

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTAAGCACATGCCTCCAGAGGTGC-3' (SEQ ID NO:426);

reverse PCR primer 5'-GTGACGTGGATGCTTGGGATGTTG-3' (SEQ ID NO:427).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA42801 sequence which had the following nucleotide sequence:

5 hybridization probe

5'-TGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCATTCTGCGTCGA-3' (SEQ ID NO:428).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO731 gene using the probe oligonucleotide and one of the PCR primers. RNA  
10 for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255). The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD;  
15 pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO731 [herein designated as UNQ395 (DNA48331-1329)] (SEQ ID NO:424) and the derived protein sequence for PRO731.

20 The entire nucleotide sequence of UNQ395 (DNA48331-1329) is shown in Figure 170 (SEQ ID NO:424). Clone UNQ395 (DNA48331-1329) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 329-331 and ending at the stop codon at nucleotide positions 3881-3883 (Figure 170). The predicted polypeptide precursor is 1184 amino acids long (Figure 171). The full-length PRO731 protein shown in Figure 171 has an estimated molecular weight of about 129,022 daltons and  
25 a pI of about 5.2. Clone UNQ395 (DNA48331-1329) was deposited with the ATCC on March 31, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO731 polypeptide suggests that portions of it possess significant identity and similarity to members of the protocadherin family, thereby indicating that  
30 PRO731 may be a novel protocadherin.

Still analyzing the amino acid sequence of SEQ ID NO:425, the putative signal peptide is at about amino acids 1-13 of SEQ ID NO:425. The transmembrane domain is at amino acids 719-739 of SEQ ID NO:425. The N-glycosylation of SEQ ID NO:425 are as follows: 415-418, 582-586, 659-662, 662-665, and 857-860. The cadherin extracellular repeated domain signatures are at about amino acids (of SEQ ID NO:425): 123-133, 232-  
35 242, 340-350, 448-458, and 553-563. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 69: Isolation of cDNA Clones Encoding Human PRO218

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA17411. Two proprietary Genentech EST sequences were employed in the consensus assembly and are shown in Figure 174 and 175. Based on the DNA17411 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that  
5 contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO218.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-AAGTGGAGCCGGAGCCTTCC-3' (SEQ ID NO:433);

reverse PCR primer 5'-TCGTTGTTTATGCAGTAGTCGG-3' (SEQ ID NO:434).

10 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA17411 sequence which had the following nucleotide sequence:

hybridization probe

5'-ATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGG-3' (SEQ ID NO:435).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was  
15 screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO218 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO218 [herein designated as UNQ192 (DNA30867-1335)] (SEQ ID NO:429) and the derived protein sequence  
20 for PRO218.

The entire nucleotide sequence of UNQ192 (DNA30867-1335) is shown in Figure 172 (SEQ ID NO:429). Clone UNQ192 (DNA30867-1335) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 150-152 and ending at the stop codon at nucleotide positions 1515-1517 (Figure 172). The predicted polypeptide precursor is 455 amino acids long (Figure 173). The full-  
25 length PRO218 protein shown in Figure 173 has an estimated molecular weight of about 52,917 daltons and a pI of about 9.5. Clone UNQ192 (DNA30867-1335) has been deposited with the ATCC on April 28, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO218 polypeptide suggests that PRO218 may  
30 be a novel transmembrane protein.

Still analyzing the amino acid sequence of SEQ ID NO:430, the putative signal peptide is at about amino acids 1 through 23 of SEQ ID NO:430. Transmembrane domains are potentially at about amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398, and 425-444 of SEQ ID NO:430. N-glycosylation sites are at about amino acids 67, 180, and 243 of SEQ ID NO:430. Eukaryotic cobalamin-binding protein is at about  
35 amino acids 151-160 of SEQ ID NO:430. The corresponding nucleotides can be routinely determined given the sequences provided herein.



EXAMPLE 70: Isolation of cDNA Clones Encoding Human PRO768

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43448. Based on the DNA43448 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO768.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GGCTGACACCGCAGTGCTCTTCAG-3' (SEQ ID NO:438);

reverse PCR primer 5'-GCTGCTGGGGACTGCAATGTAGCTG-3' (SEQ ID NO:439).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43448 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATC-3' (SEQ ID NO:440).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO768 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO768 [herein designated as UNQ406 (DNA55737-1345)] (SEQ ID NO:436) and the derived protein sequence for PRO768.

The entire nucleotide sequence of UNQ406 (DNA55737-1345) is shown in Figure 176 (SEQ ID NO:436). Clone UNQ406 (DNA55737-1345) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 20-22 and ending at the stop codon at nucleotide positions 3443-3445 (Figure 176). The predicted polypeptide precursor is 1141 amino acids long (Figure 177). The full-length PRO768 protein shown in Figure 177 has an estimated molecular weight of about 124,671 daltons and a pI of about 5.82. Clone UNQ406 (DNA55737-1345) has been deposited with the ATCC on April 6, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO768 polypeptide suggests that portions of it possess significant sequence identity and similarity with integrin 7.

Still analyzing the amino acid sequence of SEQ ID NO:437, the putative signal peptide is at about amino acids 1-33 of SEQ ID NO:437. The transmembrane domain is at amino acids 1039-1064 of SEQ ID NO:437. N-glycosylation sites are at amino acids: 86-89, 746-749, 949-952, 985-988 and 1005-1008 of SEQ ID NO:437. Integrin alpha chain protein domains are identified at about amino acids: 1064-1071, 384-409, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047 of SEQ ID NO:437. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 71: Isolation of cDNA Clones Encoding Human PRO771

A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA43330. Based on the DNA43330 sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO771.

5 A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CAGCAATATTCAGAAGCGGCAAGGG-3' (SEQ ID NO:443);

reverse PCR primer 5'-CATCATGGTCATCACCACCATCATCATC-3' (SEQ ID NO:444).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA43330 consensus sequence which had the following nucleotide sequence:

10 hybridization probe

5'-GGTTACTACAAGCCAACACAATGTCATGGCAGTGTGGACAGTGCTGG-3' (SEQ ID NO:445).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO771 gene using the probe oligonucleotide and one of the PCR primers. RNA  
15 for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB28).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO771 [herein designated as UNQ409 (DNA49829-1346)] (SEQ ID NO:441) and the derived protein sequence for PRO771.

The entire nucleotide sequence of UNQ409 (DNA49829-1346) is shown in Figure 178 (SEQ ID  
20 NO:441). Clone UNQ409 (DNA49829-1346) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1442-1444 (Figure 178). The predicted polypeptide precursor is 436 amino acids long (Figure 179). The full-length PRO771 protein shown in Figure 179 has an estimated molecular weight of about 49,429 daltons and a pI of about 4.8. Clone UNQ409 (DNA49829-1346) has been deposited with the ATCC on April 7, 1998.  
25 Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO771 polypeptide suggests that portions of it possess significant homology to the testican protein, thereby indicating that PRO771 may be a novel testican homologue.

30 Still analyzing the amino acid sequence of SEQ ID NO:442, the putative signal peptide, leucine zipper pattern, N-myristoylation sites, and thyroglobulin type-1 repeats are also shown in Figure 179. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 72: Isolation of cDNA Clones Encoding Human PRO733

35 A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA45600. Based on the DNA45600 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained

the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO733.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-CCCAGCAGGGATGGGCGACAAGA-3' (SEQ ID NO:448);

reverse PCR primer 5'-GTCTTCCAGTTTCATATCCAATA-3' (SEQ ID NO:449).

- 5 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA45600 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAGAAGGAGCACGGGGAAGGGCAGCCAGATCTTGTCGCCCCAT-3' (SEQ ID NO:450).

- 10 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO733 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human bone marrow tissue (LIB255).

- 15 DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO733 [herein designated as UNQ411 (DNA52196-1348)] (SEQ ID NO:446) and the derived protein sequence for PRO733.

- 20 The entire nucleotide sequence of UNQ411 (DNA52196-1348) is shown in Figure 180 (SEQ ID NO:446). Clone UNQ411 (DNA52196-1348) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 793-795 (Figure 180). The predicted polypeptide precursor is 229 amino acids long (Figure 181). The full-length PRO733 protein shown in Figure 181 has an estimated molecular weight of about 26,017 daltons and a pI of about 4.73. Clone UNQ411 (DNA52196-1348) has been deposited with the ATCC on April 7, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

- 25 Analysis of the amino acid sequence of the full-length PRO733 polypeptide suggests that portions of it possess significant sequence identity and similarity to the T1/ST2 receptor binding protein precursor and therefore may have a similar function in cell signaling. If it is a cytokine, it may be useful in the treatment of inflammation and cancer.

- 30 Still analyzing the amino acid sequence of SEQ ID NO:447, the putative signal peptide, transmembrane domain, N-myristoylation site, and tyrosine kinase site are also shown in Figure 181. The corresponding nucleotides can be routinely determined given the sequences provided herein.

#### EXAMPLE 73: Isolation of cDNA Clones Encoding Human PRO162

- 35 An expressed sequence tag (EST) DNA database (Merck/Washington University) was searched and an EST AA397543 was identified which showed homology to human pancreatitis-associated protein. The EST AA397543 clone was purchased and its insert obtained and sequenced and the sequence obtained is shown in Figure 182 (SEQ ID NO:451).

The entire nucleotide sequence of PRO162 is shown in Figure 182 (SEQ ID NO:451). DNA sequencing of the clone gave the full-length DNA sequence for PRO162 [herein designated as UNQ429 (DNA56965-1356)] (SEQ ID NO:451) and the derived protein sequence for PRO162. Clone UNQ429 (DNA56965-1356) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 86-88 and ending at the stop codon at nucleotide positions 611-613 (Figure 182). The predicted polypeptide precursor is 175 amino acids long (Figure 183). The full-length PRO162 protein shown in Figure 183 has an estimated molecular weight of about 19,330 daltons and a pI of about 7.25. Clone UNQ429 (DNA56965-1356) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO162 polypeptide suggests that portions of it possess significant homology to the human pancreatitis-associated protein, thereby indicating that PRO162 may be a novel pancreatitis-associated protein.

Still analyzing the amino acid sequence of SEQ ID NO:452, the putative signal peptide is at about amino acids 1-26 of SEQ ID NO:452. A C-type lectin domain signature is at about amino acids 146-171 of SEQ ID NO:452. The corresponding nucleotides can be routinely determined given the sequences provided herein.

#### EXAMPLE 74: Isolation of cDNA Clones Encoding Human PRO788

A consensus DNA sequence (designated herein as DNA49308) was assembled relative to other EST sequences using phrap as described in Example 1 above. Based upon an observed homology between the DNA49308 consensus sequence and the Incyte EST clone no. 2777282, the Incyte EST clone no. 2777282 was purchased and its insert obtained and sequenced, which gave the full-length DNA sequence for PRO788 [herein designated as UNQ430 (DNA56405-1357)] (SEQ ID NO:453) and the derived protein sequence for PRO788.

Clone UNQ430 (DNA56405-1357) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 84-86 and ending at the stop codon at nucleotide positions 459-461 (Figure 184). The predicted polypeptide precursor is 125 amino acids long (Figure 185). The full-length PRO788 protein shown in Figure 185 has an estimated molecular weight of about 13,115 daltons and a pI of about 5.90. Clone UNQ430 (DNA56405-1357) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing Figure 185, a signal peptide is shown at about amino acids 1-17 of SEQ ID NO:454. An N-glycosylation site is at about amino acids 46-49 of SEQ ID NO:454.

#### EXAMPLE 75: Isolation of cDNA Clones Encoding Human PRO1008

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated as DNA49804. An EST proprietary to Genentech was employed in the consensus assembly and is herein designated as DNA16508 (Figure 188; SEQ ID NO:457). Based upon an observed homology between the DNA49804 sequence and Merck EST clone no. AA143670, the Merck EST clone no. AA143670 was purchased and its insert obtained and sequenced. That



sequence is shown herein in Figure 186 (SEQ ID NO:455).

Sequencing gave the full length sequence for PRO1008 [herein designated as UNQ492 (DNA57530-1375)] (SEQ ID NO:455) and the derived protein sequence for PRO1008 were identified.

The entire nucleotide sequence of UNQ492 (DNA57530-1375) is shown in Figure 186 (SEQ ID NO:455). Clone UNQ492 (DNA57530-1375) contains a single open reading frame with an apparent  
5 translational initiation site at nucleotide positions 138-140 and ending at the stop codon at nucleotide positions 936-938 (Figure 186). The predicted polypeptide precursor is 266 amino acids long (Figure 187). The full-length PRO1008 protein shown in Figure 187 has an estimated molecular weight of about 28,672 daltons and a pI of about 8.85. Clone UNQ492 (DNA57530-1375) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the  
10 sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1008 polypeptide suggests that portions of it possess significant sequence identity and/or similarity with mdkk-1, thereby indicating that PRO1008 may be a novel member of this family and have head inducing activity.

Still analyzing the amino acid sequence of SEQ ID NO:456, the putative signal peptide is at about amino  
15 acids 1-23 of SEQ ID NO:456. The N-glycosylation site is at about amino acids 256-259 of SEQ ID NO:456, and the fungal zn-(2)-cys(6) binuclear cluster domain is at about amino acids 110-126 of SEQ ID NO:456. The corresponding nucleotides can of all the amino acids can be routinely determined given the sequences provided herein.

#### 20 EXAMPLE 76: Isolation of cDNA Clones Encoding Human PRO1012

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence is herein designated DNA49313. Based on the DNA49313 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for  
25 PRO1012.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-ACTCCCCAGGCTGTTCACTGCC-3' (SEQ ID NO:460);

reverse PCR primer 5'-GATCAGCCAGCCAATACCAGCAGC-3' (SEQ ID NO:461).

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA49313 consensus  
30 sequence which had the following nucleotide sequence:

hybridization probe

5'-GTGGTGATGATAGAATGCTTTGCCGAATGAAAGGAGTCAACAGCTATCCC-3' (SEQ ID NO:462).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to  
35 isolate clones encoding the PRO1012 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1012 [herein designated as UNQ495 (DNA56439-1376)] (SEQ ID NO:458) and the derived protein sequence for PRO1012.

The entire nucleotide sequence of UNQ495 (DNA56439-1376) is shown in Figure 189 (SEQ ID NO:458). Clone UNQ495 (DNA56439-1376) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 404-406 and ending at the stop codon at nucleotide positions 2645-2647 (Figure 189). The predicted polypeptide precursor is 747 amino acids long (Figure 190). The full-length PRO1012 protein shown in Figure 190 has an estimated molecular weight of about 86,127 daltons and a pI of about 7.46. Clone UNQ495 (DNA56439-1376) has been deposited with ATCC on May 14, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1012 polypeptide suggests that portions of it possess sequence identity with disulfide isomerase thereby indicating that PRO1012 may be a novel disulfide isomerase related protein.

Still analyzing the amino acid sequence of SEQ ID NO:459, the cytochrome C family heme-binding site signature is at about amino acids 158-163 of SEQ ID NO:459. The Nt-DNAJ domain signature is at about amino acids 77-96 of SEQ ID NO:459. An N-glycosylation site is at about amino acids 484-487 of SEQ ID NO:459. The ER targeting sequence is at about amino acids 744-747 of SEQ ID NO:459. It is understood that the polypeptide and nucleic acids disclosed can be routinely formed with or without, these portions as desired, in alternative embodiments. For example, it may be desirable to produce PRO1012 without the ER targeting sequence. The corresponding nucleotides can be routinely determined given the sequences provided herein.

#### EXAMPLE 77: Isolation of cDNA Clones Encoding Human PRO1014

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49811. Based upon an observed homology between the DNA49811 sequence and Incyte EST clone no. 2612207, Incyte EST clone no. 2612207 was purchased and its insert was obtained and sequenced, wherein the sequence obtained is shown in Figure 191 (SEQ ID NO:463).

DNA sequencing gave the full-length DNA sequence for PRO1014 [herein designated as UNQ497 (DNA56409-1377)] (SEQ ID NO:463) and the derived protein sequence for PRO1014.

The entire nucleotide sequence of UNQ497 (DNA56409-1377) is shown in Figure 191 (SEQ ID NO:463). Clone UNQ497 (DNA56409-1377) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 66-68 and ending at the stop codon at nucleotide positions 966-968 (Figure 191). The predicted polypeptide precursor is 300 amino acids long (Figure 192). The full-length PRO1014 protein shown in Figure 192 has an estimated molecular weight of about 33,655 daltons and a pI of about 9.31. Clone UNQ497 (DNA56409-1377) has been deposited with the ATCC on May 20, 1998. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1014 polypeptide suggests that portions of it possess sequence identity with reductase, thereby indicating that PRO1014 may be a novel member of the reductase family.

Still analyzing the amino acid sequence of SEQ ID NO:464, the putative signal peptide is at about amino acids 1-19 of SEQ ID NO:464. The cAMP and cGMP dependent protein kinase phosphorylation sites are at about amino acids 30-33 and 58-61 of SEQ ID NO:464. Short chain alcohol dehydrogenase family proteins are at about amino acids 165-202, 37-49, 112-122 and 210-219 of SEQ ID NO:464. The corresponding nucleotides of these domains and any other amino acids provided herein can be routinely determined given the sequences provided herein.

#### 10 EXAMPLE 78: Isolation of cDNA Clones Encoding Human PRO1017

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus DNA sequence is herein designated DNA53235. Based upon an observed homology between the DNA53235 consensus sequence and the Merck EST clone no. AA243086, the Merck EST clone no. AA243086 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 193 (SEQ ID NO:465). DNA sequencing gave the full-length DNA sequence for PRO1017 [herein designated as UNQ500 (DNA56112-1379)] (SEQ ID NO:465) and the derived protein sequence for PRO1017.

The entire nucleotide sequence of UNQ500 (DNA56112-1379) is shown in Figure 193 (SEQ ID NO:465). Clone UNQ500 (DNA56112-1379) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 128-130 and ending at the stop codon at nucleotide positions 1370-1372 (Figure 193). The predicted polypeptide precursor is 414 amino acids long (Figure 194). The full-length PRO1017 protein shown in Figure 194 has an estimated molecular weight of about 48,414 daltons and a pI of about 9.54. Clone UNQ500 (DNA56112-1379) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Analysis of the amino acid sequence of the full-length PRO1017 polypeptide suggests that portions of it possess sequence identity with HNK-1 sulfotransferase, thereby indicating that PRO1017 may be a novel sulfotransferase.

Still analyzing the amino acid sequence of SEQ ID NO:466, the putative signal peptide is at about amino acids 1-31 of SEQ ID NO:466. N-glycosylation sites are at about amino acids 134-137, 209-212, 280-283 and 370-273 of SEQ ID NO:466. The TNFR/NGFR family cystein-rich region protein is at about amino acids 329-332 of SEQ ID NO:466. The corresponding nucleotides can be routinely determined given the sequences provided herein. The protein can be secreted.

#### 35 EXAMPLE 79: Isolation of cDNA Clones Encoding Human PRO474

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence obtained is herein designated DNA49818. Based upon

an observed homology between the DNA49818 consensus sequence and the Merck EST clone no. H77889, the Merck EST clone no. H77889 was purchased and its insert obtained and sequenced, wherein the sequence obtained is herein shown in Figure 195 (SEQ ID NO:467). DNA sequencing gave the full-length DNA sequence for PRO474 [herein designated as UNQ502 (DNA56045-1380)] (SEQ ID NO:467) and the derived protein sequence for PRO474.

5       The entire nucleotide sequence of UNQ502 (DNA56045-1380) is shown in Figure 195 (SEQ ID NO:467). Clone UNQ502 (DNA56045-1380) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 106-108 and ending at the stop codon at nucleotide positions 916-918 (Figure 195). The predicted polypeptide precursor is 270 amino acids long (Figure 196). The full-length PRO474 protein shown in Figure 196 has an estimated molecular weight of about 28,317 daltons and a  
10       pl of about 6.0. Clone UNQ502 (DNA56045-1380) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

      Still analyzing the amino acid sequence of SEQ ID NO:468, an N-glycosylation site is at about amino acids 138-141 of SEQ ID NO:468. Short-chain alcohol dehydrogenase family proteins are at about amino acids  
15       10-22, 81-91, 134-171 and 176-185 of SEQ ID NO:468. The corresponding nucleotides can be routinely determined given the sequences provided herein.

#### EXAMPLE 80: Isolation of cDNA Clones Encoding Human PRO1031

      An initial consensus DNA sequence was assembled relative to other EST sequences using phrap as  
20       described in Example 1 above, wherein the consensus sequence obtained is herein designated as DNA47332. Based upon an observed homology between the DNA47332 sequence and the Merck EST clone no. W74558, Merck EST clone no. W74558 was purchased and its insert obtained and sequenced, wherein the sequence obtained is shown in Figure 197 (SEQ ID NO:469). DNA sequencing gave the full-length DNA sequence for PRO1031 [herein designated as UNQ516 (DNA59294-1381)] (SEQ ID NO:469) and the derived protein  
25       sequence for PRO1031.

      The entire nucleotide sequence of UNQ516 (DNA59294-1381) is shown in Figure 197 (SEQ ID NO:469). Clone UNQ516 (DNA59294-1381) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 42-44 and ending at the stop codon at nucleotide positions 582-584 (Figure 197). The predicted polypeptide precursor is 180 amino acids long (Figure 198). The full-length  
30       PRO1031 protein shown in Figure 198 has an estimated molecular weight of about 20,437 daltons and a pl of about 9.58. Clone UNQ516 (DNA59294-1381) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

      Analysis of the amino acid sequence of the full-length PRO1031 polypeptide suggests that it is a novel  
35       cytokine.

      Still analyzing the amino acid sequence of SEQ ID NO:470, the putative signal peptide is at about amino acids 1-20 of SEQ ID NO:470. An N-glycosylation site is at about amino acids 75-78 of SEQ ID NO:470.



A region having sequence identity with IL-17 is at about amino acids 96-180. The corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 81: Isolation of cDNA Clones Encoding Human PRO938

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein that consensus sequence is herein designated DNA49798. Based on the DNA49798 DNA consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO938.

A pair of PCR primers (forward and reverse) were synthesized:

forward PCR primer 5'-GTCCAGCCCATGACCGCCTCCAAC-3' (SEQ ID NO:473)  
reverse PCR primer 5'-CTCTCCTCATCCACACCAGCAGCC-3' (SEQ ID NO:474)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA49798 sequence which had the following nucleotide sequence:

hybridization probe  
5'-GTGGATGCTGAAATTTTACGCCCCATGGTGTCCATCCTGCCAGC-3' (SEQ ID NO:475)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO938 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO938 [herein designated as UNQ475 (DNA56433-1406)] (SEQ ID NO:471) and the derived protein sequence for PRO938.

The entire nucleotide sequence of UNQ475 (DNA56433-1406) is shown in Figure 199 (SEQ ID NO:471). Clone UNQ475 (DNA56433-1406) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 and ending at the stop codon at nucleotide positions 1181-1183 (Figure 199). The predicted polypeptide precursor is 349 amino acids long (Figure 200). The full-length PRO938 protein shown in Figure 200 has an estimated molecular weight of about 38,952 daltons and a pI of about 4.34. Analysis of the full-length PRO938 sequence shown in Figure 200 (SEQ ID NO:472) evidences the presence of the following features: a signal peptide from amino 1 to about amino acid 22, a transmembrane domain from about amino acid 191 to about amino acid 211, a potential N-glycosylation site from about amino acid 46 to about amino acid 49, a region homologous to disulfide isomerase from about amino acid 56 to about amino acid 72, and a region having sequence identity with flavodoxin proteins from about amino acid 173 to about amino acid 187.

Clone UNQ475 (DNA56433-1406) has been deposited with ATCC on May 12, 1998, and is assigned ATCC Accession No. 209857.

Analysis of the amino acid sequence of the full-length PRO938 polypeptide suggests that it possesses significant sequence similarity to protein disulfide isomerase, thereby indicating that PRO938 may be a novel

protein disulfide isomerase. An analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO938 amino acid sequence and the following Dayhoff sequences, P\_W03626, P\_W03627, P\_R70491, GARP\_PLAFF, XLU85970\_1, ACADISPROA\_1, IE68\_HSVSA, KSU52064\_1, U93872\_83, P\_R97866.

5 EXAMPLE 82: Isolation of cDNA Clones Encoding Human PRO1082

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above, wherein the consensus sequence is herein designated DNA38097. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1082.

10 A set of PCR primers (two forward and one reverse) were synthesized:

forward primer 1 5'-GTCCACAGACAGTCATCTCAGGAGCAG-3' (SEQ ID NO:478);

forward primer 2 5'-ACAAGTGTCTTCCCAACCTG-3' (SEQ ID NO:479);

reverse primer 1 5'-ATCCTCCCAGAGCCATGGTACCTC-3' (SEQ ID NO:480).

15 Additionally, a synthetic oligonucleotide hybridization probe was constructed from the DNA38097 consensus sequence which had the following nucleotide sequence:

hybridization probe

5'-CCAAGGATAGCTGTTGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCT-3' (SEQ ID NO:481).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primers identified above. A positive library was then used to  
20 isolate clones encoding the PRO1082 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1082 [herein designated as UNQ539 (DNA53912-1457)] (SEQ ID NO:476) and the derived protein sequence for PRO1082.

25 The entire nucleotide sequence of UNQ539 (DNA53912-1457) is shown in Figure 201 (SEQ ID NO:476). Clone UNQ539 (DNA53912-1457) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 160-162 and ending at the stop codon at nucleotide positions 763-765 (Figure 201). The predicted polypeptide precursor is 201 amino acids long (Figure 202). The full-length PRO1082 protein shown in Figure 202 has an estimated molecular weight of about 22,563 daltons and  
30 a pI of about 4.87. Clone UNQ539 (DNA53912-1457) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

35 Still analyzing the amino acid sequence of SEQ ID NO:477, the transmembrane domain is at about amino acids 45-65 of SEQ ID NO:477. A cAMP- and cGMP-dependent protein kinase phosphorylation site is at about amino acids 197-200 of SEQ ID NO:477. N-myristoylation sites are at about amino acids 35-40 and 151-156 of SEQ ID NO:477. The regions which share sequence identity with the LDL receptor are at about amino acids 34-67 and 70-200 of SEQ ID NO:477. The corresponding nucleotides of these amino acid regions

and others can be routinely determined given the sequences provided herein.

EXAMPLE 83: Isolation of cDNA Clones Encoding Human PRO1083

A cDNA sequence was identified using the amylase screening technique described in Example 2 above, wherein that cDNA sequence is designated herein as DNA24256 (Figure 205; SEQ ID NO:484). That cDNA  
5 sequence was then compared and aligned with other known EST sequences as described in Example 1 above to obtain a consensus DNA sequence which is designated herein as DNA43422. Based on the DNA 43422 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO1083.

10 A pair of PCR primers (forward and reverse) were synthesized:  
forward PCR primer 5'-GGCATTGGAGCAGTGCTGGGTG-3' (SEQ ID NO:485);  
reverse PCR primer 5'-TGGAGGCCTAGATGCGGCTGGACG-3' (SEQ ID NO:486).

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to  
15 isolate clones encoding the PRO1083 gene using the reverse PCR primer. RNA for construction of the cDNA libraries was isolated from human fetal kidney tissue (LIB227).

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO1083 [herein designated as UNQ540 (DNA50921-1458)] (SEQ ID NO:482) and the derived protein sequence for PRO1083.

20 The entire nucleotide sequence of UNQ540 (DNA50921-1458) is shown in Figure 203 (SEQ ID NO:482). Clone UNQ540 (DNA50921-1458) contains a single open reading frame with an apparent translational initiation site at nucleotide positions 214-216 and ending at the stop codon at nucleotide positions 2293-2295 (Figure 203). The predicted polypeptide precursor is 693 amino acids long (Figure 204). The full-length PRO1083 protein shown in Figure 204 has an estimated molecular weight of about 77,738 daltons and  
25 a pI of about 8.87. Clone UNQ540 (DNA50921-1458) has been deposited with the ATCC. Regarding the sequence, it is understood that the deposited clone contains the correct sequence, and the sequences provided herein are based on known sequencing techniques.

Still analyzing the amino acid sequence of SEQ ID NO:483, the putative signal peptide is at about amino acids 1-25 of SEQ ID NO:483. The transmembrane domains are at about amino acids 382-398, 402-420, 445-  
30 468, 473-491, 519-537, 568-590 and 634-657 of SEQ ID NO:483. A microbodies C-terminal targeting signal is at about amino acids 691-693 of SEQ ID NO:483. cAMP- and cGMP-dependent protein kinase phosphorylation sites are at about amino acids 198-201 and 370-373 of SEQ ID NO:483. N-glycosylation sites are at about amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-227 and 341-344 of SEQ ID NO:483. A G-protein coupled receptor family domain is at about amino acids 475-504 of SEQ ID NO:483. The  
35 corresponding nucleotides can be routinely determined given the sequences provided herein.

EXAMPLE 84: Isolation of cDNA Clones Encoding Human PRO200

Probes based on an expressed sequence tag (EST) identified from the Incyte Pharmaceuticals database due to homology with VEGF were used to screen a cDNA library derived from the human glioma cell line G61. In particular, Incyte Clone "INC1302516" was used to generate the following four probes:

(SEQ ID NO:489) ACTTCTCAGTGTCCATAAGGG;

5 (SEQ ID NO:490) GAACTAAAGAGAACCGATAACCATTTTCTGGCCAGGTTGTC;

(SEQ ID NO:491) CACCACAGCGTTTAACCAGG; and

(SEQ ID NO:492) ACAACAGGCACAGTTCCCAC.

Nine positives were identified and characterized. Three clones contained the full coding region and were identical in sequence. Partial clones were also identified from a fetal lung library and were identical with  
10 the glioma-derived sequence with the exception of one nucleotide change which did not alter the encoded amino acid.

EXAMPLE 85: Expression Constructs for PRO200

For mammalian protein expression, the entire open reading frame (ORF) was cloned into a CMV-based  
15 expression vector. An epitope-tag (FLAG, Kodak) and Histidine-tag (His8) were inserted between the ORF and stop codon. VEGF-E-His8 and VEGF-E-FLAG were transfected into human embryonic kidney 293 cells by SuperFect (Qiagen) and pulse-labeled for 3 hours with [<sup>35</sup>S]methionine and [<sup>35</sup>C]cysteine. Both epitope-tagged proteins co-migrate when 20 microliters of 15-fold concentrated serum-free conditioned medium were electrophoresed on a polyacrylamide gel (Novex) in sodium dodecyl sulfate sample buffer (SDS-PAGE). The  
20 VEGF-E-IgG expression plasmid was constructed by cloning the ORF in front of the human Fc (IgG) sequence.

The VEGF-E-IgG plasmid was co-transfected with Baculogold Baculovirus DNA (Pharmingen) using Lipofectin (GibcoBRL) into 10<sup>5</sup> Sf9 cells grown in Hink's TNM-FH medium (JRH Biosciences) supplemented with 10% fetal bovine serum. Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9 cells at an approximate multiplicity of infection  
25 (MOI) of 10. Cells were incubated for 3 days, then supernatant harvested, and expression of the recombinant plasmid determined by binding of 1 ml of supernatant to 30 µl of Protein-A Sepharose CL-4B beads (Pharmacia) followed by subsequent SDS-PAGE analysis. The first amplification supernatant was used to infect a 500 ml spinner culture of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were treated as above, except harvested supernatant was sterile filtered. Specific protein was purified  
30 by binding to Protein-A Sepharose 4 Fast Flow (Pharmacia) column.

EXAMPLE 86: Northern Blot Analyses for PRO200

Blots of human poly(A)+ RNA from multiple adult and fetal tissues and tumor cell lines were obtained from Clontech (Palo Alto, CA). Hybridization was carried out using <sup>32</sup>P-labeled probes containing the entire  
35 coding region and washed in 0.1 x SSC, 0.1% SDS at 63°C.

VEGF-E mRNA was detectable in fetal lung, kidney, brain, liver and adult heart, placenta, liver, skeletal muscle, kidney, and pancreas. VEGF-E mRNA was also found in A549 lung adenocarcinoma and HeLa



cervical adenocarcinoma cell lines.

EXAMPLE 87: In Situ Hybridization of Human Fetal Tissue Sections for PRO200

Formalin-fixed, paraffin-embedded human fetal brain, liver, lower limb, small intestine, thyroid, lymph node, thymus, stomach, trachea, skin, spleen, spinal cord, adrenal, placenta, cord, and adult liver, pancreas, lung, spleen, lymph node, adrenal, heart, aorta, and skin were sectioned, deparaffinized, deproteinized in proteinase K (20  $\mu$ g/ml) for 15 minutes at 37°C, and further processed for in situ hybridization as described by Lu LH and Gillett NA (Cell Vision 1:169-176, 1994). A [ $\alpha$ -<sup>33</sup>-P]UTP-labeled antisense riboprobe was generated from a PCR product of 980 bp (primers GGCGGAATCCAACCTGAGTAG and GCGGCTATCCTCCTGTGCTC, SEQ ID NOS: 493 and 494, respectively). The slides were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

VEGF-E mRNA expression included localization at the growth plate region and embracing fetal myocytes.

EXAMPLE 88: Myocyte Hypertrophy Assay for PRO200

Myocytes from neonatal Harlan Sprague Dawley rat heart ventricle (23 days gestation) were plated in duplicate at 75000 cells/ml in a 96-well plate. Cells were treated for 48h with 2000, 200, 20, or 2 ng/ml VEGF-E-IgG. Myocytes were stained with crystal violet to visualize morphology and scored on a scale of 3 to 7, 3 being nonstimulated and 7 being full-blown hypertrophy.

2000 ng/ml and 200 ng/ml VEGF-E caused hypertrophy, scored as a 5.

EXAMPLE 89: Cell Proliferation Assay for PRO200

Mouse embryonic fibroblast C3H10T1/2 cells (ATCC) were grown in 50:50 Ham's F-12: low glucose DMEM medium containing 10% fetal calf serum (FCS). Cells were plated in duplicate in a 24-well plate at 1000, 2000, and 4000 cells/well. After 48 hours, cells were switched to medium containing 2% FCS and were incubated for 72 hours with 200, 800, or 2000 ng/ml VEGF-E or no growth factor added.

Approximately 1.5 fold greater number of cells were measured in the presence of 200 ng/ml VEGF-E as in its absence, at all three cell densities.

EXAMPLE 90: Endothelial Cell Survival Assay for PRO200

Human umbilical vein endothelial cells (HUVEC, Cell Systems) were maintained in Complete Media (Cell Systems) and plated in triplicate in serum-free medium (Basic Media from Cell Systems containing 0.1% BSA) at 20,000 cells/well of a 48-well plate. Cells were incubated for 5 days with 200 or 400 ng/ml VEGF-E-IgG, 100 ng/ml VEGF, 20 ng/ml basic FGF, or no addition.

Survival was 2-3 times greater with VEGF-E as compared to lack of growth factor addition. VEGF and basic FGF were included as positive controls.

EXAMPLE 91: Isolation of cDNA Clones Encoding Human PRO285

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#2243209) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

5 TAAAGACCCAGCTGTGACCG (SEQ ID NO:499)

ATCCATGAGCCTCTGATGGG (SEQ ID NO: 500), and

a probe:

ATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTC (SEQ ID NO: 501)

were synthesized.

10 mRNA for construction of the cDNA libraries was isolated from human placenta tissue. The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA (Fast Track 2). The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into the cloning vector pCR2.1 (Invitrogen, Inc.)  
15 using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). The double stranded cDNA was sized to greater than 1000 bp and the cDNA was cloned into BamHI/NotI cleaved vector. pCR2.1 is a commercially available plasmid, designed for easy cloning of PCR fragments, that carries AmpR and KanR genes for selection, and LacZ gene for blue-white selection.

20 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO285 gene using the probe oligonucleotide and one of the PCR primers.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA40021-1154 (encoding PRO285) is shown in Figure 208 (SEQ ID NO:495). Clone DNA40021-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 61-63 (Figure 208). The  
25 predicted polypeptide precursor is 1049 amino acids long, including a putative signal peptide at amino acid positions 1-29, a putative transmembrane domain between amino acid positions 837-860, and a leucine zipper pattern at amino acid positions 132-153 and 704-725, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA40021-1154 has been deposited with ATCC (designation: DNA40021-1154) and is assigned ATCC deposit no.209389.

30 Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

35

EXAMPLE 92: Isolation of cDNA Clones Encoding Human PRO286

A proprietary expressed sequence tag (EST) DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) was searched and an EST (#694401) was identified which showed homology to the *Drosophila* Toll protein.

Based on the EST, a pair of PCR primers (forward and reverse):

5 GCCGAGACAAAACGTTCTCC (SEQ ID NO:502)  
 CATCCATGTTCTCATCCATTAGCC (SEQ ID NO: 503), and

a probe:

TCGACAACCTCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATT (SEQ ID NO: 504)

were synthesized.

10 mRNA for construction of the cDNA libraries was isolated from human placenta tissue. This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased  
 15 adaptors, cleaved with NotI, sized to greater than 1000 bp appropriately by gel electrophoresis, and cloned in a defined orientation into XhoI/NotI-cleaved pRK5D.

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO286 gene using the probe oligonucleotide identified above and one of the PCR  
 20 primers.

A cDNA clone was sequenced in entirety. The entire nucleotide sequence of DNA42663-1154 (encoding PRO286) is shown in Figure 210 (SEQ ID NO:497). Clone DNA42663-1154 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 57-59 (Figure 211). The predicted polypeptide precursor is 1041 amino acids long, including a putative signal peptide at amino acid  
 25 positions 1-26, a potential transmembrane domain at amino acid positions 826-848, and leucine zipper patterns at amino acids 130-151, 206-227, 662-684, 669-690 and 693-614, respectively. It is noted that the indicated boundaries are approximate, and the actual limits of the indicated regions might differ by a few amino acids. Clone DNA42663-1154 has been deposited with ATCC (designation: DNA42663-1154) and is assigned ATCC deposit no. 209386.

30 Based on a BLAST and FastA sequence alignment analysis (using the ALIGN computer program) of the full-length sequence of PRO286, it is a human analogue of the *Drosophila* Toll protein, and is homologous to the following human Toll proteins: Toll1 (DNAX# HSU88540-1, which is identical with the random sequenced full-length cDNA #HUMRSC786-1); Toll2 (DNAX# HSU88878-1); Toll3 (DNAX# HSU88879-1); and Toll4 (DNAX# HSU88880-1).

35

EXAMPLE 93: NF- $\kappa$ B Assay for PRO285 and PRO286

As the Toll proteins signal through the NF- $\kappa$ B pathway, their biological activity can be tested in an NF- $\kappa$ B assay. In this assay Jurkat cells are transiently transfected using Lipofectamine reagent (Gibco BRL) according to the manufacturer's instructions. 1 $\mu$ g pB2XLuc plasmid, containing NF- $\kappa$ B-driven luciferase gene, is cotransfected with 1 $\mu$ g pSR $\alpha$ N expression vector with or without the insert encoding PRO285 or PRO286.

5 For a positive control, cells are treated with PMA (phorbol myristyl acetate; 20 ng/ml) and PHA (phytohaemagglutinin, 2 $\mu$ g/ml) for three to four hours. Cells are lysed 2 or 3 days later for measurement of luciferase activity using reagents from Promega.

EXAMPLE 94: Isolation of cDNA Clones Encoding Human PRO213-1, PRO1330 and PRO1449

10 A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA28735. Based on the DNA28735 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO213-1, PRO1330 and/or PRO1449. A pair of PCR primers (forward and reverse) were synthesized:

15 forward PCR primer 5'-TGGAGCAGCAATATGCCAGCC-3' (SEQ ID NO:511)

reverse PCR primer 5'-TTTTCCAATCCTGTCGGGTTGG-3' (SEQ ID NO:512)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA28735 sequence which had the following nucleotide sequence:

hybridization probe

20 5'-GGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGG-3' (SEQ ID NO:513)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO213-1, PRO1330 and/or PRO1449 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal lung tissue.

25 DNA sequencing of the clones isolated as described above gave the full-length DNA sequence encoding PRO213-1, PRO1330 and/or PRO1449 [DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively].

The entire nucleotide sequences corresponding to DNA30943-1-1163-1 (SEQ ID NO:505), DNA64907-1163-1 (SEQ ID NO:507) and DNA64908-1163-1 (SEQ ID NO:509), respectively. DNA30943-1163, 30 DNA64907-1163-1 and DNA64908-1163-1 contain a single open reading frame with an apparent translational initiation site at nucleotide positions 336-338, 488-490 and 326-328, respectively, and ending at the stop codon at nucleotide positions 1221-1223, 1307-1309 and 1145-1147, respectively (Figures 212, 214 and 216). The predicted polypeptide precursor is 295, 273 and 273 amino acids long, respectively (Figures 213, 215 and 217). DNA30943-1-1163-1, DNA64907-1163-1 and DNA64908-1163-1 have been deposited with ATCC and are 35 assigned ATCC deposit no. 209791, 203242 and 203243, respectively.

Analysis of the amino acid sequence of the full-length PRO213-1 polypeptide suggests that a portion of it possess significant homology to the human growth arrest-specific gene 6 protein. More specifically, an



analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced significant homology between the PRO213 amino acid sequence and the following Dayhoff sequences, HSMHC3W5A\_6 and B48089.

Additional analysis of the amino acid sequence of the full-length PRO1330 and PRO1449 polypeptide indicates significant identity with notch4. More specifically, an analysis of the Dayhoff database (version 35.130 SwissProt 35) evidenced significant identity between PRO1330 and the following Dayhoff sequences, D86566\_1  
5 and NEL\_HUMAN.

EXAMPLE 95: Isolation of cDNA Clones Encoding Human PRO298

A cDNA isolated in the amylase screen described in Example 2 above is herein designated DNA26832 (Figure 220; SEQ ID NO:516). The sequence of DNA26832 was then used to search expressed sequence tag (EST) databases. The EST databases included public EST databases (e.g., GenBank) and a proprietary EST database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or BLAST2 (Altschul et al., Methods in Enzymology 266: 469-480 [1996]). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington,  
15 Seattle, Washington; <http://bozeman.mbt.washington.edu/phrap.docs/phrap.html>).

A consensus DNA sequence was assembled relative to other EST sequences using phrap. A consensus sequence was determined, which was then extended using repeated cycles of BLAST and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above. The extended assembly sequence was designated DNA35861. Based on the DNA35861 consensus sequence, oligonucleotides  
20 were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence of PRO298. Forward and reverse primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequence is typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries  
25 for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel et al., Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

PCR primers (forward and reverse) and a hybridization probe were synthesized:

forward PCR primer 1 CAACGTGATTTC AAAGCTGGGCTC (SEQ ID NO:517)  
30 forward PCR primer 2 GCCTCGTATCAAGAATTTC (SEQ ID NO:518)  
forward PCR primer 3 AGTGGAAGTCGACCTCCC (SEQ ID NO:519)  
reverse PCR primer 1 CTCACCTGAAATCTCTCATAGCCC (SEQ ID NO:520)  
hybridization probe 1 CGCAAAACCCATTTTGGGAGCAGGAATTC CAATCATGTCTGTGATGGTGG  
(SEQ ID NO:521)

35 In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO298 gene using the probe oligonucleotide and one of the PCR primers.

RNA for construction of the cDNA libraries was isolated from human fetal lung tissue (LIB25). The cDNA libraries used to isolated the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for PRO298 (herein designated UNQ261 [DNA39975-1210]) (SEQ ID NO:514), and the derived protein sequence for PRO298 (SEQ ID NO:515).

The entire nucleotide sequence of UNQ261 (DNA39975-1210) is shown in Figure 218 (SEQ ID NO:514). Clone DNA39975-1210 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 375-377. The predicted polypeptide precursor is 364 amino acids long. The protein contains four putative transmembrane domains between amino acid positions 36-55 (type II TM), 65-84, 188-208, and 229-245, respectively. A putative N-linked glycosylation site starts at amino acid position 253. In addition, the following features have been identified in the protein sequence: cAMP- and cGMP-dependent protein kinase phosphorylation site, starting at position 8; N-myristoylation sites starting a position 173 and 262, respectively; and a ZP domain between amino acid positions 45-60. Clone DNA39975-1210 has been deposited with ATCC (April 21, 1998) and is assigned ATCC deposit no.209783.

#### 20 EXAMPLE 96: Isolation of cDNA Clones Encoding Human PRO337

A cDNA sequence identified in the amylase screen described in Example 2 above is herein designated DNA42301 (Figure 223, SEQ ID NO:524). The DNA42301 sequence was then compared to other EST sequences using phrap as described in Example 1 above and a consensus sequence designated herein as DNA28761 was identified. Based on this consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence. In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO337 gene using the probe oligonucleotide and one of the PCR primers. RNA for construction of the cDNA libraries was isolated from human fetal brain.

A cDNA clone was sequenced in its entirety. The full length nucleotide sequence of DNA43316-1237 is shown in Figure 221 (SEQ ID NO:522). Clone DNA43316-1237 contains a single open reading frame with an apparent translational initiation site at nucleotide positions 134-136 (Figure 221; SEQ ID NO:522). The predicted polypeptide precursor is 344 amino acids long. Clone DNA43316-1237 has been deposited with ATCC and is assigned ATCC deposit no. 209487

Based on a BLAST-2 and FastA sequence alignment analysis of the full-length sequence, PRO337 shows amino acid sequence identity to rat neurotrimin (97%).

EXAMPLE 97: Isolation of cDNA Clones Encoding Human PRO403Introduction:

Human thrombopoietin (THPO) is a glycosylated hormone of 352 amino acids consisting of two domains. The N-terminal domain, sharing 50% similarity to erythropoietin, is responsible for the biological activity. The C-terminal region is required for secretion. The gene for thrombopoietin (THPO) maps to human chromosome 3q27-q28 where the six exons of this gene span 7 kilobase base pairs of genomic DNA (Chang et al., Genomics 26: 636-7 (1995); Foster et al., Proc. Natl. Acad. Sci. USA 91: 13023-7 (1994); Gurney et al., Blood 85: 981-988 (1995)). In order to determine whether there were any genes encoding THPO homologues located in close proximity to THPO, genomic DNA fragments from this region were identified and sequenced. Three P1 clones and one PAC clones (Genome Systems Inc., St. Louis, MO; cat. Nos. P1-2535 and PAC-6539) encompassing the THPO locus were isolated and a 140 kb region was sequenced using the ordered shotgun strategy (Chen et al., Genomics 17: 651-656 (1993)), coupled with a PCR-based gap filling approach. Analysis reveals that the region is gene-rich with four additional genes located very close to THPO: tumor necrosis factor-receptor type 1 associated protein 2 (TRAP2) and elongation initiation factor gamma (eIF4), chloride channel 2 (CLCN2) and RNA polymerase II subunit hRPB17. While no THPO homolog was found in the region, four novel genes have been predicted by computer-assisted gene detection (GRAIL)(Xu et al., Gen. Engin. 16: 241-253 (1994), the presence of CpG islands (Cross, S. and Bird, A., Curr. Opin. Genet. & Devel. 5: 109-314 (1995), and homology to known genes (as detected by WU-BLAST2.0)(Altschul and Gish, Methods Enzymol. 266: 460-480 (1996) (<http://blast.wustl.edu/blast/README.html>).

Procedures:P1 and PAC clones:

The initial human P1 clone was isolated from a genomic P1 library (Genome Systems Inc., St. Louis, MO; cat. no.: P1-2535) screened with PCR primers designed from the THPO genomic sequence (A.L. Gurney, et al., Blood 85: 981-88 (1995)). PCR primers were designed from the end sequences derived from this P1 clone were then used to screen P1 and PAC libraries (Genome Systems, Cat. Nos.: P1-2535 & PAC-6539) to identify overlapping clones (PAC1, p1.t, and P1.u). The 3'-end sequence from PAC.z was used to define the primers used for the screening of a human BAC library (Genome Systems Inc., St. Louis, MO; Cat. No.: BDTW-4533A).

Ordered Shotgun Strategy:

The Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-656 (1993)) involves the mapping and sequencing of large genomic DNA clones with a hierarchical approach. The P1 or PAC clone was sonicated and the fragments subcloned into lambda vector ( $\lambda$ BlueStar) (Novagen, Inc., Madison, WI; cat. no. 69242-3). The lambda subclone inserts were isolated by long-range PCR (Barnes, W. Proc. Natl. Acad. Sci. USA 91: 2216-2220 (1994) and the ends sequenced. The lambda-end sequences were overlapped to create a partial map of the original clone. Those lambda clones with overlapping end-sequences were identified, the insets subcloned into a plasmid vector (pUC18 or pUC19, Hoefer Pharmacia Biotech, Inc., San Francisco, CA, Cat. Nos. 27-4949-01 and 27-4951-01) and the ends of the plasmid subclones were sequenced and assembled to generate a contiguous sequence. This directed sequencing strategy minimizes the redundancy required while allowing one

to scan for and concentrate on interesting regions.

In order to define better the THPO locus and to search for other genes related to the hematopoietin family, five genomic clones were isolated from this region by PCR screening of human P1 and PAC libraries (Genome System, Inc., Cat. Nos.: P1-2535 and PAC-6539).

The sizes of the genomic fragments are as follows: P1.t is 40 kb; P1.g is 70 kb; P1.u is 70 kb; PAC.z is 200 kb; and BAC.1 is 80 kb. Approximately 75% (140 kb) of the 190 kb genomic DNA region was sequenced by the Ordered Shotgun Strategy (OSS) (Chen et al., Genomics 17: 651-56 (1993), and assembled into contigs using AutoAssembler<sup>TM</sup> (Applied Biosystems, Perkin Elmer, Foster City, CA, cat. no. 903227). The preliminary order of these contigs was determined by manual analysis. There were 47 contigs the 140 kb region. A PCR-based approach to ordering the contigs and filling in the gaps was employed. The following summarizes the number and sizes of the gaps. The 50 kb of sequence unique to BAC.1 was sequenced by a total shotgun approach with a ten-fold redundancy.

<u>Size of gap</u>	<u>number</u>
< 50 bp	13
50-150 bp	7
150-300 bp	7
300-1000 bp	10
1000-5000 bp	7
> 5000 bp	2 ((15,000 bp)

#### 20 DNA sequencing:

ABI DYE-primer<sup>TM</sup> chemistry (PE Applied Biosystems, Foster City, CA; Cat. No.: 402112) was used to end-sequence the lambda and plasmid subclones. ABI DYE-terminator<sup>TM</sup> chemistry (PE Applied Biosystems, Foster City, CA, Cat. No: 403044) was used to sequence the PCR products with their respective PCR primers. The sequences were collected with an ABI377 instrument. For PCR products larger than 1kb, walking primers were used. The sequences of contigs generated by the OSS strategy in AutoAssembler<sup>TM</sup> (PE Applied Biosystems, Foster City, CA; Cat. No: 903227) and the gap-filling sequencing trace files were imported into Sequencher<sup>TM</sup> (Gene Codes Corp., Ann Arbor, MI) for overlapping and editing. The sequences generated by the total shotgun strategy were assembled using Phred and Phrap and edited using Consed (<http://chimera.biotech.washington.edu/uwgc/projects.htm>) and GFP (Genome Reconstruction Manager for Phrap), version 1.2 (<http://stork.cellb.bcm.tmc.edu/gfp/>).

#### 30 PCR-Based gap filling Strategy:

Primers were designed based on the 5'- and 3'-end sequenced of each contig, avoiding repetitive and low quality sequence regions. All primers were designed to be 19-24-mers with 50-70% G/C content. Oligos were synthesized and gel-purified by standard methods.

35 Since the orientation and order of the contigs were unknown, permutations of the primers were used in the amplification reactions. Two PCR kits were used: first, XL PCR kit (Perkin Elmer, Norwalk, CT; Cat. No.: N8080205), with extension times of approximately 10 minutes; and second, the Taq polymerase PCR kit



(Qiagen Inc., Valencia, CA; Cat. No.: 201223) was used under high stringency conditions if smeared or multiple products were observed with the XL PCR kit. The main PCR product from each successful reaction was extracted from a 0.9% low melting agarose gel and purified with the GeneClean DNA Purification kit prior to sequencing.

#### Analysis:

5 The identification and characterization of coding regions was carried out as follows: First, repetitive sequences were masked using RepeatMasker (A.F.A. Smit & P. Green, [http://ftp.genome.washington.edu/RM/RM\\_details.html](http://ftp.genome.washington.edu/RM/RM_details.html)) which screens DNA sequences in FastA format against a library of repetitive elements and returns a masked query sequence. Repeats not masked were identified by comparing the sequence to the GenBank database using WUBLAST2.0 [Altschul, S & Gish, W., Methods  
10 Enzymol. 266: 460-480 (1996); <http://blast.wustl.edu/blast/README.html>] and were masked manually.

Next, known genes were revealed by comparing the genomic regions against Genentech's protein database using the WUBLAST2.0 algorithm and then annotated by aligning the genomic and cDNA sequences for each gene, respectively, using a Needleman-Wunch (Needleman and Wunsch, J. Mol. Biol. 48: 443-453 (1970) algorithm to find regions of local identity between sequences. The strategy results in detection of all  
15 exons of the five known genes in the region, THPO, TRAP2, eIF4g, CLCN2 and hRPB17 (see below).

<u>Known genes</u>	<u>Map position</u>
eukaryotic translation initiation factor 4 gamma	3q27-qter
thrombopoietin	3q26-q27
20 chloride channel 2	3q26-qter
TNF receptor associated protein 2	not previously mapped
RNA polymerase II subunit hRPB17	not previously mapped

Finally, novel transcription units were predicted using a number of approaches. CpG islands (S. Cross  
25 & Bird, A., Curr. Opin. Genet. Dev. 5: 109-314 (1995) islands were used to define promoter regions and were identified as clusters of sites cleaved by enzymes recognizing GC-rich, 6 or 8-mer palindromic sequences (NotI, NarI, BssHII, XhoI. CpG islands are usually associated with promoter regions of genes. WUBLAST2.0 analysis of short genomic regions (10-20 kb) versus GenBank revealed matches to ESTs. The individual EST sequences (or where possible, their sequence chromatogram files) were retrieved and assembled with Sequencer  
30 to provide a theoretical cDNA sequence (DNA36443). GRAIL2 (ApoCom Inc., Knoxville, TN, command line version for the DEC alpha) was used to predict a novel exon. The five known genes in the region served as internal controls for the success of the GRAIL algorithm.

#### Isolation:

A partial endothelin converting enzyme-2 (ECE-2) cDNA clone was isolated by first splicing in silico  
35 the ECE-2 exons predicted in the genomic sequence to generate a putative sequence (DNA36443). An oligonucleotide probe: GAAGCAGTGCAGCCAGCAGTAGAGAGGCACCTGCTAAGA) (SEQ ID NO:530) was designed and used to screen a human fetal small intestine library (LIB110) and internal PCR primers

(36443f1) (ECE2.f:ACGCAGCTGGAGCTGGTCTTAGCA) (SEQ ID NO:531) and (36443r1) (ECE2.r) (GGTACTGGACCCCTAGGGCCACAA) (SEQ ID NO:532) were used to confirm clones hybridizing to the probe prior to sequencing. One positive clone was obtained, however this cDNA (DNA49830) represented a partially spliced transcript containing appropriately spliced exons 1 through 6, followed by intron 6 sequence. The oligo dT primer annealed to a polyA-stretch within an Alu element present in intron 6. An additional ECE-2  
 5 cDNA fragment (DNA49831) was obtained by PCR from a human fetal kidney library (LIB227) with primers designed from the presumed cDNA sequence [36443f3: CCTCCCAGCCGAGACCAAGTGG (SEQ ID NO:533) and 36443r2: GGTCCTATAAGGGCCAAGACC (SEQ ID NO:534)]. This PCR product extended from exon 13 into the 3' untranslated region in exon 18.

A full length endothelin converting enzyme 2 (ECE-2) cDNA clone (DNA55800-1263) was isolated  
 10 from an oligo-dT-primed human fetal brain library. RNA from human fetal brain tissue (20 weeks gestation, #283005)(SRC175) was isolated by guanidine thiocyanate and 5  $\mu$ g used to generate double stranded cDNA which was cloned into the vector pRK5E. The 3' -primer (pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTTT) (SEQ ID NO:535) and the 5 -linker (pCGGACGCGTGGGTCGA) (SEQ ID NO:536) were designed to introduce XhoI and NotI restriction sites.  
 15 The library was screened with PCR primers [36443pcrf1: CGGCCGTGATGGCTGGTGACG (SEQ ID NO:537) and 36443r3: GGCAGACTCCTTCCTATGGG (SEQ ID NO:538)] designed from the partial human ECE-2 cDNA sequences (DNA49830 and DNA49831). PCR products were cloned into the vector pCR2.1-TOPO (Invitrogen Corp., Carlsbad, CA, Cat. No. K4500-01) and sequenced with DYE-terminator chemistry as described above.

20

#### EXAMPLE 98: Northern Blot and in situ RNA Hybridization Analysis for PRO403

Expression of PRO403 mRNA in human tissues was examined by Northern blot analysis. Human polyA+ RNA blots derived from human fetal and adult tissues (Clontech, Palo Alto, CA; Cat. Nos. 7760-1, 7756-1 and 7755-1) were hybridized to a [32P- $\alpha$ ]dATP-labelled cDNA fragments from probe based on the full  
 25 length PRO403 cDNA. Blots were incubated with the probes in hybridization buffer (5X SSPE; 2X Denhardt's solution; 100 mg/mL denatured sheared salmon sperm DNA; 50% formamide; 2% SDS) for 18 hours at 42°C, washed to high stringency (0.1XSSC, 0.1% SDS, 50°C) and autoradiographed. The blots were developed after overnight exposure by phosphorimager analysis (Fuji).

PRO403 mRNA transcripts were detected. Analysis of the expression pattern showed the strongest  
 30 signal of the expected 3.3 kb transcript in adult brain (highest in the cerebellum, putamen, medulla, and temporal lobe, and lower in the cerebral cortex, occipital lobe and frontal lobe), spinal cord, lung and pancreas and higher levels of a 4.5 kb transcript in fetal brain and kidney.

#### EXAMPLE 99: Use of PRO Polypeptide-Encoding Nucleic Acid as Hybridization Probes

35 The following method describes use of a nucleotide sequence encoding a PRO polypeptide as a hybridization probe.

DNA comprising the coding sequence of a PRO polypeptide of interest as disclosed herein may be employed as a probe or used as a basis from which to prepare probes to screen for homologous DNAs (such as those encoding naturally-occurring variants of the PRO polypeptide) in human tissue cDNA libraries or human tissue genomic libraries.

5 Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO polypeptide-encoding nucleic acid-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

10 DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO polypeptide can then be identified using standard techniques known in the art.

EXAMPLE 100: Expression of PRO Polypeptides in *E. coli*

This example illustrates preparation of an unglycosylated form of a desired PRO polypeptide by recombinant expression in *E. coli*.

15 The DNA sequence encoding the desired PRO polypeptide is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. 20 The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the specific PRO polypeptide coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in 25 Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

30 Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO polypeptide can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

35 PRO181, PRO195, PRO200, PRO237, PRO273, PRO540, PRO322, PRO1017, PRO938, PRO162, PRO1114, PRO827 and PRO1008 were expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA encoding the PRO polypeptide was initially amplified using selected PCR primers. The

primers contained restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences were then ligated into an expression vector, which was used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants were first grown  
5 in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 was reached. Cultures were then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 0.71 g sodium citrate·2H<sub>2</sub>O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM MgSO<sub>4</sub>) and grown for approximately 20-30 hours at 30°C with shaking. Samples were removed to verify expression by SDS-PAGE analysis, and the bulk culture  
10 is centrifuged to pellet the cells. Cell pellets were frozen until purification and refolding.

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) was resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution was stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution was centrifuged  
15 at 40,000 rpm in a Beckman Ultracentrifuge for 30 min. The supernatant was diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. Depending the clarified extract was loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column was washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein was eluted with buffer containing 250 mM imidazole.  
20 Fractions containing the desired protein were pooled and stored at 4°C. Protein concentration was estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins were refolded by diluting sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes were chosen so that the final protein concentration was between 50 to 100 micrograms/ml.  
25 The refolding solution was stirred gently at 4°C for 12-36 hours. The refolding reaction was quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution was filtered through a 0.22 micron filter and acetonitrile was added to 2-10% final concentration. The refolded protein was chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions  
30 with A280 absorbance were analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein were pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase  
35 step also removes endotoxin from the samples.

Fractions containing the desired folded PRO proteins were pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins were formulated into 20 mM Hepes, pH 6.8 with



0.14 M sodium chloride and 4 % mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides described herein were successfully expressed as described above.

EXAMPLE 101: Expression of PRO Polypeptides in Mammalian Cells

5 This example illustrates preparation of a glycosylated form of a desired PRO polypeptide by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO polypeptide-encoding DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO polypeptide DNA using ligation methods such as described in Sambrook et al., supra. The  
10 resulting vector is called pRK5-PRO polypeptide.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10  $\mu$ g pRK5-PRO polypeptide DNA is mixed with about 1  $\mu$ g DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500  
15  $\mu$ l of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M  $\text{CaCl}_2$ . To this mixture is added, dropwise, 500  $\mu$ l of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM  $\text{NaPO}_4$ , and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

20 Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200  $\mu$ Ci/ml  $^{35}\text{S}$ -cysteine and 200  $\mu$ Ci/ml  $^{35}\text{S}$ -methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in  
25 serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO polypeptide may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700  $\mu$ g pRK5-PRO polypeptide DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate  
30 is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5  $\mu$ g/ml bovine insulin and 0.1  $\mu$ g/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO polypeptide can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

35 In another embodiment, PRO polypeptides can be expressed in CHO cells. The pRK5-PRO polypeptide can be transfected into CHO cells using known reagents such as  $\text{CaPO}_4$  or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing

a radiolabel such as  $^{35}\text{S}$ -methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO polypeptide can then be concentrated and purified by any selected method.

Epitope-tagged PRO polypeptide may also be expressed in host CHO cells. The PRO polypeptide may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO polypeptide insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO polypeptide can then be concentrated and purified by any selected method, such as by  $\text{Ni}^{2+}$ -chelate affinity chromatography.

Stable expression in CHO cells was performed using the following procedure. The proteins were expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins were fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs were subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., *Current Protocols of Molecular Biology*, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., *Nucl. Acids Res.* 24: 9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA were introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect<sup>®</sup> (Quiagen), Dosper<sup>®</sup> or Fugene<sup>®</sup> (Boehringer Mannheim). The cells were grown and described in Lucas et al., supra. Approximately  $3 \times 10^7$  cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA were thawed by placement into water bath and mixed by vortexing. The contents were pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant was aspirated and the cells were resuspended in 10 mL of selective media (0.2  $\mu\text{m}$  filtered PS20 with 5% 0.2  $\mu\text{m}$  diafiltered fetal bovine serum). The cells were then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells were transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, a 250 mL, 500 mL and 2000 mL spinners were seeded with  $3 \times 10^5$  cells/mL. The cell media was exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in US Patent No. 5,122,469, issued June 16, 1992 was actually used. 3L production spinner is seeded at  $1.2 \times 10^6$  cells/mL. On day 0, the cell number pH were determined. On day 1, the spinner was sampled and sparging with filtered air was commenced. On day 2, the spinner was sampled,

the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion). Throughout the production, pH was adjusted as necessary to keep at around 7.2. After 10 days, or until viability dropped below 70%, the cell culture was harvested by centrifugation and filtering through a 0.22 µm filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

5 For the poly-His tagged constructs, the proteins were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media was pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The  
10 highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs were purified from the conditioned media as follows. The conditioned medium was pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer  
15 before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 µL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity was assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides described herein were successfully expressed as described above.

20

#### EXAMPLE 102: Expression of PRO Polypeptides in Yeast

The following method describes recombinant expression of a desired PRO polypeptide in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO polypeptides from the ADH2/GAPDH promoter. DNA encoding a desired PRO polypeptide, a selected signal  
25 peptide and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of the PRO polypeptide. For secretion, DNA encoding the PRO polypeptide can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, the yeast alpha-factor secretory signal/leader sequence, and linker sequences (if needed) for expression of the PRO polypeptide.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described  
30 above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO polypeptide can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge  
35 filters. The concentrate containing the PRO polypeptide may further be purified using selected column chromatography resins.

Many of the PRO polypeptides described herein were successfully expressed as described above.

EXAMPLE 103: Expression of PRO Polypeptides in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO polypeptides in Baculovirus-infected insect cells.

The desired PRO polypeptide is fused upstream of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG).  
5 A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression  
10 vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4-5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression is performed as described by O'Reilley et al.,  
15 Baculovirus expression vectors: A laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO polypeptide can then be purified, for example, by Ni<sup>2+</sup>-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., *Nature*, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM MgCl<sub>2</sub>; 0.1 mM EDTA; 10% Glycerol; 0.1 % NP-40; 0.4 M KCl), and sonicated  
20 twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% Glycerol, pH 7.8) and filtered through a 0.45 µm filter. A Ni<sup>2+</sup>-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline A<sub>280</sub> with loading buffer, at  
25 which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% Glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching A<sub>280</sub> baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or western blot with Ni<sup>2+</sup>-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted His<sub>10</sub>-tagged PRO  
30 polypeptide are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO polypeptide can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

PRO195, PRO526, PRO540, PRO846, PRO362, PRO363, PRO700, PRO707, PRO322, PRO719, PRO1083, PRO868, PRO866, PRO768, PRO788, PRO938, PRO827 and PRO1031 were successfully expressed  
35 in baculovirus infected Sf9 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations. The proteins were expressed as an IgG construct (immunoadhesin), in which the protein extracellular region was fused to an IgG1 constant region sequence



containing the hinge, CH2 and CH3 domains and/or in poly-His tagged forms.

For expression in baculovirus infected Sf9 cells, following PCR amplification, the respective coding sequences were subcloned into a baculovirus expression vector (pb.PH.IgG for IgG fusions and pb.PH.His.c for poly-His tagged proteins), and the vector and Baculogold® baculovirus DNA (Pharmingen) were co-transfected into 105 *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711), using Lipofectin (Gibco BRL).  
5 pb.PH.IgG and pb.PH.His are modifications of the commercially available baculovirus expression vector pVL1393 (Pharmingen), with modified polylinker regions to include the His or Fc tag sequences. The cells were grown in Hink's TNM-FH medium supplemented with 10% FBS (Hyclone). Cells were incubated for 5 days at 28°C. The supernatant was harvested and subsequently used for the first viral amplification by infecting Sf9  
10 cells in Hink's TNM-FH medium supplemented with 10% FBS at an approximate multiplicity of infection (MOI) of 10. Cells were incubated for 3 days at 28°C. The supernatant was harvested and the expression of the constructs in the baculovirus expression vector was determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

15 The first viral amplification supernatant was used to infect a spinner culture (500 ml) of Sf9 cells grown in ESF-921 medium (Expression Systems LLC) at an approximate MOI of 0.1. Cells were incubated for 3 days at 28°C. The supernatant was harvested and filtered. Batch binding and SDS-PAGE analysis was repeated, as necessary, until expression of the spinner culture was confirmed.

The conditioned medium from the transfected cells (0.5 to 3 L) was harvested by centrifugation to  
20 remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein construct were purified using a Ni-NTA column (Qiagen). Before purification, imidazole was added to the conditioned media to a concentration of 5 mM. The conditioned media were pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column was washed with additional equilibration buffer and the  
25 protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein was subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins were purified from the conditioned media as follows. The conditioned media were pumped onto a 5 ml Protein A column (Pharmacia) which had been  
30 equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column was washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein was immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein was subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of the proteins was verified by SDS polyacrylamide gel (PAGE) electrophoresis and  
35 N-terminal amino acid sequencing by Edman degradation.

PRO181, PRO195, PRO200, PRO320, PRO237, PRO273, PRO285, PRO337, PRO526, PRO540, PRO846, PRO362, PRO363, PRO617, PRO322, PRO1083, PRO868, 768, PRO792, PRO788, PRO162,

PRO1114, PRO827, PRO1075 and PRO1031 were successfully expressed in baculovirus infected Hi5 insect cells. While the expression was actually performed in a 0.5-2 L scale, it can be readily scaled up for larger (e.g. 8 L) preparations.

For expression in baculovirus-infected Hi5 insect cells, the PRO polypeptide-encoding DNA may be amplified with suitable systems, such as Pfu (Stratagene), or fused upstream (5'-of) of an epitope tag contained with a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the PRO polypeptide or the desired portion of the PRO polypeptide (such as the sequence encoding the extracellular domain of a transmembrane protein) is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector. For example, derivatives of pVL1393 can include the Fc region of human IgG (pb.PH.IgG) or an 8 histidine (pb.PH.His) tag downstream (3'-of) the NAME sequence. Preferably, the vector construct is sequenced for confirmation.

Hi5 cells are grown to a confluency of 50% under the conditions of, 27°C, no CO<sub>2</sub>, NO pen/strep. For each 150 mm plate, 30 ug of pIE based vector containing PRO polypeptide is mixed with 1 ml Ex-Cell medium (Media: Ex-Cell 401 + 1/100 L-Glu JRH Biosciences #14401-78P (note: this media is light sensitive)), and in a separate tube, 100 ul of CellFectin (CellFECTIN (GibcoBRL #10362-010) (vortexed to mix)) is mixed with 1 ml of Ex-Cell medium. The two solutions are combined and allowed to incubate at room temperature for 15 minutes. 8 ml of Ex-Cell media is added to the 2ml of DNA/CellFECTIN mix and this is layered on Hi5 cells that have been washed once with Ex-Cell media. The plate is then incubated in darkness for 1 hour at room temperature. The DNA/CellFECTIN mix is then aspirated, and the cells are washed once with Ex-Cell to remove excess CellFECTIN. 30 ml of fresh Ex-Cell media is added and the cells are incubated for 3 days at 28°C. The supernatant is harvested and the expression of the PRO polypeptide in the baculovirus expression vector can be determined by batch binding of 1 ml of supernatant to 25 mL of Ni-NTA beads (QIAGEN) for histidine tagged proteins or Protein-A Sepharose CL-4B beads (Pharmacia) for IgG tagged proteins followed by SDS-PAGE analysis comparing to a known concentration of protein standard by Coomassie blue staining.

The conditioned media from the transfected cells (0.5 to 3 L) is harvested by centrifugation to remove the cells and filtered through 0.22 micron filters. For the poly-His tagged constructs, the protein comprising the PRO polypeptide is purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc containing) constructs of proteins are purified from the conditioned media as follows. The conditioned media is pumped onto a 5 ml Protein A column (Pharmacia) which had been

equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 mL of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity of PRO polypeptide can be assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation and other analytical procedures as desired or necessary.

Many of the PRO polypeptides described herein were successfully expressed as described above.

#### EXAMPLE 104: Preparation of Antibodies that Bind to PRO Polypeptides

This example illustrates preparation of monoclonal antibodies which can specifically bind to a PRO polypeptide.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, *supra*. Immunogens that may be employed include purified PRO polypeptide, fusion proteins containing the PRO polypeptide, and cells expressing recombinant PRO polypeptide on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO polypeptide immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO polypeptide antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO polypeptide. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against the PRO polypeptide. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against the PRO polypeptide is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO polypeptide monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 105: Chimeric PRO Polypeptides

PRO polypeptides may be expressed as chimeric proteins with one or more additional polypeptide domains added to facilitate protein purification. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS<sup>TM</sup> extension/affinity purification system (Immunex Corp., Seattle Wash.). The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (Invitrogen, San Diego Calif.) between the purification domain and the PRO polypeptide sequence may be useful to facilitate expression of DNA encoding the PRO polypeptide.

EXAMPLE 106: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE<sup>TM</sup> (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (e.g., high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (e.g., a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 107: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located



intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (i) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PRO polypeptide.

#### EXAMPLE 108: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins.

In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

5 It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then  
10 be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques  
15 in place of or in addition to x-ray crystallography.

EXAMPLE 109: Ability of PRO Polypeptides to Inhibit Vascular Endothelial Growth Factor (VEGF) Stimulated Proliferation of Endothelial Cell Growth (Assay 9)

The ability of various PRO polypeptides to inhibit VEGF stimulated proliferation of endothelial cells  
20 was tested. Polypeptides testing positive in this assay are useful for inhibiting endothelial cell growth in mammals where such an effect would be beneficial, e.g., for inhibiting tumor growth.

Specifically, bovine adrenal cortical capillary endothelial cells (ACE) (from primary culture, maximum of 12-14 passages) were plated in 96-well plates at 500 cells/well per 100 microliter. Assay media included low glucose DMEM, 10% calf serum, 2 mM glutamine, and 1X penicillin/streptomycin/fungizone. Control wells  
25 included the following: (1) no ACE cells added; (2) ACE cells alone; (3) ACE cells plus 5 ng/ml FGF; (4) ACE cells plus 3 ng/ml VEGF; (5) ACE cells plus 3 ng/ml VEGF plus 1 ng/ml TGF-beta; and (6) ACE cells plus 3 ng/ml VEGF plus 5 ng/ml LIF. The test samples, poly-his tagged PRO polypeptides (in 100 microliter volumes), were then added to the wells (at dilutions of 1%, 0.1% and 0.01%, respectively). The cell cultures were incubated for 6-7 days at 37°C/5% CO<sub>2</sub>. After the incubation, the media in the wells was aspirated, and  
30 the cells were washed 1X with PBS. An acid phosphatase reaction mixture (100 microliter; 0.1M sodium acetate, pH 5.5, 0.1% Triton X-100, 10 mM p-nitrophenyl phosphate) was then added to each well. After a 2 hour incubation at 37°C, the reaction was stopped by addition of 10 microliters 1N NaOH. Optical density (OD) was measured on a microplate reader at 405 nm.

The activity of PRO polypeptides was calculated as the percent inhibition of VEGF (3 ng/ml) stimulated  
35 proliferation (as determined by measuring acid phosphatase activity at OD 405 nm) relative to the cells without stimulation. TGF-beta was employed as an activity reference at 1 ng/ml, since TGF-beta blocks 70-90% of VEGF-stimulated ACE cell proliferation. The results are indicative of the utility of the PRO polypeptides in

cancer therapy and specifically in inhibiting tumor angiogenesis. Numerical values (relative inhibition) are determined by calculating the percent inhibition of VEGF stimulated proliferation by the PRO polypeptides relative to cells without stimulation and then dividing that percentage into the percent inhibition obtained by TGF- $\beta$  at 1 ng/ml which is known to block 70-90% of VEGF stimulated cell proliferation. The results are considered positive if the PRO polypeptide exhibits 30% or greater inhibition of VEGF stimulation of endothelial cell growth (relative inhibition 30% or greater).

The following polypeptides tested positive in this assay: PRO200, PRO322 and PRO320.

EXAMPLE 110: Retinal Neuron Survival (Assay 52)

This example demonstrates that certain PRO polypeptides have efficacy in enhancing the survival of retinal neuron cells and, therefore, are useful for the therapeutic treatment of retinal disorders or injuries including, for example, treating sight loss in mammals due to retinitis pigmentosum, AMD, etc.

Sprague Dawley rat pups at postnatal day 7 (mixed population: glia and retinal neuronal types) are killed by decapitation following CO<sub>2</sub> anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca<sup>2+</sup>, Mg<sup>2+</sup>-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well in 96 well plates in DMEM/F12 supplemented with N2 and with or without the specific test PRO polypeptide. Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5% CO<sub>2</sub>. After 2-3 days in culture, cells are stained with calcein AM then fixed using 4% paraformaldehyde and stained with DAPI for determination of total cell count. The total cells (fluorescent) are quantified at 20X objective magnification using CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The effect of various concentration of PRO polypeptides are reported herein where percent survival is calculated by dividing the total number of calcein AM positive cells at 2-3 days in culture by the total number of DAPI-labeled cells at 2-3 days in culture. Anything above 30% survival is considered positive.

The following PRO polypeptides tested positive in this assay using polypeptide concentrations within the range of 0.01% to 1.0% in the assay: PRO200, PRO322, PRO540, PRO846 and PRO617.

EXAMPLE 111: Rod Photoreceptor Survival (Assay 56)

This assay shows that certain polypeptides of the invention act to enhance the survival/proliferation of rod photoreceptor cells and, therefore, are useful for the therapeutic treatment of retinal disorders or injuries including, for example, treating sight loss in mammals due to retinitis pigmentosum, AMD, etc. Sprague Dawley rat pups at 7 day postnatal (mixed population: glia and retinal neuronal cell types) are killed by decapitation following CO<sub>2</sub> anesthesia and the eyes are removed under sterile conditions. The neural retina is dissected away from the pigment epithelium and other ocular tissue and then dissociated into a single cell suspension using 0.25% trypsin in Ca<sup>2+</sup>, Mg<sup>2+</sup>-free PBS. The retinas are incubated at 37°C for 7-10 minutes after which the trypsin is inactivated by adding 1 ml soybean trypsin inhibitor. The cells are plated at 100,000 cells per well

in 96 well plates in DMEM/F12 supplemented with  $N_2$ . Cells for all experiments are grown at 37°C in a water saturated atmosphere of 5%  $CO_2$ . After 2-3 days in culture, cells are fixed using 4% paraformaldehyde, and then stained using CellTracker Green CMFDA. Rho 4D2 (ascites or IgG 1:100), a monoclonal antibody directed towards the visual pigment rhodopsin is used to detect rod photoreceptor cells by indirect immunofluorescence. The results are calculated as % survival: total number of calcein - rhodopsin positive cells at 2-3 days in culture, divided by the total number of rhodopsin positive cells at time 2-3 days in culture. The total cells (fluorescent) are quantified at 20x objective magnification using a CCD camera and NIH image software for MacIntosh. Fields in the well are chosen at random.

The following polypeptides tested positive in this assay: PRO200, PRO322, PRO540, PRO846 and PRO617.

EXAMPLE 112: Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

The metacarpophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5%  $CO_2$  in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100 $\mu$ g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional 24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1 $\alpha$ , a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, Biochem. Biophys. Acta 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1 $\alpha$  and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. The polypeptides testing positive in this assay are: PRO200.

EXAMPLE 113: In Vitro Antiproliferative Assay (Assay 161)

The antiproliferative activity of various PRO polypeptides was determined in the investigational, disease-oriented *in vitro* anti-cancer drug discovery assay of the National Cancer Institute (NCI), using a sulforhodamine B (SRB) dye binding assay essentially as described by Skehan et al., J. Natl. Cancer Inst. 82:1107-1112 (1990). The 60 tumor cell lines employed in this study ("the NCI panel"), as well as conditions for their maintenance



and culture *in vitro* have been described by Monks et al., J. Natl. Cancer Inst. 83:757-766 (1991). The purpose of this screen is to initially evaluate the cytotoxic and/or cytostatic activity of the test compounds against different types of tumors (Monks et al., *supra*; Boyd, Cancer: Princ. Pract. Oncol. Update 3(10):1-12 [1989]).

Cells from approximately 60 human tumor cell lines were harvested with trypsin/EDTA (Gibco), washed once, resuspended in IMEM and their viability was determined. The cell suspensions were added by  
5 pipet (100  $\mu$ L volume) into separate 96-well microtiter plates. The cell density for the 6-day incubation was less than for the 2-day incubation to prevent overgrowth. Inoculates were allowed a preincubation period of 24 hours at 37°C for stabilization. Dilutions at twice the intended test concentration were added at time zero in 100  $\mu$ L aliquots to the microtiter plate wells (1:2 dilution). Test compounds were evaluated at five half-log dilutions (1000 to 100,000-fold). Incubations took place for two days and six days in a 5% CO<sub>2</sub> atmosphere and 100%  
10 humidity.

After incubation, the medium was removed and the cells were fixed in 0.1 ml of 10% trichloroacetic acid at 40°C. The plates were rinsed five times with deionized water, dried, stained for 30 minutes with 0.1 ml of 0.4% sulforhodamine B dye (Sigma) dissolved in 1% acetic acid, rinsed four times with 1% acetic acid to remove unbound dye, dried, and the stain was extracted for five minutes with 0.1 ml of 10 mM Tris base  
15 [tris(hydroxymethyl)aminomethane], pH 10.5. The absorbance (OD) of sulforhodamine B at 492 nm was measured using a computer-interfaced, 96-well microtiter plate reader.

A test sample is considered positive if it shows at least 50% growth inhibitory effect at one or more concentrations. PRO polypeptides testing positive in this assay are shown in Table 7, where the abbreviations are as follows:

20 NSCL = non-small cell lung carcinoma  
CNS = central nervous system

Table 7

	<u>Test compound</u>	<u>Tumor Cell Line Type</u>	<u>Cell Line Designation</u>
	PRO181	Leukemia	RPMI-8226
	PRO181	NSCL	NCI-H226; NCI-H522
	PRO181	Melanoma	MALME-3M; SK-MEL-5
5	PRO181	Ovarian	OVCAR-4
	PRO181	Breast	NCI/ADR-RES
	PRO181	Leukemia	MOLT-4
	PRO181	NSCL	NCI-H226*
	PRO181	CNS	SNB-19
10	PRO181	Ovarian	OVCAR-3; OVCAR-8
	PRO181	Renal	A498
	PRO181	Breast	MDA-MB-231/ATCC; MDA-N
	PRO181	Melanoma	LOX IMVI
	PRO181	Leukemia	CCRF-CEM; RPMI-8226*
15	PRO181	NSCL	HOP-62
	PRO181	Leukemia	HL-60 (TB)
	PRO237	Leukemia	K-562
	PRO237	NSCL	NCI-H322M
	PRO237	Colon	HCC-2998; HCT-15
20	PRO237	Colon	KM12
	PRO237	Prostate	DU-145
	PRO237	Breast	MDA-N
	PRO526	NSCL	HOP-62; NCI-H322M
	PRO526	Colon	HCT-116
25	PRO526	Melanoma	LOX IMVI; SK-MEL-2
	PRO526	Ovarian	OVCAR-3
	PRO526	Prostate	PC-3
	PRO526	NSCL	NCI-H226
	PRO526	CNS	SF-539
30	PRO526	Renal	CAKI-1; RXF 393
	PRO362	NSCL	NCI-H322M
	PRO362	Colon	HCT-116
	PRO362	CNS	SF-295
	PRO362	Melanoma	LOX IMVI
35	PRO362	Leukemia	MOLT-4; RPMI-8226; SR
	PRO362	Colon	COLO 205
	PRO362	Breast	HS 578T; MDA-N
	PRO362	Prostate	PC-3
	PRO362	Leukemia	HL-60 (TB); K-562
40	PRO362	NSCL	EKVX; NCI-H23
	PRO362	Colon	HCC-2998
	PRO362	CNS	U251
	PRO362	Melanoma	UACC-257; UACC-62
	PRO362	Ovarian	OVCAR-8
45	PRO362	Breast	T-47D
	PRO362	NSCL	NCI-H522
	PRO362	Renal	RXF 393; UO-31
	PRO362	Breast	MDA-MB-435
	PRO362	NSCL	HOP-62; NCI-H522
50	PRO362	Colon	KM12
	PRO362	Melanoma	MALME-3M; SK-MEL-2
	PRO362	Melanoma	SK-MEL-28; SK-MEL-5
	PRO362	Ovarian	OVCAR-3; OVCAR-4
	PRO362	Breast	MCF7
55	PRO866	Leukemia	HL-60 (TB); MOLT-4; SR

Table 7 (Continued)

	<u>Test compound</u>	<u>Tumor Cell Line Type</u>	<u>Cell Line Designation</u>
	PRO866	NSCL	HOP-62
	PRO866	NSCL	HOP-92
	PRO866	Colon	KM12
5	PRO866	CNS	SF-295
	PRO866	Ovarian	IGROV1
	PRO866	Breast	MDA-MB-435
	PRO866	Melanoma	LOX IMVI
	PRO320	Leukemia	CCRF-CEM; RPMI-8226
10	PRO320	NSCL	HOP62; NCI H322M
	PRO320	Colon	HCT-116
	PRO320	Renal	SN12C
	PRO320	Breast	MDA-N
	PRO320	Ovarian	OVCAR-3
15	PRO320	Melanoma	MALME-3M

\* cytotoxic

The results of these assays demonstrate that the positive testing PRO polypeptides are useful for inhibiting neoplastic growth in a number of different tumor cell types and may be used therapeutically therefor.

20 Antibodies against these PRO polypeptides are useful for affinity purification of these useful polypeptides. Nucleic acids encoding these PRO polypeptides are useful for the recombinant preparation of these polypeptides.

#### EXAMPLE 114: Gene Amplification in Tumors

25 This example shows that certain PRO polypeptide-encoding genes are amplified in the genome of certain human lung, colon and/or breast cancers and/or cell lines. Amplification is associated with overexpression of the gene product, indicating that the polypeptides are useful targets for therapeutic intervention in certain cancers such as colon, lung, breast and other cancers and diagnostic determination of the presence of those cancers. Therapeutic agents may take the form of antagonists of the PRO polypeptide, for example, murine-human chimeric, humanized or human antibodies against a PRO polypeptide.

30 The starting material for the screen was genomic DNA isolated from a variety cancers. The DNA is quantitated precisely, *e.g.*, fluorometrically. As a negative control, DNA was isolated from the cells of ten normal healthy individuals which was pooled and used as assay controls for the gene copy in healthy individuals (not shown). The 5' nuclease assay (for example, TaqMan™) and real-time quantitative PCR (for example, ABI Prizm 7700 Sequence Detection System™ (Perkin Elmer, Applied Biosystems Division, Foster City, CA)), were  
35 used to find genes potentially amplified in certain cancers. The results were used to determine whether the DNA encoding the PRO polypeptide is over-represented in any of the primary lung or colon cancers or cancer cell lines or breast cancer cell lines that were screened. The primary lung cancers were obtained from individuals with tumors of the type and stage as indicated in Table 8. An explanation of the abbreviations used for the designation of the primary tumors listed in Table 8 and the primary tumors and cell lines referred to throughout  
40 this example are given below.

The results of the TaqMan™ are reported in delta ( $\Delta$ ) Ct units. One unit corresponds to 1 PCR cycle or approximately a 2-fold amplification relative to normal, two units corresponds to 4-fold, 3 units to 8-fold amplification and so on. Quantitation was obtained using primers and a TaqMan™ fluorescent probe derived

from the PRO polypeptide-encoding gene. Regions of the PRO polypeptide-encoding gene which are most likely to contain unique nucleic acid sequences and which are least likely to have spliced out introns are preferred for the primer and probe derivation, *e.g.*, 3'-untranslated regions. The sequences for the primers and probes (forward, reverse and probe) used for the PRO polypeptide gene amplification analysis were as follows:

PRO853 (DNA48227-1350)

- 5 48227.tm.fl  
5'-GGCACTTCATGGTCCTTGAAA-3' (SEQ ID NO:539)  
48227.tm.pl  
5'-CGGATGTGTGTGAGGCCATGCC-3' (SEQ ID NO:540)  
48227.tm.rl  
10 5'-GAAAGTAACCACGGAGGTCAAGAT-3' (SEQ ID NO:541)

PRO1017 (DNA56112-1379):

- 56112.tm.fl  
5'-CCTCCTCCGAGACTGAAAGCT-3' (SEQ ID NO:542)  
15 56112.tm.pl  
5'-TCGCGTTGCTTTTTCTCGCGTG-3' (SEQ ID NO:543)  
56112.tm.rl  
5'-GCGTGCGTCAGGTTCCA-3' (SEQ ID NO:544)

20 PRO213-1 (DNA30943-1163-1):

- 30943.tm.f3:  
5'-CGTTCGTGCAGCGTGTGTA-3' (SEQ ID NO:545)  
30943.tm.p3:  
5'-CTTCCTCACCACCTGCGACGGG-3' (SEQ ID NO:546)  
25 30943.tm.r3:  
5'-GGTAGGCGGTCCTATAGATGGTT-3' (SEQ ID NO:547)  
30943.tm.fl:  
5'-AGATGTGGATGAATGCAGTGCTA-3' (SEQ ID NO:548)  
30943.tm.pl:  
30 5'-ATCAACACCGCCGGCAGTTACTGG-3' (SEQ ID NO:549)  
30943.tm.rl:  
5'-ACAGAGTGTACCGTCTGCAGACA-3' (SEQ ID NO:550)  
30943.3trn-5:  
5'-AGCCTCCTGGTGCACTCCT-3' (SEQ ID NO:551)  
35 30943.3trn-probe:  
5'-CGACTCCCTGAGCGAGCAGATTTC-3' (SEQ ID NO:552)



30943.3tm-3:

5'-GCTGGGCAGTCACGAGTCTT-3' (SEQ ID NO:553)

PRO237 (DNA34353-1428):

34353.tm.f:

5 5'-AATCCTCCATCTCAGATCTTCCAG-3' (SEQ ID NO:554)

34353.tm.p:

5'-CCTCAGCGGTAACAGCCGGCC-3' (SEQ ID NO:555)

34353.tm.r:

5'-TGGGCCAAGGGCTGC-3' (SEQ ID NO:556)

10

PRO324 (DNA36343-1310):

36343.tmf1:

5'-TGGTGGATAACCAACAAGATGG-3' (SEQ ID NO:557)

36343.tmp1:

15 5'-GAGTCTGCATCCACACCACTCTTAAAGTTCTCAA-3' (SEQ ID NO:558)

36343.tmr1:

5'-CAGGTGCTCTTTTCAGTCATGTTT-3' (SEQ ID NO:559)

PRO351 (DNA40571-1315):

20 40571.tm.fl:

5'-TGGCCATTCTCAGGACAAGAG-3' (SEQ ID NO:560)

40571.tm.p1:

5'-CAGTAATGCCATTTGCCTGCCTGCAT-3' (SEQ ID NO:561)

40571.tm.r1:

25 5'-TGCCTGGAATCACATGACA-3' (SEQ ID NO:562)

PRO362 (DNA45416-1251):

45416.tm.fl:

5'-TGTGGCACAGACCCAATCCT-3' (SEQ ID NO:563)

30 45416.tm.p1:

5'-GACCCTGAAGGCCTCCGGCCT-3' (SEQ ID NO:564)

45416.tm.r1:

5'-GAGAGAGGGAAGGCAGCTATGTC-3' (SEQ ID NO:565)

35 PRO615 (DNA48304-1323):

48304.tm.fl:

5'-CAGCCCCTCTCTTTCACCTGT-3' (SEQ ID NO:566)

48304.tm.p1:

5'-CCATCCTGTGCAGCTGACACACAGC-3'

(SEQ ID NO:567)

48304.tm.r1:

5'-GC CAGGCTATGA GGCTCCTT-3'

(SEQ ID NO:568)

5 PRO531 (DNA48314-1320):

48314.tm.f1:

5'-TTCAAGTTCCTGAAGCCGATTAT-3'

(SEQ ID NO:569)

48814.tm.p1:

5'-CCAACTTCCCTCCCCAGTGCCCT-3'

(SEQ ID NO:570)

10 48814.tm.r1:

5'-TTGGGGAAGGTAGAATTCCTTGTAT-3'

(SEQ ID NO:571)

PRO618 (DNA49152-1324):

49152.tm.f1:

15 5'-CCCTTCTGCCTCCCAATTCT-3'

(SEQ ID NO:572)

49152.tm.p1:

5'-TCTCCTCCGTCCCCTTCCTCCACT-3'

(SEQ ID NO:573)

49152.tm.r1:

5'-TGAGCCACTGCCTTGCATTA-3'

(SEQ ID NO:574)

20

PRO772 (DNA49645-1347):

49645.tm.f2:

5'-TCTGCAGACGCGATGGATAA-3'

(SEQ ID NO:575)

49645.tm.p2:

25 5'-CCGAAAATAAAACATCGCCCCTTCTGC-3'

(SEQ ID NO:576)

49645.tm.r2:

5'-CACGTGGCCTTTCACACTGA-3'

(SEQ ID NO:577)

49645.tm.f1:

5'-ACTTGTGACAGCAGTATGCTGTCTT-3'

(SEQ ID NO:578)

30 49645.tm.p1:

5'-AAGCTTCTGTTCAATCCCAGCGGTCC-3'

(SEQ ID NO:579)

49645.tm.r1:

5'-ATGCACAGGCTTTTTCTGGTAA-3'

(SEQ ID NO:580)

35 PRO703 (DNA50913-1287):

50913.tm.f1:

5'-GCAGGAAACCTTCGAATCTGAG-3'

(SEQ ID NO:581)

50913.tm.p1:

5'-ACACCTGAGGCACCTGAGAGAGGAACTCT-3' (SEQ ID NO:582)

50913.tm.r1:

5'-GACAGCCCAGTACACCTGCAA-3' (SEQ ID NO:583)

5 PRO792 (DNA56352-1358):

56352.tm.fl:

5'-GACGGCTGGATCTGTGAGAAA-3' (SEQ ID NO:584)

56352.tm.p1:

5'-CACAAGTCTGACCCCGCCCA-3' (SEQ ID NO:585)

10 56352.tm.r1:

5'-CCAGGATACGACATGCTGCAA-3' (SEQ ID NO:586)

PRO474 (DNA56045-1380):

56045.tm.fl:

15 5'-AAACTCCAACCTGTATCAGATGCA-3' (SEQ ID NO:587)

56045.tm.p1:

5'-CCCCCAAGCCCTTAGACTCTAAGCCC-3' (SEQ ID NO:588)

56045.tm.r1:

5'-GACCCGGCACCTTGCTAAC-3' (SEQ ID NO:589)

20

PRO274 (DNA39987-1184):

39987.tm.f:

5'-GGACGGTCAGTCAGGATGACA-3' (SEQ ID NO:590)

39987.tm.p:

25 5'-TTCGGCATCATCTCTTCCCTCTCCC-3' (SEQ ID NO:591)

39987.tm.r:

5'-ACAAAAAAAAAGGGAACAAAATACGA-3' (SEQ ID NO:592)

PRO381 (DNA44194-1317)

30 44194.tm.f :

5'-CTTTGAATAGAAGACTTCTGGACAATTT-3' (SEQ ID NO:593)

44194.tm.p:

5'-TTGCAACTGGGAATATACCACGACATGAGA-3' (SEQ ID NO:594)

44194.tm.r:

35 5'-TAGGGTGCTAATTTGTGCTATAACCT-3' (SEQ ID NO:595)

44194.tm.f2:

5'-GGCTCTGAGTCTCTGCTTGA-3' (SEQ ID NO:596)

44194.tm.p2:

5'-TCCAACAACCATTTTCCTCTGGTCC-3' (SEQ ID NO:597)

44194.tm.r2:

5'-AAGCAGTAGCCATTAACAAGTCA-3' (SEQ ID NO:598)

5 PRO717 (DNA50988-1326):

50988.tm.f3:

5'-CAAGCGTCCAGGTTTATTGA-3' (SEQ ID NO:599)

50988.tm.r3:

5'-GACTACAAGGCGCTCAGCTA-3' (SEQ ID NO:600)

10 50988.tm.p3:

5'-CCGGCTGGGTCTCACTCCTCC-3' (SEQ ID NO:601)

PRO1330 and PRO1449 (DNA64907-1163 and DNA64908-1163, respectively):

30943.tm.f3:

15 5'-CGTTCGTGCAGCGTGTGTA-3' (SEQ ID NO:602)

30943.tm.p3:

5'-CTTCCTCACACCTGCGACG GG-3' (SEQ ID NO:603)

30943.tm.r3:

5'-GGTAGGCGGTCCTATAGATGGTT-3' (SEQ ID NO:604)

20 30943.tm.f1:

5'-AGATG TGGATGAATG CAGTGCTA-3' (SEQ ID NO:605)

30943.tm.p1:

5'-ATCAACACCGCCGGCAGTTACTGG-3' (SEQ ID NO:606)

30943.tm.r1:

25 5'-ACAGAGTGTACCGTCTGCAGACA-3' (SEQ ID NO:607)

30943.3trn-5:

5'-AGCCTCCTGGTGCACTCCT-3' (SEQ ID NO:608)

30943.3trn-probe:

5'-CGACTCCCTGAGCGAGCAGATTTCC-3' (SEQ ID NO:609)

30 30943.3trn-3:

5'-GCTGGGCAGTCACGAGTCTT-3' (SEQ ID NO:610)

35 The 5' nuclease assay reaction is a fluorescent PCR-based technique which makes use of the 5' exonuclease activity of Taq DNA polymerase enzyme to monitor amplification in real time. Two oligonucleotide primers (forward [.f] and reverse [.r]) are used to generate an amplicon typical of a PCR reaction. A third oligonucleotide, or probe (.p), is designed to detect nucleotide sequence located between the two PCR primers. The probe is non-extendible by Taq DNA polymerase enzyme, and is labeled with a reporter fluorescent dye



and a quencher fluorescent dye. Any laser-induced emission from the reporter dye is quenched by the quenching dye when the two dyes are located close together as they are on the probe. During the amplification reaction, the Taq DNA polymerase enzyme cleaves the probe in a template-dependent manner. The resultant probe fragments disassociate in solution, and signal from the released reporter dye is free from the quenching effect of the second fluorophore. One molecule of reporter dye is liberated for each new molecule synthesized, and  
5 detection of the unquenched reporter dye provides the basis for quantitative interpretation of the data.

The 5' nuclease procedure is run on a real-time quantitative PCR device such as the ABI Prism 7700™ Sequence Detection. The system consists of a thermocycler, laser, charge-coupled device (CCD) camera and computer. The system amplifies samples in a 96-well format on a thermocycler. During amplification, laser-induced fluorescent signal is collected in real-time through fiber optics cables for all 96 wells, and detected  
10 at the CCD. The system includes software for running the instrument and for analyzing the data.

5' Nuclease assay data are initially expressed as Ct, or the threshold cycle. This is defined as the cycle at which the reporter signal accumulates above the background level of fluorescence. The  $\Delta C_t$  values are used as quantitative measurement of the relative number of starting copies of a particular target sequence in a nucleic acid sample when comparing cancer DNA results to normal human DNA results.

15 Table 8 describes the stage, T stage and N stage of various primary tumors which were used to screen the PRO polypeptide compounds of the invention.

Table 8  
Primary Lung and Colon Tumor Profiles

	Primary Tumor Stage	Stage	Other Stage	Dukes Stage	T Stage	N Stage
5	Human lung tumor AdenoCa (SRCC724) [LT1]	IIA			T1	N1
	Human lung tumor SqCCa (SRCC725) [LT1a]	IIB			T3	N0
	Human lung tumor AdenoCa (SRCC726) [LT2]	IB			T2	N0
	Human lung tumor AdenoCa (SRCC727) [LT3]	IIIA			T1	N2
	Human lung tumor AdenoCa (SRCC728) [LT4]	IB			T2	N0
10	Human lung tumor SqCCa (SRCC729) [LT6]	IB			T2	N0
	Human lung tumor Aden/SqCCa (SRCC730) [LT7]	IA			T1	N0
	Human lung tumor AdenoCa (SRCC731) [LT9]	IB			T2	N0
	Human lung tumor SqCCa (SRCC732) [LT10]	IIB			T2	N1
	Human lung tumor SqCCa (SRCC733) [LT11]	IIA			T1	N1
15	Human lung tumor AdenoCa (SRCC734) [LT12]	IV			T2	N0
	Human lung tumor AdenoSqCCa (SRCC735) [LT13]	IB			T2	N0
	Human lung tumor SqCCa (SRCC736) [LT15]	IB			T2	N0
	Human lung tumor SqCCa (SRCC737) [LT16]	IB			T2	N0
	Human lung tumor SqCCa (SRCC738) [LT17]	IIB			T2	N1
20	Human lung tumor SqCCa (SRCC739) [LT18]	IB			T2	N0
	Human lung tumor SqCCa (SRCC740) [LT19]	IB			T2	N0
	Human lung tumor LCCa (SRCC741) [LT21]	IIB			T3	N1
	Human lung AdenoCa (SRCC811) [LT22]	IA			T1	N0
	Human colon AdenoCa (SRCC742) [CT2]		M1	D	pT4	N0
25	Human colon AdenoCa (SRCC743) [CT3]			B	pT3	N0
	Human colon AdenoCa (SRCC744) [CT8]			B	T3	N0
	Human colon AdenoCa (SRCC745) [CT10]			A	pT2	N0
	Human colon AdenoCa (SRCC746) [CT12]		MO, R1	B	T3	N0
	Human colon AdenoCa (SRCC747) [CT14]		pMO, RO	B	pT3	pN0
30	Human colon AdenoCa (SRCC748) [CT15]		M1, R2	D	T4	N2
	Human colon AdenoCa (SRCC749) [CT16]		pMO	B	pT3	pN0
	Human colon AdenoCa (SRCC750) [CT17]			C1	pT3	pN1
	Human colon AdenoCa (SRCC751) [CT1]		MO, R1	B	pT3	N0
	Human colon AdenoCa (SRCC752) [CT4]			B	pT3	M0
35	Human colon AdenoCa (SRCC753) [CT5]		G2	C1	pT3	pN0
	Human colon AdenoCa (SRCC754) [CT6]		pMO, RO	B	pT3	pN0
	Human colon AdenoCa (SRCC755) [CT7]		G1	A	pT2	pN0
	Human colon AdenoCa (SRCC756) [CT9]		G3	D	pT4	pN2
	Human colon AdenoCa (SRCC757) [CT11]			B	T3	N0
40	Human colon AdenoCa (SRCC758) [CT18]		MO, RO	B	pT3	pN0

#### DNA Preparation:

DNA was prepared from cultured cell lines, primary tumors, normal human blood. The isolation was performed using purification kit, buffer set and protease and all from Quiagen, according to the manufacturer's instructions and the description below.

#### 45 Cell culture lysis:

Cells were washed and trypsinized at a concentration of  $7.5 \times 10^8$  per tip and pelleted by centrifuging at 1000 rpm for 5 minutes at 4°C, followed by washing again with 1/2 volume of PBS recentrifugation. The pellets were washed a third time, the suspended cells collected and washed 2x with PBS. The cells were then suspended into 10 ml PBS. Buffer C1 was equilibrated at 4°C. Qiagen protease #19155 was diluted into 6.25 ml cold ddH<sub>2</sub>O to a final concentration of 20 mg/ml and equilibrated at 4°C. 10 ml of G2 Buffer was prepared by diluting Qiagen RNase A stock (100 mg/ml) to a final concentration of 200 µg/ml.

Buffer C1 (10 ml, 4°C) and ddH<sub>2</sub>O (40 ml, 4°C) were then added to the 10 ml of cell suspension, mixed by inverting and incubated on ice for 10 minutes. The cell nuclei were pelleted by centrifuging in a Beckman swinging bucket rotor at 2500 rpm at 4°C for 15 minutes. The supernatant was discarded and the nuclei were suspended with a vortex into 2 ml Buffer C1 (at 4°C) and 6 ml ddH<sub>2</sub>O, followed by a second 4°C centrifugation at 2500 rpm for 15 minutes. The nuclei were then resuspended into the residual buffer using 200  $\mu$ l per tip.

5 G2 buffer (10 ml) was added to the suspended nuclei while gentle vortexing was applied. Upon completion of buffer addition, vigorous vortexing was applied for 30 seconds. Quiagen protease (200  $\mu$ l, prepared as indicated above) was added and incubated at 50°C for 60 minutes. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*, incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

*Solid human tumor sample preparation and lysis:*

10 Tumor samples were weighed and placed into 50 ml conical tubes and held on ice. Processing was limited to no more than 250 mg tissue per preparation (1 tip/preparation). The protease solution was freshly prepared by diluting into 6.25 ml cold ddH<sub>2</sub>O to a final concentration of 20 mg/ml and stored at 4°C. G2 buffer (20 ml) was prepared by diluting DNase A to a final concentration of 200 mg/ml (from 100 mg/ml stock). The tumor tissue was homogenated in 19 ml G2 buffer for 60 seconds using the large tip of the polytron in a laminar-flow TC hood in order to avoid inhalation of aerosols, and held at room temperature. Between samples, the polytron was cleaned by spinning at 2 x 30 seconds each in 2L ddH<sub>2</sub>O, followed by G2 buffer (50 ml). If tissue was still present on the generator tip, the apparatus was disassembled and cleaned.

15

Quiagen protease (prepared as indicated above, 1.0 ml) was added, followed by vortexing and incubation at 50°C for 3 hours. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*, incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

20

*Human blood preparation and lysis:*

Blood was drawn from healthy volunteers using standard infectious agent protocols and citrated into 10 ml samples per tip. Quiagen protease was freshly prepared by dilution into 6.25 ml cold ddH<sub>2</sub>O to a final concentration of 20 mg/ml and stored at 4°C. G2 buffer was prepared by diluting RNase A to a final concentration of 200  $\mu$ g/ml from 100 mg/ml stock. The blood (10 ml) was placed into a 50 ml conical tube and 10 ml C1 buffer and 30 ml ddH<sub>2</sub>O (both previously equilibrated to 4°C) were added, and the components mixed by inverting and held on ice for 10 minutes. The nuclei were pelleted with a Beckman swinging bucket rotor at 2500 rpm, 4°C for 15 minutes and the supernatant discarded. With a vortex, the nuclei were suspended into 2 ml C1 buffer (4°C) and 6 ml ddH<sub>2</sub>O (4°C). Vortexing was repeated until the peller was white. The nuclei were then suspended into the residual buffer using a 200  $\mu$ l tip. G2 buffer (10 ml) were added to the suspended nuclei while gently vortexing, followed by vigorous vortexing for 30 seconds. Quiagen protease was added (200  $\mu$ l) and incubated at 50°C for 60 minutes. The incubation and centrifugation was repeated until the lysates were clear (*e.g.*, incubating additional 30-60 minutes, pelleting at 3000 x g for 10 min., 4°C).

25

30

*Purification of cleared lysates:*

35 (1) Isolation of genomic DNA:

Genomic DNA was equilibrated (1 sample per maxi tip preparation) with 10 ml QBT buffer. QF elution buffer was equilibrated at 50°C. The samples were vortexed for 30 seconds, then loaded onto equilibrated tips

and drained by gravity. The tips were washed with 2 x 15 ml QC buffer. The DNA was eluted into 30 ml silanized, autoclaved 30 ml Corex tubes with 15 ml QF buffer (50°C). Isopropanol (10.5 ml) was added to each sample, the tubes covered with parafin and mixed by repeated inversion until the DNA precipitated. Samples were pelleted by centrifugation in the SS-34 rotor at 15,000 rpm for 10 minutes at 4°C. The pellet location was marked, the supernatant discarded, and 10 ml 70% ethanol (4°C) was added. Samples were pelleted again by  
 5 centrifugation on the SS-34 rotor at 10,000 rpm for 10 minutes at 4°C. The pellet location was marked and the supernatant discarded. The tubes were then placed on their side in a drying rack and dried 10 minutes at 37°C, taking care not to overdry the samples.

After drying, the pellets were dissolved into 1.0 ml TE (pH 8.5) and placed at 50°C for 1-2 hours. Samples were held overnight at 4°C as dissolution continued. The DNA solution was then transferred to 1.5 ml  
 10 tubes with a 26 gauge needle on a tuberculin syringe. The transfer was repeated 5x in order to shear the DNA. Samples were then placed at 50°C for 1-2 hours.

(2) Quantitation of genomic DNA and preparation for gene amplification assay:

The DNA levels in each tube were quantified by standard  $A_{260}$ ,  $A_{280}$  spectrophotometry on a 1:20 dilution (5  $\mu$ l DNA + 95  $\mu$ l ddH<sub>2</sub>O) using the 0.1 ml quartz cuvetts in the Beckman DU640 spectrophotometer.  
 15  $A_{260}/A_{280}$  ratios were in the range of 1.8-1.9. Each DNA samples was then diluted further to approximately 200 ng/ml in TE (pH 8.5). If the original material was highly concentrated (about 700 ng/ $\mu$ l), the material was placed at 50°C for several hours until resuspended.

Fluorometric DNA quantitation was then performed on the diluted material (20-600 ng/ml) using the manufacturer's guidelines as modified below. This was accomplished by allowing a Hoeffer DyNA Quant 200  
 20 fluorometer to warm-up for about 15 minutes. The Hoechst dye working solution (#H33258, 10  $\mu$ l, prepared within 12 hours of use) was diluted into 100 ml 1 x TNE buffer. A 2 ml cuvette was filled with the fluorometer solution, placed into the machine, and the machine was zeroed. pGEM 3Zf(+) (2  $\mu$ l, lot #360851026) was added to 2 ml of fluorometer solution and calibrated at 200 units. An additional 2  $\mu$ l of pGEM 3Zf(+) DNA was then tested and the reading confirmed at 400 +/- 10 units. Each sample was then read at least in triplicate.  
 25 When 3 samples were found to be within 10% of each other, their average was taken and this value was used as the quantification value.

The fluorometrically determined concentration was then used to dilute each sample to 10 ng/ $\mu$ l in ddH<sub>2</sub>O. This was done simultaneously on all template samples for a single TaqMan plate assay, and with enough material to run 500-1000 assays. The samples were tested in triplicate with Taqman<sup>TM</sup> primers and probe both B-actin  
 30 and GAPDH on a single plate with normal human DNA and no-template controls. The diluted samples were used provided that the CT value of normal human DNA subtracted from test DNA was +/- 1 Ct. The diluted, lot-qualified genomic DNA was stored in 1.0 ml aliquots at -80°C. Aliquots which were subsequently to be used in the gene amplification assay were stored at 4°C. Each 1 ml aliquot is enough for 8-9 plates or 64 tests.

*Gene amplification assay:*

35 The PRO polypeptide compounds of the invention were screened in the following primary tumors and the resulting  $\Delta$ Ct values greater than or equal to 1.0 are reported in Table 9 below.



Table 9

 $\Delta$ Ct values in lung and colon primary tumor and cell line models

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT-1	1.60	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.60
LT-1a	1.24	1.04	---	---	---	---	1.70	---	1.785	---	1.33	1.22	1.16	1.94	---	---	---	1.24
LT2	---	---	---	---	1.39	---	---	---	---	---	---	---	---	---	---	---	---	---
LT3	1.51	1.74	---	---	---	1.31	1.95	---	2.38	1.03	1.11	1.77	1.10	2.55	---	---	---	1.51
						1.55	1.24							1.52				
						1.44												
LT4	2.26	---	---	---	1.00	---	1.46	---	---	---	---	---	---	---	1.24	---	---	2.26
LT6	1.56	1.16	---	---	---	1.00	2.07	---	2.80	---	1.07	1.15	1.81	2.10	---	---	---	1.56
														2.28				
LT7	2.45	1.44	---	---	---	1.09	---	---	1.12	---	---	1.44	---	1.06	---	---	---	2.45
						1.03												
LT9	1.24	---	---	1.19	---	1.04	1.10	---	2.74	1.39	1.62	---	1.99	2.56	---	---	---	1.24
						1.14				1.11				2.59				
LT10	---	1.20	---	1.06	1.69	1.18	1.96	---	3.52	1.29	1.46	1.48	2.00	2.63	---	---	---	---
						1.11	1.16			1.29				2.85				
LT11	2.26	---	1.34	1.02	---	1.46	1.79	1.03	1.54	1.84	1.45	1.90	1.20	1.36	---	---	---	2.26
	2.85					1.72			2.94			1.83		5.21				2.85
	2.25					1.27			1.41									2.25
	1.79					1.25												1.79
						1.06												

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT12	1.86	---	1.92	---	---	2.08	1.86	1.18	1.77	---	---	1.38	---	1.64	---	---	---	1.86
	4.32					1.87			3.02			1.62		5.01				4.32
	2.59					1.41			1.82									2.59
	1.55					1.50												1.55
LT13	1.98	1.05	---	1.23	---	1.39	2.53	1.33	1.55	---	1.18	1.33	1.33	1.03	---	---	7.03	1.98
	2.52					1.09	2.06		2.14			1.20		1.00				2.52
	2.38					1.03	1.31		2.03					4.54				2.38
														1.14				
LT15	1.40	---	---	1.14	---	1.67	2.56	1.28	2.23	---	1.47	1.45	1.04	1.35	---	---	2.71	1.40
	1.58					1.47	2.95		2.01			1.44		1.86				1.58
	2.69					1.09	1.31		2.50					4.97				2.69
						1.05								1.52				
LT16	1.22	1.22	1.63	1.09	---	1.32	---	1.33	2.98	---	---	1.07	---	4.23	1.00	---	5.48	1.22
	2.77					1.38			1.77					1.52				2.77
	1.75													1.17				1.75
LT17	4.58	1.07	1.75	1.46	---	1.66	1.12	1.21	2.90	1.04	1.42	1.24	1.35	1.40	---	---	---	4.58
	3.73					1.59	1.53		1.62			1.61	1.115	5.45				3.73
	5.55					1.21												5.55
						1.50												
LT18	---	---	---	1.07	---	---	---	---	3.28	---	---	---	---	5.31	1.61	---	---	---
									1.68									

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
LT19	1.03	--	1.90	1.33	--	1.59	2.08	--	2.54	--	1.60	1.38	1.62	1.59	--	--	--	1.03
	1.22					1.50	2.95		2.98			1.19		1.84				1.22
	1.26					1.03			1.21					4.84				1.26
LT21	1.86	--	1.15	1.27	--	1.19	--	--	3.14	--	--	1.22	--	5.15	--	--	--	1.86
	1.83					1.09												1.83
	3.21					1.06												3.21
LT22	1.61	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.61
CT2	1.61	--	--	--	--	1.36	2.21	2.4	3.72	--	--	2.10	1.46	2.67	--	--	--	1.61
	2.11					1.25	2.55		2.55					1.65				2.11
							1.90							1.48				
CT3	--	--	--	--	--	1.12	1.50	1.52	3.91	--	--	1.62	--	2.41	--	--	--	--
CT8									1.58					1.02				
	2.80	--	--	--	--	--	1.15	1.55	2.66	--	--	1.06	--	2.34	--	--	--	2.80
CT10							1.34											
	2.39	--	--	--	--	1.55	1.75	1.97	3.57	--	--	1.96	--	2.23	--	--	--	2.39
CT12							1.47		1.78					1.21				
	3.45	--	--	--	--	1.08	1.93	1.36	3.50	--	--	1.57	--	2.46	--	--	--	3.45
CT14							1.30		1.08									
	3.79	--	--	--	--	1.76	1.47	1.75	3.88	--	--	1.19	--	2.83	--	--	--	3.79
CT15							1.11		1.86									
	3.66	--	--	--	--	1.23	2.44	1.75	3.62	--	--	1.70	--	2.89	--	--	2.61	3.66
CT16							1.33											
	2.66	--	--	--	--	1.29	1.95	1.11	3.12	--	--	1.51	--	2.60	--	--	2.21	2.66
CT17	3.63	--	--	--	--	1.44	2.19	1.11	3.34	--	--	1.31	--	2.33	--	--	3.31	3.63

Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
CT1	--	--	--	--	--	--	--	1.09	--	--	--	1.08	--	1.00	--	--	--	--
CT4	1.18	--	--	--	--	1.17 1.07	--	1.16	1.11	--	--	1.63	--	1.13	--	--	--	1.18
CT5	1.25	--	--	--	--	1.12 1.16 2.11	1.59 1.35 2.11	1.95	2.21	--	--	1.50	--	1.84 2.05	--	--	--	1.25
CT6	1.27	--	--	--	--	--	--	--	1.12	--	--	1.38	--	1.24 1.36	--	--	--	1.27
CT7	--	--	--	--	--	--	--	1.14	--	--	--	1.50	--	--	--	--	--	--
CT9	--	--	--	--	--	--	1.28	--	1.29	--	--	--	--	--	--	--	--	--
CT11	--	--	--	--	--	1.74 1.17	1.49	1.88	1.48	--	--	1.99	--	2.11 2.13	--	--	--	--
CT18	--	--	--	--	--	1.36	--	--	--	--	--	1.15	--	9.66	--	--	--	--
Calu-1	1.35 2.95	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.77	1.35 2.95
H441	2.00	--	--	--	--	--	--	1.71	--	--	--	--	--	--	--	--	2.57	2.00
H522	--	--	--	--	--	--	--	1.03	--	--	--	--	--	--	--	--	3.78	--
H810	2.76	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.84	2.76
HT29	1.31	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.71	1.31
SW403	2.08	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	2.09	2.08
LS174T	1.61	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	2.90	1.61
HCT15	1.22	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.46	1.22
HCC2998	1.73	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1.20	1.73



Tumor or Cell Line	PRO 213-1	PRO 237	PRO 324	PRO 351	PRO 362	PRO 615	PRO 531	PRO 853	PRO 1017	PRO 618	PRO 772	PRO 703	PRO 792	PRO 474	PRO 274	PRO 381	PRO 717	PRO1330 and PRO1449
HF- 000643	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	4.83	---	---
HF- 000840	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.08	---	---
HF- 000811	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.09 3.15	---	---
HF- 001294	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.14 1.08	---	---
HF- 001296	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	3.18 3.53	---	---
HF- 001291	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.17	---	---
A549	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.66	---
H460	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.50	---
SKMES1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.15	---
SW620	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	2.36	---
Colo320	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.99 2.73	---
HCT116	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.90	---
SKCO1	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	3.13	---
Colo205	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.48	---
KM12	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	1.67	---

Summary

Because amplification of the various DNA's as described above occurs in various tumors, it is likely associated with tumor formation and/or growth. As a result, antagonists (*e.g.*, antibodies) directed against these polypeptides would be expected to be useful in cancer therapy.

5 EXAMPLE 115: Induction of c-fos in Endothelial Cells (Assay 34)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in endothelial cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO  
10 polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50% Ham's F12 w/o GHT: low glucose, and 50% DMEM without glycine: with NaHCO<sub>3</sub>, 1% glutamine, 10 mM HEPES, 10% FBS, 10 ng/ml bFGF) were plated on 96-well microtiter plates at a cell density of  $1 \times 10^4$  cells/well. The  
15 day after plating, the cells were starved by removing the growth media and treating the cells with 100  $\mu$ l/well test samples and controls (positive control = growth media; negative control = Protein 32 buffer = 10 mM HEPES, 140 mM NaCl, 4% (w/v) mannitol, pH 6.8). The cells were incubated for 30 minutes at 37°C, in 5% CO<sub>2</sub>. The samples were removed, and the first part of the bDNA kit protocol (Chiron Diagnostics, cat. #6005-037) was followed, where each capitalized reagent/buffer listed below was available from the kit.

20 Briefly, the amounts of the TM Lysis Buffer and Probes needed for the tests were calculated based on information provided by the manufacturer. The appropriate amounts of thawed Probes were added to the TM Lysis Buffer. The Capture Hybridization Buffer was warmed to room temperature. The bDNA strips were set up in the metal strip holders, and 100  $\mu$ l of Capture Hybridization Buffer was added to each b-DNA well needed, followed by incubation for at least 30 minutes. The test plates with the cells were removed from the incubator,  
25 and the media was gently removed using the vacuum manifold. 100  $\mu$ l of Lysis Hybridization Buffer with Probes were quickly pipetted into each well of the microtiter plates. The plates were then incubated at 55°C for 15 minutes. Upon removal from the incubator, the plates were placed on the vortex mixer with the microtiter adapter head and vortexed on the #2 setting for one minute. 80  $\mu$ l of the lysate was removed and added to the bDNA wells containing the Capture Hybridization Buffer, and pipetted up and down to mix. The plates were  
30 incubated at 53°C for at least 16 hours.

On the next day, the second part of the bDNA kit protocol was followed. Specifically, the plates were removed from the incubator and placed on the bench to cool for 10 minutes. The volumes of additions needed were calculated based upon information provided by the manufacturer. An Amplifier Working Solution was prepared by making a 1:100 dilution of the Amplifier Concentrate (20 fm/ $\mu$ l) in AL Hybridization Buffer. The  
35 hybridization mixture was removed from the plates and washed twice with Wash A. 50  $\mu$ l of Amplifier Working Solution was added to each well and the wells were incubated at 53°C for 30 minutes. The plates were then removed from the incubator and allowed to cool for 10 minutes. The Label Probe Working Solution was

prepared by making a 1:100 dilution of Label Concentrate (40 pmoles/ $\mu$ l) in AL Hybridization Buffer. After the 10-minute cool-down period, the amplifier hybridization mixture was removed and the plates were washed twice with Wash A. 50  $\mu$ l of Label Probe Working Solution was added to each well and the wells were incubated at 53°C for 15 minutes. After cooling for 10 minutes, the Substrate was warmed to room temperature. Upon addition of 3  $\mu$ l of Substrate Enhancer to each ml of Substrate needed for the assay, the plates were  
5 allowed to cool for 10 minutes, the label hybridization mixture was removed, and the plates were washed twice with Wash A and three times with Wash D. 50  $\mu$ l of the Substrate Solution with Enhancer was added to each well. The plates were incubated for 30 minutes at 37°C and RLU was read in an appropriate luminometer.

The replicates were averaged and the coefficient of variation was determined. The measure of activity of the fold increase over the negative control (Protein 32/HEPES buffer described above) value was indicated  
10 by chemiluminescence units (RLU). The results are considered positive if the PRO polypeptide exhibits at least a two-fold value over the negative buffer control. Negative control = 1.00 RLU at 1.00% dilution. Positive control = 8.39 RLU at 1.00% dilution.

The following PRO polypeptides tested positive in this assay: PRO938, PRO200, PRO865, PRO788 and PRO1013.

15

EXAMPLE 116: Proliferation of Rat Utricular Supporting Cells (Assay 54)

This assay shows that certain polypeptides of the invention act as potent mitogens for inner ear supporting cells which are auditory hair cell progenitors and, therefore, are useful for inducing the regeneration of auditory hair cells and treating hearing loss in mammals. The assay is performed as follows. Rat UEC-4  
20 utricular epithelial cells are aliquoted into 96 well plates with a density of 3000 cells/well in 200  $\mu$ l of serum-containing medium at 33°C. The cells are cultured overnight and are then switched to serum-free medium at 37°C. Various dilutions of PRO polypeptides (or nothing for a control) are then added to the cultures and the cells are incubated for 24 hours. After the 24 hour incubation, <sup>3</sup>H-thymidine (1  $\mu$ Ci/well) is added and the cells are then cultured for an additional 24 hours. The cultures are then washed to remove unincorporated radiolabel,  
25 the cells harvested and Cpm per well determined. Cpm of at least 30% or greater in the PRO polypeptide treated cultures as compared to the control cultures is considered a positive in the assay.

The following polypeptide tested positive in this assay: PRO337, PRO363 and PRO1012.

EXAMPLE 117: Detection of PRO Polypeptides That Affect Glucose or FFA Uptake by Primary Rat Adipocytes (Assay 94)

30

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by adipocyte cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by adipocytes would be beneficial including, for example, obesity, diabetes or hyper- or hypo-insulinemia.

35

In a 96 well format, PRO polypeptides to be assayed are added to primary rat adipocytes, and allowed to incubate overnight. Samples are taken at 4 and 16 hours and assayed for glycerol, glucose and FFA uptake. After the 16 hour incubation, insulin is added to the media and allowed to incubate for 4 hours. At this time, a

sample is taken and glycerol, glucose and FFA uptake is measured. Media containing insulin without the PRO polypeptide is used as a positive reference control. As the PRO polypeptide being tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as stimulators of glucose and/or FFA uptake in this assay: PRO181, PRO200, PRO337, PRO362, PRO363, PRO731, PRO534, PRO1114 and PRO1075.

The following PRO polypeptides tested positive as inhibitors of glucose and/or FFA uptake in this assay: PRO195, PRO322, PRO862, PRO868, PRO865 and PRO162.

10 EXAMPLE 118: Detection of Polypeptides That Affect Glucose and/or FFA Uptake in Skeletal Muscle (Assay 106)

This assay is designed to determine whether PRO polypeptides show the ability to affect glucose or FFA uptake by skeletal muscle cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of disorders where either the stimulation or inhibition of glucose uptake by skeletal muscle would be beneficial including, for example, diabetes or hyper- or hypo-insulinemia.

15 In a 96 well format, PRO polypeptides to be assayed are added to primary rat differentiated skeletal muscle, and allowed to incubate overnight. Then fresh media with the PRO polypeptide and +/- insulin are added to the wells. The sample media is then monitored to determine glucose and FFA uptake by the skeletal muscle cells. The insulin will stimulate glucose and FFA uptake by the skeletal muscle, and insulin in media without the PRO polypeptide is used as a positive control, and a limit for scoring. As the PRO polypeptide being  
20 tested may either stimulate or inhibit glucose and FFA uptake, results are scored as positive in the assay if greater than 1.5 times or less than 0.5 times the insulin control.

The following PRO polypeptides tested positive as either stimulators or inhibitors of glucose and/or FFA uptake in this assay: PRO181, PRO200, PRO1083, PRO865, PRO162, PRO1008 and PRO1330.

25 EXAMPLE 119: Stimulation of Heart Neonatal Hypertrophy (Assay 1)

This assay is designed to measure the ability of PRO polypeptides to stimulate hypertrophy of neonatal heart. PRO polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of various cardiac insufficiency disorders.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells (180  $\mu$ l at  $7.5 \times 10^4$ /ml, serum <0.1%, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO polypeptide or growth medium only (negative control) (20  $\mu$ l/well) are added directly to the wells on day 1. PGF (20  $\mu$ l/well) is then added on day 2 at final concentration of  $10^{-6}$  M. The cells are then stained on day 4 and visually scored on day 5, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as  
35 compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. A positive result in the assay is a score of 1.0 or greater.

The following polypeptides tested positive in this assay: PRO195, PRO200, PRO526 and PRO792.



EXAMPLE 120: Enhancement of Heart Neonatal Hypertrophy Induced by F2a (Assay 37)

This assay is designed to measure the ability of PRO polypeptides to stimulate hypertrophy of neonatal heart. PRO polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of various cardiac insufficiency disorders.

Cardiac myocytes from 1-day old Harlan Sprague Dawley rats were obtained. Cells (180  $\mu$ l at  $7.5 \times 10^4$ /ml, serum <0.1%, freshly isolated) are added on day 1 to 96-well plates previously coated with DMEM/F12 + 4% FCS. Test samples containing the test PRO polypeptide (20  $\mu$ l/well) are added directly to the wells on day 1. PGF (20  $\mu$ l/well) is then added on day 2 at a final concentration of  $10^{-6}$  M. The cells are then stained on day 4 and visually scored on day 5. Visual scores are based on cell size, wherein cells showing no increase in size as compared to negative controls are scored 0.0, cells showing a small to moderate increase in size as compared to negative controls are scored 1.0 and cells showing a large increase in size as compared to negative controls are scored 2.0. A score of 1.0 or greater is considered positive.

No PBS is included, since calcium concentration is critical for assay response. Plates are coated with DMEM/F12 plus 4% FCS (200  $\mu$ l/well). Assay media included: DMEM/F12 (with 2.44 gm bicarbonate), 10  $\mu$ g/ml transferrin, 1  $\mu$ g/ml insulin, 1  $\mu$ g/ml aprotinin, 2 mmol/L glutamine, 100 U/ml penicillin G, 100  $\mu$ g/ml streptomycin. Protein buffer containing mannitol (4%) gave a positive signal (score 3.5) at 1/10 (0.4%) and 1/100 (0.04%), but not at 1/1000 (0.004%). Therefore the test sample buffer containing mannitol is not run.

The following PRO polypeptides tested positive in this assay: PRO195.

EXAMPLE 121: Guinea Pig Vascular Leak (Assays 32 and 51)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce vascular permeability. Polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of conditions which would benefit from enhanced vascular permeability including, for example, conditions which may benefit from enhanced local immune system cell infiltration.

Hairless guinea pigs weighing 350 grams or more were anesthetized with Ketamine (75-80 mg/kg) and 5 mg/kg Xylazine intramuscularly. Test samples containing the PRO polypeptide or a physiological buffer without the test polypeptide are injected into skin on the back of the test animals with 100  $\mu$ l per injection site intradermally. There were approximately 16-24 injection sites per animal. One ml of Evans blue dye (1% in PBS) is then injected intracardially. Skin vascular permeability responses to the compounds (*i.e.*, blemishes at the injection sites of injection) are visually scored by measuring the diameter (in mm) of blue-colored leaks from the site of injection at 1 and 6 hours post administration of the test materials. The mm diameter of blueness at the site of injection is observed and recorded as well as the severity of the vascular leakage. Blemishes of at least 5 mm in diameter are considered positive for the assay when testing purified proteins, being indicative of the ability to induce vascular leakage or permeability. A response greater than 7 mm diameter is considered positive for conditioned media samples. Human VEGF at 0.1  $\mu$ g/100  $\mu$ l is used as a positive control, inducing a response of 15-23 mm diameter.

The following PRO polypeptides tested positive in this assay: PRO200.



EXAMPLE 122: Skin Vascular Permeability Assay (Assay 64)

This assay shows that certain polypeptides of the invention stimulate an immune response and induce inflammation by inducing mononuclear cell, eosinophil and PMN infiltration at the site of injection of the animal. Compounds which stimulate an immune response are useful therapeutically where stimulation of an immune response is beneficial. This skin vascular permeability assay is conducted as follows. Hairless guinea pigs weighing 350 grams or more are anesthetized with ketamine (75-80 mg/Kg) and 5 mg/Kg xylazine intramuscularly (IM). A sample of purified polypeptide of the invention or a conditioned media test sample is injected intradermally onto the backs of the test animals with 100  $\mu$ l per injection site. It is possible to have about 10-30, preferably about 16-24, injection sites per animal. One  $\mu$ l of Evans blue dye (1% in physiologic buffered saline) is injected intracardially. Blemishes at the injection sites are then measured (mm diameter) at 1 hr and 6 hr post injection. Animals were sacrificed at 6 hrs after injection. Each skin injection site is biopsied and fixed in formalin. The skins are then prepared for histopathologic evaluation. Each site is evaluated for inflammatory cell infiltration into the skin. Sites with visible inflammatory cell inflammation are scored as positive. Inflammatory cells may be neutrophilic, eosinophilic, monocytic or lymphocytic. At least a minimal perivascular infiltrate at the injection site is scored as positive, no infiltrate at the site of injection is scored as negative.

The following polypeptide tested positive in this assay: PRO200, PRO362 and PRO1031.

EXAMPLE 123: Induction of c-fos in Cortical Neurons (Assay 83)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in cortical neurons. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of nervous system disorders and injuries where neuronal proliferation would be beneficial.

Cortical neurons are dissociated and plated in growth medium at 10,000 cells per well in 96 well plates. After approximately 2 cellular divisions, the cells are treated for 30 minutes with the PRO polypeptide or nothing (negative control). The cells are then fixed for 5 minutes with cold methanol and stained with an antibody directed against phosphorylated CREB. mRNA levels are then calculated using chemiluminescence. A positive in the assay is any factor that results in at least a 2-fold increase in c-fos message as compared to the negative controls.

The following PRO polypeptides tested positive in this assay: PRO200.

EXAMPLE 124: Mouse Kidney Mesangial Cell Proliferation Assay (Assay 92)

This assay shows that certain polypeptides of the invention act to induce proliferation of mammalian kidney mesangial cells and, therefore, are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with Schönlein-Henoch purpura, celiac disease, dermatitis herpetiformis or Crohn disease. The assay is performed as follows. On day one, mouse kidney mesangial cells are plated on a 96 well plate in growth media (3:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium, 95% fetal bovine serum, 5% supplemented with 14 mM HEPES) and grown overnight. On day 2, PRO polypeptides are diluted at 2 concentrations (1% and 0.1%) in serum-free

medium and added to the cells. Control samples are serum-free medium alone. On day 4, 20 $\mu$ l of the Cell Titer 96 Aqueous one solution reagent (Progenia) was added to each well and the colorimetric reaction was allowed to proceed for 2 hours. The absorbance (OD) is then measured at 490 nm. A positive in the assay is anything that gives an absorbance reading which is at least 15% above the control reading.

The following polypeptide tested positive in this assay: PRO200, PRO363, PRO731, PRO534, PRO866  
5 and PRO1031.

EXAMPLE 125: Pericyte c-Fos Induction (Assay 93)

This assay shows that certain polypeptides of the invention act to induce the expression of c-fos in pericyte cells and, therefore, are useful not only as diagnostic markers for particular types of pericyte-associated  
10 tumors but also for giving rise to antagonists which would be expected to be useful for the therapeutic treatment of pericyte-associated tumors. Specifically, on day 1, pericytes are received from VEC Technologies and all but 5 ml of media is removed from flask. On day 2, the pericytes are trypsinized, washed, spun and then plated onto 96 well plates. On day 7, the media is removed and the pericytes are treated with 100  $\mu$ l of PRO  
15 polypeptide test samples and controls (positive control = DME+5% serum +/- PDGF at 500 ng/ml; negative control = protein 32). Replicates are averaged and SD/CV are determined. Fold increase over Protein 32 (buffer control) value indicated by chemiluminescence units (RLU) luminometer reading verses frequency is plotted on a histogram. Two-fold above Protein 32 value is considered positive for the assay. ASY Matrix: Growth media = low glucose DMEM = 20% FBS + 1X pen strep + 1X fungizone. Assay Media = low glucose DMEM +5% FBS.

20 The following polypeptides tested positive in this assay: PRO200.

EXAMPLE 126: Chondrocyte Re-differentiation Assay (Assay 110)

This assay shows that certain polypeptides of the invention act to induce redifferentiation of chondrocytes, therefore, are expected to be useful for the treatment of various bone and/or cartilage disorders  
25 such as, for example, sports injuries and arthritis. The assay is performed as follows. Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of metacarpophalangeal joints of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4  $\mu$ g/ml gentamycin. The culture media is changed every third day and the cells are then seeded in 96 well plates at 5,000 cells/well in 100 $\mu$ l of the same media without serum and 100  $\mu$ l of the test PRO polypeptide, 5  
30 nM staurosporin (positive control) or medium alone (negative control) is added to give a final volume of 200  $\mu$ l/well. After 5 days of incubation at 37°C, a picture of each well is taken and the differentiation state of the chondrocytes is determined. A positive result in the assay occurs when the redifferentiation of the chondrocytes is determined to be more similar to the positive control than the negative control.

The following polypeptide tested positive in this assay: PRO200, PRO285, PRO337, PRO526, PRO362,  
35 PRO363, PRO531, PRO1083, PRO862, PRO733, PRO1017, PRO792, PRO788, PRO1008, PRO1075, PRO725 and PRO1031.

EXAMPLE 127: Fetal Hemoglobin Induction in an Erythroblastic Cell Line (Assay 107)

This assay is useful for screening PRO polypeptides for the ability to induce the switch from adult hemoglobin to fetal hemoglobin in an erythroblastic cell line. Molecules testing positive in this assay are expected to be useful for therapeutically treating various mammalian hemoglobin-associated disorders such as the various thalassemias. The assay is performed as follows. Erythroblastic cells are plated in standard growth medium at 1000 cells/well in a 96 well format. PRO polypeptides are added to the growth medium at a concentration of 0.2% or 2% and the cells are incubated for 5 days at 37°C. As a positive control, cells are treated with 100µM hemin and as a negative control, the cells are untreated. After 5 days, cell lysates are prepared and analyzed for the expression of gamma globin (a fetal marker). A positive in the assay is a gamma globin level at least 2-fold above the negative control.

The following polypeptides tested positive in this assay: PRO237, PRO381, PRO362, PRO724, PRO866, PRO1114, PRO725 and PRO1071.

EXAMPLE 128: Induction of Pancreatic β-Cell Precursor Proliferation (Assay 117)

This assay shows that certain polypeptides of the invention act to induce an increase in the number of pancreatic β-cell precursor cells and, therefore, are useful for treating various insulin deficient states in mammals, including diabetes mellitus. The assay is performed as follows. The assay uses a primary culture of mouse fetal pancreatic cells and the primary readout is an alteration in the expression of markers that represent either β-cell precursors or mature β-cells. Marker expression is measured by real time quantitative PCR (RTQ-PCR); wherein the marker being evaluated is a transcription factor called Pdx1.

The pancreata are dissected from E14 embryos (CD1 mice). The pancreata are then digested with collagenase/dispase in F12/DMEM at 37°C for 40 to 60 minutes (collagenase/dispase, 1.37 mg/ml, Boehringer Mannheim, #1097113). The digestion is then neutralized with an equal volume of 5% BSA and the cells are washed once with RPMI1640. At day 1, the cells are seeded into 12-well tissue culture plates (pre-coated with laminin, 20µg/ml in PBS, Boehringer Mannheim, #124317). Cells from pancreata from 1-2 embryos are distributed per well. The culture medium for this primary culture is 14F/1640. At day 2, the media is removed and the attached cells washed with RPMI/1640. Two mls of minimal media are added in addition to the protein to be tested. At day 4, the media is removed and RNA prepared from the cells and marker expression analyzed by real time quantitative RT-PCR. A protein is considered to be active in the assay if it increases the expression of the relevant β-cell marker as compared to untreated controls.

14F/1640 is RPMI1640 (Gibco) plus the following:

group A 1:1000

group B 1:1000

recombinant human insulin 10 µg/ml

Aprotinin (50µg/ml) 1:2000 (Boehringer manheim #981532)

Bovine pituitary extract (BPE) 60µg/ml

Gentamycin 100 ng/ml

Group A : (in 10ml PBS)

Transferrin, 100mg (Sigma T2252)

Epidermal Growth Factor, 100 $\mu$ g (BRL 100004)

Triiodothyronine, 10 $\mu$ l of 5x10<sup>-6</sup> M (Sigma T5516)

Ethanolamine, 100 $\mu$ l of 10<sup>-1</sup> M (Sigma E0135)

5 Phosphoethalamine, 100 $\mu$ l of 10<sup>-1</sup> M (Sigma P0503)

Selenium, 4 $\mu$ l of 10<sup>-1</sup> M (Aesar #12574)

Group C : (in 10ml 100% ethanol)

Hydrocortisone, 2 $\mu$ l of 5X10<sup>-3</sup> M (Sigma #H0135)

Progesterone, 100 $\mu$ l of 1X10<sup>-3</sup> M (Sigma #P6149)

10 Forskolin, 500 $\mu$ l of 20mM (Calbiochem #344270)

Minimal media:

RPMI 1640 plus transferrin (10  $\mu$ g/ml), insulin (1  $\mu$ g/ml), gentamycin (100ng/ml), aprotinin (50  $\mu$ g/ml) and BPE (15  $\mu$ g/ml).

Defined media:

15 RPMI 1640 plus transferrin (10  $\mu$ g/ml), insulin (1  $\mu$ g/ml), gentamycin (100 ng/ml) and aprotinin (50  $\mu$ g/ml).

The following polypeptides tested positive in this assay: PRO237 and PRO731.

EXAMPLE 129: Stimulatory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 24)

20 This example shows that certain polypeptides of the invention are active as a stimulator of the proliferation of stimulated T-lymphocytes. Compounds which stimulate proliferation of lymphocytes are useful therapeutically where enhancement of an immune response is beneficial. A therapeutic agent may take the form of antagonists of the polypeptide of the invention, for example, murine-human chimeric, humanized or human antibodies against the polypeptide.

25 The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

30 More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO<sub>2</sub>) and then washed and resuspended to 3x10<sup>6</sup> cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

35 The assay is prepared by plating in triplicate wells a mixture of:

100:1 of test sample diluted to 1% or to 0.1%,

50 :1 of irradiated stimulator cells, and



50 :1 of responder PBMC cells.

100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO<sub>2</sub> for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mC/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice.

5 The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to 1x10<sup>7</sup> cells/ml of assay media. The assay is then conducted as described above.

10 Positive increases over control are considered positive with increases of greater than or equal to 180% being preferred. However, any value greater than control indicates a stimulatory effect for the test protein.

The following PRO polypeptides tested positive in this assay: PRO273, PRO526, PRO381, PRO719, PRO866 and PRO1031.

15 EXAMPLE 130: Inhibitory Activity in Mixed Lymphocyte Reaction (MLR) Assay (Assay 67)

This example shows that one or more of the polypeptides of the invention are active as inhibitors of the proliferation of stimulated T-lymphocytes. Compounds which inhibit proliferation of lymphocytes are useful therapeutically where suppression of an immune response is beneficial.

20 The basic protocol for this assay is described in Current Protocols in Immunology, unit 3.12; edited by J E Coligan, A M Kruisbeek, D H Marglies, E M Shevach, W Strober, National Institutes of Health, Published by John Wiley & Sons, Inc.

25 More specifically, in one assay variant, peripheral blood mononuclear cells (PBMC) are isolated from mammalian individuals, for example a human volunteer, by leukopheresis (one donor will supply stimulator PBMCs, the other donor will supply responder PBMCs). If desired, the cells are frozen in fetal bovine serum and DMSO after isolation. Frozen cells may be thawed overnight in assay media (37°C, 5% CO<sub>2</sub>) and then washed and resuspended to 3x10<sup>6</sup> cells/ml of assay media (RPMI; 10% fetal bovine serum, 1% penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate). The stimulator PBMCs are prepared by irradiating the cells (about 3000 Rads).

The assay is prepared by plating in triplicate wells a mixture of:

30 100:1 of test sample diluted to 1% or to 0.1%,  
50 :1 of irradiated stimulator cells, and  
50 :1 of responder PBMC cells.

35 100 microliters of cell culture media or 100 microliter of CD4-IgG is used as the control. The wells are then incubated at 37°C, 5% CO<sub>2</sub> for 4 days. On day 5, each well is pulsed with tritiated thymidine (1.0 mC/well; Amersham). After 6 hours the cells are washed 3 times and then the uptake of the label is evaluated.

In another variant of this assay, PBMCs are isolated from the spleens of Balb/c mice and C57B6 mice. The cells are teased from freshly harvested spleens in assay media (RPMI; 10% fetal bovine serum, 1%



penicillin/streptomycin, 1% glutamine, 1% HEPES, 1% non-essential amino acids, 1% pyruvate) and the PBMCs are isolated by overlaying these cells over Lympholyte M (Organon Teknika), centrifuging at 2000 rpm for 20 minutes, collecting and washing the mononuclear cell layer in assay media and resuspending the cells to  $1 \times 10^7$  cells/ml of assay media. The assay is then conducted as described above.

Any decreases below control is considered to be a positive result for an inhibitory compound, with decreases of less than or equal to 80% being preferred. However, any value less than control indicates an inhibitory effect for the test protein.

The following polypeptide tested positive in this assay: PRO273, PRO526, PRO381, PRO701, PRO363, PRO531, PRO1083, PRO865, PRO788 and PRO1114.

10 EXAMPLE 131: Fibroblast (BHK-21) Proliferation (Assay 98)

This assay shows that certain PRO polypeptides of the invention act to induce proliferation of mammalian fibroblast cells in culture and, therefore, function as useful growth factors in mammalian systems. The assay is performed as follows. BHK-21 fibroblast cells plated in standard growth medium at 2500 cells/well in a total volume of 100  $\mu$ l. The PRO polypeptide,  $\beta$ -FGF (positive control) or nothing (negative control) are then added to the wells in the presence of 1  $\mu$ g/ml of heparin for a total final volume of 200  $\mu$ l. The cells are then incubated at 37°C for 6 to 7 days. After incubation, the media is removed, the cells are washed with PBS and then an acid phosphatase substrate reaction mixture (100  $\mu$ l/well) is added. The cells are then incubated at 37°C for 2 hours. 10  $\mu$ l per well of 1N NaOH is then added to stop the acid phosphatase reaction. The plates are then read at OD 405nm. A positive in the assay is acid phosphatase activity which is at least 50% above the negative control.

The following PRO polypeptide tested positive in this assay: PRO273 and PRO731.

EXAMPLE 132: Induction of Endothelial Cell Apoptosis (ELISA) (Assay 109)

The ability of PRO polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems) using a 96-well format, in 0% serum media supplemented with 100 ng/ml VEGF, 0.1% BSA, 1X penn/strep. A positive result in this assay indicates the usefulness of the polypeptide for therapeutically treating any of a variety of conditions associated with undesired endothelial cell growth including, for example, the inhibition of tumor growth. The 96-well plates used were manufactured by Falcon (No. 3072). Coating of 96 well plates were prepared by allowing gelatinization to occur for >30 minutes with 100  $\mu$ l of 0.2% gelatin in PBS solution. The gelatin mix was aspirated thoroughly before plating HUVEC cells at a final concentration of  $2 \times 10^4$  cells/ml in 10% serum containing medium - 100  $\mu$ l volume per well. The cells were grown for 24 hours before adding test samples containing the PRO polypeptide of interest.

To all wells, 100  $\mu$ l of 0% serum media (Cell Systems) complemented with 100 ng/ml VEGF, 0.1% BSA, 1X penn/strep was added. Test samples containing PRO polypeptides were added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only were used as a negative control. As a positive control, 1:3 serial dilutions of 50  $\mu$ l of a 3x stock of staurosporine were used.

The cells were incubated for 24 to 35 hours prior to ELISA.

ELISA was used to determine levels of apoptosis preparing solutions according to the Boehringer Manual [Boehringer, Cell Death Detection ELISA plus, Cat No. 1 920 685]. Sample preparations: 96 well plates were spun down at 1 krpm for 10 minutes (200g); the supernatant was removed by fast inversion, placing the plate upside down on a paper towel to remove residual liquid. To each well, 200  $\mu$ l of 1X Lysis buffer was added and incubation allowed at room temperature for 30 minutes without shaking. The plates were spun down for 10 minutes at 1 krpm, and 20  $\mu$ l of the lysate (cytoplasmic fraction) was transferred into streptavidin coated MTP. 80  $\mu$ l of immunoreagent mix was added to the 20  $\mu$ l lysate in each well. The MTP was covered with adhesive foil and incubated at room temperature for 2 hours by placing it on an orbital shaker (200 rpm). After two hours, the supernatant was removed by suction and the wells rinsed three times with 250  $\mu$ l of 1X incubation buffer per well (removed by suction). Substrate solution was added (100  $\mu$ l) into each well and incubated on an orbital shaker at room temperature at 250 rpm until color development was sufficient for a photometric analysis (approx. after 10-20 minutes). A 96 well reader was used to read the plates at 405 nm, reference wavelength, 492 nm. The levels obtained for PIN 32 (control buffer) was set to 100%. Samples with levels > 130% were considered positive for induction of apoptosis.

The following PRO polypeptides tested positive in this assay: PRO846.

#### EXAMPLE 133: Induction of Endothelial Cell Apoptosis (Assay 73)

The ability of PRO polypeptides to induce apoptosis in endothelial cells was tested in human venous umbilical vein endothelial cells (HUVEC, Cell Systems). A positive test in the assay is indicative of the usefulness of the polypeptide in therapeutically treating tumors as well as vascular disorders where inducing apoptosis of endothelial cells would be beneficial.

The cells were plated on 96-well microtiter plates (Amersham Life Science, cytostar-T scintillating microplate, RPNQ160, sterile, tissue-culture treated, individually wrapped), in 10% serum (CSG-medium, Cell Systems), at a density of  $2 \times 10^4$  cells per well in a total volume of 100  $\mu$ l. On day 2, test samples containing the PRO polypeptide were added in triplicate at dilutions of 1%, 0.33% and 0.11%. Wells without cells were used as a blank and wells with cells only were used as a negative control. As a positive control 1:3 serial dilutions of 50  $\mu$ l of a 3x stock of staurosporine were used. The ability of the PRO polypeptide to induce apoptosis was determined by processing of the 96 well plates for detection of Annexin V, a member of the calcium and phospholipid binding proteins, to detect apoptosis.

0.2 ml Annexin V - Biotin stock solution (100  $\mu$ g/ml) was diluted in 4.6 ml  $2 \times \text{Ca}^{2+}$  binding buffer and 2.5% BSA (1:25 dilution). 50  $\mu$ l of the diluted Annexin V - Biotin solution was added to each well (except controls) to a final concentration of 1.0  $\mu$ g/ml. The samples were incubated for 10-15 minutes with Annexin-Biotin prior to direct addition of  $^{35}\text{S}$ -Streptavidin.  $^{35}\text{S}$ -Streptavidin was diluted in  $2 \times \text{Ca}^{2+}$  Binding buffer, 2.5% BSA and was added to all wells at a final concentration of  $3 \times 10^4$  cpm/well. The plates were then sealed, centrifuged at 1000 rpm for 15 minutes and placed on orbital shaker for 2 hours. The analysis was performed on a 1450 Microbeta Trilux (Wallac). Percent above background represents the percentage amount of counts per minute above the negative controls. Percents greater than or equal to 30% above background are considered

positive.

The following PRO polypeptides tested positive in this assay: PRO719.

EXAMPLE 134: Human Venous Endothelial Cell Calcium Flux Assay (Assay 68)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to stimulate calcium flux in human umbilical vein endothelial cells (HUVEC, Cell Systems). Calcium influx is a well documented response upon binding of certain ligands to their receptors. A test compound that results in a positive response in the present calcium influx assay can be said to bind to a specific receptor and activate a biological signaling pathway in human endothelial cells. This could ultimately lead, for example, to endothelial cell division, inhibition of endothelial cell proliferation, endothelial tube formation, cell migration, apoptosis, etc.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50:50 without glycine, 1% glutamine, 10mM Hepes, 10% FBS, 10 ng/ml bFGF), were plated on 96-well microtiter ViewPlates-96 (Packard Instrument Company Part #6005182) microtiter plates at a cell density of  $2 \times 10^4$  cells/well. The day after plating, the cells were washed three times with buffer (HBSS plus 10 mM Hepes), leaving 100  $\mu$ l/well. Then 100  $\mu$ l/well of 8  $\mu$ M Fluo-3 (2x) was added. The cells were incubated for 1.5 hours at 37°C/5% CO<sub>2</sub>. After incubation, the cells were then washed 3x with buffer (described above) leaving 100  $\mu$ l/well. Test samples of the PRO polypeptides were prepared on different 96-well plates at 5x concentration in buffer. The positive control corresponded to 50  $\mu$ M ionomycin (5x); the negative control corresponded to Protein 32. Cell plate and sample plates were run on a FLIPR (Molecular Devices) machine. The FLIPR machine added 25  $\mu$ l of test sample to the cells, and readings were taken every second for one minute, then every 3 seconds for the next three minutes.

The fluorescence change from baseline to the maximum rise of the curve ( $\Delta$  change) was calculated, and replicates averaged. The rate of fluorescence increase was monitored, and only those samples which had a  $\Delta$  change greater than 1000 and a rise within 60 seconds, were considered positive.

The following PRO polypeptides tested positive in the present assay: PRO771.

EXAMPLE 135: Induction of c-fos in Endothelial Cells (Assay 34)

This assay is designed to determine whether PRO polypeptides show the ability to induce c-fos in endothelial cells. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Human venous umbilical vein endothelial cells (HUVEC, Cell Systems) in growth media (50% Ham's F12 w/o GHT: low glucose, and 50% DMEM without glycine: with NaHCO<sub>3</sub>, 1% glutamine, 10 mM HEPES, 10% FBS, 10 ng/ml bFGF) were plated on 96-well microtiter plates at a cell density of  $1 \times 10^4$  cells/well. The day after plating, the cells were starved by removing the growth media and treating the cells with 100  $\mu$ l/well

test samples and controls (positive control = growth media; negative control = Protein 32 buffer = 10 mM HEPES, 140 mM NaCl, 4% (w/v) mannitol, pH 6.8). The cells were incubated for 30 minutes at 37°C, in 5% CO<sub>2</sub>. The samples were removed, and the first part of the bDNA kit protocol (Chiron Diagnostics, cat. #6005-037) was followed, where each capitalized reagent/buffer listed below was available from the kit.

5 Briefly, the amounts of the TM Lysis Buffer and Probes needed for the tests were calculated based on information provided by the manufacturer. The appropriate amounts of thawed Probes were added to the TM Lysis Buffer. The Capture Hybridization Buffer was warmed to room temperature. The bDNA strips were set up in the metal strip holders, and 100 µl of Capture Hybridization Buffer was added to each b-DNA well needed, followed by incubation for at least 30 minutes. The test plates with the cells were removed from the incubator, and the media was gently removed using the vacuum manifold. 100 µl of Lysis Hybridization Buffer with  
10 Probes were quickly pipetted into each well of the microtiter plates. The plates were then incubated at 55°C for 15 minutes. Upon removal from the incubator, the plates were placed on the vortex mixer with the microtiter adapter head and vortexed on the #2 setting for one minute. 80 µl of the lysate was removed and added to the bDNA wells containing the Capture Hybridization Buffer, and pipetted up and down to mix. The plates were incubated at 53°C for at least 16 hours.

15 On the next day, the second part of the bDNA kit protocol was followed. Specifically, the plates were removed from the incubator and placed on the bench to cool for 10 minutes. The volumes of additions needed were calculated based upon information provided by the manufacturer. An Amplifier Working Solution was prepared by making a 1:100 dilution of the Amplifier Concentrate (20 fm/µl) in AL Hybridization Buffer. The hybridization mixture was removed from the plates and washed twice with Wash A. 50 µl of Amplifier Working  
20 Solution was added to each well and the wells were incubated at 53°C for 30 minutes. The plates were then removed from the incubator and allowed to cool for 10 minutes. The Label Probe Working Solution was prepared by making a 1:100 dilution of Label Concentrate (40 pmoles/µl) in AL Hybridization Buffer. After the 10-minute cool-down period, the amplifier hybridization mixture was removed and the plates were washed twice with Wash A. 50 µl of Label Probe Working Solution was added to each well and the wells were  
25 incubated at 53°C for 15 minutes. After cooling for 10 minutes, the Substrate was warmed to room temperature. Upon addition of 3 µl of Substrate Enhancer to each ml of Substrate needed for the assay, the plates were allowed to cool for 10 minutes, the label hybridization mixture was removed, and the plates were washed twice with Wash A and three times with Wash D. 50 µl of the Substrate Solution with Enhancer was added to each well. The plates were incubated for 30 minutes at 37°C and RLU was read in an appropriate luminometer.

30 The replicates were averaged and the coefficient of variation was determined. The measure of activity of the fold increase over the negative control (Protein 32/HEPES buffer described above) value was indicated by chemiluminescence units (RLU). The results are considered positive if the PRO polypeptide exhibits at least a two-fold value over the negative buffer control. Negative control = 1.00 RLU at 1.00% dilution. Positive control = 8.39 RLU at 1.00% dilution.

35 The following PRO polypeptides tested positive in this assay: PRO474.



EXAMPLE 136: Induction of Pancreatic  $\beta$ -Cell Precursor Differentiation (Assay 89)

This assay shows that certain polypeptides of the invention act to induce differentiation of pancreatic  $\beta$ -cell precursor cells into mature pancreatic  $\beta$ -cells and, therefore, are useful for treating various insulin deficient states in mammals, including diabetes mellitus. The assay is performed as follows. The assay uses a primary culture of mouse fetal pancreatic cells and the primary readout is an alteration in the expression of markers that represent either  $\beta$ -cell precursors or mature  $\beta$ -cells. Marker expression is measured by real time quantitative PCR (RTQ-PCR); wherein the marker being evaluated is insulin.

The pancreata are dissected from E14 embryos (CD1 mice). The pancreata are then digested with collagenase/dispase in F12/DMEM at 37°C for 40 to 60 minutes (collagenase/dispase, 1.37 mg/ml, Boehringer Mannheim, #1097113). The digestion is then neutralized with an equal volume of 5% BSA and the cells are washed once with RPMI1640. At day 1, the cells are seeded into 12-well tissue culture plates (pre-coated with laminin, 20 $\mu$ g/ml in PBS, Boehringer Mannheim, #124317). Cells from pancreata from 1-2 embryos are distributed per well. The culture medium for this primary culture is 14F/1640. At day 2, the media is removed and the attached cells washed with RPMI/1640. Two mls of minimal media are added in addition to the protein to be tested. At day 4, the media is removed and RNA prepared from the cells and marker expression analyzed by real time quantitative RT-PCR. A protein is considered to be active in the assay if it increases the expression of the relevant  $\beta$ -cell marker as compared to untreated controls.

14F/1640 is RPMI1640 (Gibco) plus the following:

group A 1:1000  
group B 1:1000  
recombinant human insulin 10  $\mu$ g/ml  
Aprotinin (50 $\mu$ g/ml) 1:2000 (Boehringer manheim #981532)  
Bovine pituitary extract (BPE) 60 $\mu$ g/ml  
Gentamycin 100 ng/ml

Group A : (in 10ml PBS)

Transferrin, 100mg (Sigma T2252)  
Epidermal Growth Factor, 100 $\mu$ g (BRL 100004)  
Triiodothyronine, 10 $\mu$ l of 5x10<sup>-6</sup> M (Sigma T5516)  
Ethanolamine, 100 $\mu$ l of 10<sup>-1</sup> M (Sigma E0135)  
Phosphoethalamine, 100 $\mu$ l of 10<sup>-1</sup> M (Sigma P0503)  
Selenium, 4 $\mu$ l of 10<sup>-1</sup> M (Aesar #12574)

Group C : (in 10ml 100% ethanol)

Hydrocortisone, 2 $\mu$ l of 5X10<sup>-3</sup> M (Sigma #H0135)  
Progesterone, 100 $\mu$ l of 1X10<sup>-3</sup> M (Sigma #P6149)  
Forskolin, 500 $\mu$ l of 20mM (Calbiochem #344270)

Minimal media:

RPMI 1640 plus transferrin (10  $\mu$ g/ml), insulin (1  $\mu$ g/ml), gentamycin (100 ng/ml), aprotinin (50  $\mu$ g/ml) and BPE (15  $\mu$ g/ml).



Defined media:

RPMI 1640 plus transferrin (10  $\mu\text{g/ml}$ ), insulin (1  $\mu\text{g/ml}$ ), gentamycin (100 ng/ml) and aprotinin (50  $\mu\text{g/ml}$ ).

The following polypeptides were positive in this assay: PRO788 and PRO162.

5 EXAMPLE 137: Stimulation of Endothelial Cell Proliferation (Assay 8)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to stimulate adrenal cortical capillary endothelial cell (ACE) growth. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of conditions or disorders where angiogenesis would be beneficial including, for example, wound healing, and the like (as would agonists of these PRO polypeptides). Antagonists of the PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of cancerous tumors.

Bovine adrenal cortical capillary endothelial (ACE) cells (from primary culture, maximum of 12-14 passages) were plated in 96-well plates at 500 cells/well per 100 microliter. Assay media included low glucose DMEM, 10% calf serum, 2 mM glutamine, and 1X penicillin/streptomycin/fungizone. Control wells included the following: (1) no ACE cells added; (2) ACE cells alone; (3) ACE cells plus VEGF (5 ng/ml); and (4) ACE cells plus FGF (5ng/ml). The control or test sample, (in 100 microliter volumes), was then added to the wells (at dilutions of 1%, 0.1% and 0.01%, respectively). The cell cultures were incubated for 6-7 days at 37°C/5% CO<sub>2</sub>. After the incubation, the media in the wells was aspirated, and the cells were washed 1X with PBS. An acid phosphatase reaction mixture (100 microliter; 0.1M sodium acetate, pH 5.5, 0.1% Triton X-100, 10 mM p-nitrophenyl phosphate) was then added to each well. After a 2 hour incubation at 37°C, the reaction was stopped by addition of 10 microliters 1N NaOH. Optical density (OD) was measured on a microplate reader at 405 nm.

The activity of a PRO polypeptide was calculated as the fold increase in proliferation (as determined by the acid phosphatase activity, OD 405 nm) relative to (1) cell only background, and (2) relative to maximum stimulation by VEGF. VEGF (at 3-10 ng/ml) and FGF (at 1-5 ng/ml) were employed as an activity reference for maximum stimulation. Results of the assay were considered "positive" if the observed stimulation was  $\geq$  50% increase over background. VEGF (5 ng/ml) control at 1% dilution gave 1.24 fold stimulation; FGF (5 ng/ml) control at 1% dilution gave 1.46 fold stimulation.

The following PRO polypeptides tested positive in this assay: PRO1075.

30 EXAMPLE 138: Mouse Mesengial Cell Inhibition Assay (Assay 114)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to inhibit the proliferation of mouse mesengial cells in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of such diseases or conditions where inhibition of mesengial cell proliferation would be beneficial such as, for example, cystic renal dysplasia, polycystic kidney disease, or other kidney disease assoiciated with abnormal mesengial cell proliferation, renal tumors, and the like.

On day 1, mouse mesengial cells are plated on a 96 well plate in growth medium (a 3:1 mixture of Dulbecco's modified Eagle's medium and Ham's F12 medium, 95 %; fetal bovine serum, 5 %; supplemented with 14mM HEPES) and then are allowed to grow overnight. On day 2, the PRO polypeptide is diluted at 2 different concentrations (1 %, 0.1 %) in serum-free medium and is added to the cells. The negative control is growth medium without added PRO polypeptide. After the cells are allowed to incubate for 48 hours, 20  $\mu$ l of the Cell  
5 Titer 96 Aqueous one solution reagent (Promega) is added to each well and the colormetric reaction is allowed to proceed for 2 hours. The absorbance (OD) is then measured at 490 nm. A positive in the assay is an absorbance reading which is at least 10 % above the negative control.

The following PRO polypeptides tested positive in this assay: PRO200 and PRO697.

10 EXAMPLE 139: Chondrocyte Proliferation Assay (Assay 111)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce the proliferation and/or redifferentiation of chondrocytes in culture. PRO polypeptides testing positive in this assay would be expected to be useful for the therapeutic treatment of various bone and/or cartilage disorders such as, for example, sports injuries and arthritis.

15 Porcine chondrocytes are isolated by overnight collagenase digestion of articular cartilage of the metacarpophalangeal joint of 4-6 month old female pigs. The isolated cells are then seeded at 25,000 cells/cm<sup>2</sup> in Ham F-12 containing 10% FBS and 4  $\mu$ g/ml gentamycin. The culture media is changed every third day and the cells are reseeded to 25,000 cells/cm<sup>2</sup> every five days. On day 12, the cells are seeded in 96 well plates at 5,000 cells/well in 100 $\mu$ l of the same media without serum and 100  $\mu$ l of either serum-free medium (negative  
20 control), staurosporin (final concentration of 5 nM; positive control) or the test PRO polypeptide are added to give a final volume of 200  $\mu$ l/well. After 5 days at 37°C, 20  $\mu$ l of Alamar blue is added to each well and the plates are incubated for an additional 3 hours at 37°C. The fluorescence is then measured in each well (Ex:530 nm; Em: 590 nm). The fluorescence of a plate containing 200  $\mu$ l of the serum-free medium is measured to obtain the background. A positive result in the assay is obtained when the fluorescence of the PRO polypeptide  
25 treated sample is more like that of the positive control than the negative control.

The following PRO polypeptides tested positive in this assay: PRO181, PRO200 and PRO322.

EXAMPLE 140: Rat DRG Neuronal Survival Inhibition Assay

This assay is designed to determine whether PRO polypeptides of the present invention show the ability  
30 to inhibit the survival of neural cells in culture. Polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of neuropathic conditions which are associated with undesirable neural cell proliferation including, for example, neuroblastomas, gliomas, glioblastomas, and the like.

A heterogeneous population of neural cells freshly isolated from E14 rat embryo dorsal root ganglia are diluted in complete medium and are plated at 5,000 cells/well on polyurethane pretreated plates containing 50 $\mu$ l  
35 F12 complete media. Test PRO polypeptides (50  $\mu$ l, one concentration) with 50 $\mu$ l additional assay media are then added to test for survival inhibition activity. Negative controls are treated with 100 $\mu$ l of complete medium alone. After 3 days incubation, the cells are stained with CMFDA and fixed after 1 hour with 4%

paraformaldehyde. Cells are then quantified by NIH image analysis. A positive in the assay is cell numbers in the treated well(s) being less than 0.5 of the untreated control well(s).

The following PRO polypeptides tested positive in this assay: PRO195 and PRO701.

#### EXAMPLE 141: Tissue Expression Distribution

- 5 Oligonucleotide probes were constructed from some of the PRO polypeptide-encoding nucleotide sequences shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human adult and/or fetal tissue sources and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tissues tested. Knowledge of the expression pattern or the differential expression of the PRO polypeptide-encoding nucleic acid in various different human tissue types provides a diagnostic marker useful for tissue typing, with or without other tissue-specific markers, for determining the primary tissue source of a metastatic tumor, and the like. These assays provided the following results.

	<u>DNA Molecule</u>	<u>Tissues With Significant Expression</u>	<u>Tissues Lacking Significant Expression</u>
	DNA40954-1233	liver, lung	brain
	DNA41404-1352	lung, kidney	liver, retina, pancreas
	DNA44179-1362	liver	lung, brain
20	DNA45234-1277	kidney	liver, placenta, brain
	DNA45415-1318	thyroid, brain, kidney	liver, bone marrow
	DNA45417-1432	thyroid, brain, kidney, bone marrow	liver
	DNA45493-1349	liver, kidney	brain
	DNA48306-1291	brain, kidney	pancreas, liver
25	DNA48328-1355	thyroid, brain, liver, kidney	bone marrow
	DNA48329-1290	brain, bone marrow, kidney	liver, thyroid
	DNA49624-1279	placenta	liver, lung, kidney, brain
	DNA50911-1288	brain	placenta
	DNA50914-1289	brain, kidney, liver	placenta
30	DNA53906-1368	lung, kidney	brain
	DNA53912-1457	lung, liver, kidney, pancreas	brain
	DNA53977-1371	lung, liver, kidney, bone marrow	brain, pancreas
	DNA54002-1367	bone marrow, liver, kidney	lung, thyroid, brain
	DNA55737-1345	bone marrow, kidney	liver, brain
35	DNA57039-1402	pigment epithelium	lung, brain, liver, kidney
	DNA57253-1382	lung, brain, liver, kidney	placenta
	DNA58747-1384	lung, brain, kidney, liver	pancreas, thyroid
	DNA23318-1211	spleen, brain, heart, colon tumor, prostate	cartilage
	DNA39975-1210	brain, colon tumor, heart	THP-1 macrophages
40	DNA39979-1213	dendrocytes, cartilage, heart	spleen, substantia nigra, uterus, prostate
	DNA41386-1316	HUVEC, cartilage, dendrocytes	substantia nigra, colon tumor, uterus
	DNA50919-1361	HUVEC, brain, spleen, colon tumor	prostate, cartilage, heart, uterus
	DNA52185-1370	dendrocytes	substantia nigra, hippocampus, uterus
	DNA42663-1154	uterus, spleen, bone marrow	cartilage, HUVEC, colon tumor
45	DNA50980-1286	placenta, adrenal gland, prostate	bone marrow, uterus, cartilage

EXAMPLE 142: *In situ* Hybridization

*In situ* hybridization is a powerful and versatile technique for the detection and localization of nucleic acid sequences within cell or tissue preparations. It may be useful, for example, to identify sites of gene expression, analyze the tissue distribution of transcription, identify and localize viral infection, follow changes in specific mRNA synthesis and aid in chromosome mapping.

- 5        *In situ* hybridization was performed following an optimized version of the protocol by Lu and Gillett, Cell Vision 1:169-176 (1994), using PCR-generated <sup>33</sup>P-labeled riboprobes. Briefly, formalin-fixed, paraffin-embedded human tissues were sectioned, deparaffinized, deproteinized in proteinase K (20 g/ml) for 15 minutes at 37°C, and further processed for *in situ* hybridization as described by Lu and Gillett, *supra*. A [<sup>33</sup>-P] UTP-labeled antisense riboprobe was generated from a PCR product and hybridized at 55°C overnight. The slides  
10        were dipped in Kodak NTB2 nuclear track emulsion and exposed for 4 weeks.

<sup>33</sup>P-Riboprobe synthesis

6.0 µl (125 mCi) of <sup>33</sup>P-UTP (Amersham BF 1002, SA < 2000 Ci/mmol) were speed vac dried. To each tube containing dried <sup>33</sup>P-UTP, the following ingredients were added:

- 15        2.0 µl 5x transcription buffer  
         1.0 µl DTT (100 mM)  
         2.0 µl NTP mix (2.5 mM : 10 µ; each of 10 mM GTP, CTP & ATP + 10 µl H<sub>2</sub>O)  
         1.0 µl UTP (50 µM)  
         1.0 µl Rnasin  
         1.0 µl DNA template (1 µg)  
20        1.0 µl H<sub>2</sub>O  
         1.0 µl RNA polymerase (for PCR products T3 = AS, T7 = S, usually)

- The tubes were incubated at 37°C for one hour. 1.0 µl RQ1 DNase were added, followed by incubation at 37°C for 15 minutes. 90 µl TE (10 mM Tris pH 7.6/1mM EDTA pH 8.0) were added, and the mixture was pipetted onto DE81 paper. The remaining solution was loaded in a Microcon-50 ultrafiltration unit, and spun  
25        using program 10 (6 minutes). The filtration unit was inverted over a second tube and spun using program 2 (3 minutes). After the final recovery spin, 100 µl TE were added. 1 µl of the final product was pipetted on DE81 paper and counted in 6 ml of Biofluor II.

- The probe was run on a TBE/urea gel. 1-3 µl of the probe or 5 µl of RNA Mrk III were added to 3 µl of loading buffer. After heating on a 95°C heat block for three minutes, the gel was immediately placed on  
30        ice. The wells of gel were flushed, the sample loaded, and run at 180-250 volts for 45 minutes. The gel was wrapped in saran wrap and exposed to XAR film with an intensifying screen in -70°C freezer one hour to overnight.

<sup>33</sup>P-HybridizationA. Pretreatment of frozen sections

- 35        The slides were removed from the freezer, placed on aluminium trays and thawed at room temperature for 5 minutes. The trays were placed in 55°C incubator for five minutes to reduce condensation. The slides were fixed for 10 minutes in 4% paraformaldehyde on ice in the fume hood, and washed in 0.5 x SSC for 5



minutes, at room temperature (25 ml 20 x SSC + 975 ml SQ H<sub>2</sub>O). After deproteinization in 0.5 µg/ml proteinase K for 10 minutes at 37°C (12.5 µl of 10 mg/ml stock in 250 ml prewarmed RNase-free RNase buffer), the sections were washed in 0.5 x SSC for 10 minutes at room temperature. The sections were dehydrated in 70 %, 95 %, 100 % ethanol, 2 minutes each.

B. Pretreatment of paraffin-embedded sections

5 The slides were deparaffinized, placed in SQ H<sub>2</sub>O, and rinsed twice in 2 x SSC at room temperature, for 5 minutes each time. The sections were deproteinated in 20 µg/ml proteinase K (500 µl of 10 mg/ml in 250 ml RNase-free RNase buffer; 37°C, 15 minutes) - human embryo, or 8 x proteinase K (100 µl in 250 ml RNase buffer, 37°C, 30 minutes) - formalin tissues. Subsequent rinsing in 0.5 x SSC and dehydration were performed as described above.

10 C. Prehybridization

The slides were laid out in a plastic box lined with Box buffer (4 x SSC, 50 % formamide) - saturated filter paper. The tissue was covered with 50 µl of hybridization buffer (3.75g Dextran Sulfate + 6 ml SQ H<sub>2</sub>O), vortexed and heated in the microwave for 2 minutes with the cap loosened. After cooling on ice, 18.75 ml formamide, 3.75 ml 20 x SSC and 9 ml SQ H<sub>2</sub>O were added, the tissue was vortexed well, and incubated at 15 42°C for 1-4 hours.

D. Hybridization

1.0 x 10<sup>6</sup> cpm probe and 1.0 µl tRNA (50 mg/ml stock) per slide were heated at 95°C for 3 minutes. The slides were cooled on ice, and 48 µl hybridization buffer were added per slide. After vortexing, 50 µl <sup>33</sup>P mix were added to 50 µl prehybridization on slide. The slides were incubated overnight at 55°C.

20 E. Washes

Washing was done 2 x 10 minutes with 2xSSC, EDTA at room temperature (400 ml 20 x SSC + 16 ml 0.25M EDTA, V<sub>f</sub>=4L), followed by RNaseA treatment at 37°C for 30 minutes (500 µl of 10 mg/ml in 250 ml RNase buffer = 20 µg/ml). The slides were washed 2 x 10 minutes with 2 x SSC, EDTA at room temperature. The stringency wash conditions were as follows: 2 hours at 55°C, 0.1 x SSC, EDTA (20 ml 20 x SSC + 16 ml EDTA, V<sub>f</sub>=4L).

F. Oligonucleotides

*In situ* analysis was performed on a variety of DNA sequences disclosed herein. The oligonucleotides employed for these analyses were derived from the nucleotide sequences disclosed herein and generally range from about 40 to 55 nucleotides in length.

30 G. Results

*In situ* analysis was performed on a variety of DNA sequences disclosed herein. The results from these analyses are as follows.

(1) DNA29101-1122 (PRO200)

35 Fetal: Lower limb expression in developing lower limb bones at the edge of the cartilagenous anlage (i.e. around the outside edge); in developing tendons, in vascular smooth muscle and in cells embracing developing skeletal muscle myocytes and myotubes. Expression also observed at the epiphyseal growth plate. Lymph node expression in marginal sinus of developing lymph nodes. Thymus expression in the subcapsular



region of the thymic cortex, possibly representing either the subcapsular epithelial cells or the proliferating, double negative, thymocytes that are found in this region. Spleen is negative. Trachea expression in smooth muscle. Brain (cerebral cortex) focal expression in cortical neurones. Spinal cord negative. Small intestine expression in smooth muscle. Thyroid - generalized expression over thyroid epithelium. Adrenal is negative. Liver expression in ductal plate cells. Stomach expression in mural smooth muscle. Fetal skin expression in basal layer of squamous epithelium. Placenta expression in interstitial cells in trophoblastic villi. Cord expression in wall of arteries and vein.

Comments: Expression pattern suggests that PRO200 may be involved in cell differentiation/proliferation.

High expression was observed at the following additional sites: Chimp ovary - granulosa cells of maturing follicles, lower intensity signal observed over thecal cells. Chimp parathyroid - high expression over chief cells. Human fetal testis - moderate expression over stromal cells surrounding developing tubules. Human fetal lung - high expression over chondrocytes in developing bronchial tree, and low level expression over branching bronchial epithelium. Specific expression was not observed over the renal cell, gastric and colonic carcinomas. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

20

(2) DNA30867-1335 (PRO218)

Low level expression over numerous epithelia including fetal small intestine, fetal thyroid, chimp gastric epithelium. Expression also seen over malignant cells in a renal cell carcinoma. Expression in fetal brain, over cortex. The distribution does not suggest an obvious function. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues examined: kidney (normal and end-stage), bladder, adrenal, spleen, lymph node, pancreas, lung, skin, eye (inc. retina), colon, bladder, liver (normal, cirrhotic, acute failure), heart, clear cell carcinoma of kidney, gastric adenocarcinoma, colorectal carcinoma. Non-human primate tissues examined: Chimp tissues: salivary gland, stomach, thyroid, parathyroid, tongue, thymus, ovary, lymph node, peripheral nerve. Rhesus Monkey tissues: cerebral cortex, hippocampus, cerebellum, penis.

25

30

(3) DNA40021-1154 (PRO285)

Low levels of expression observed in the placenta and over hematopoietic cells in the mouse fetal liver. No expression was detected in either human fetal, adult or chimp lymph node and no expression was detected in human fetal or human adult spleen. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen,

35

thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), cerebellum(rm), brain infarct (human), cerebritis (human), penis, eye, bladder, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

5

(4) DNA39523-1192 (PRO273)

Expression over epithelium of mouse embryo skin as well as over basal epithelium and dermis of human fetal skin. Basal epithelial pegs of the squamous mucosa of the chimp tongue are also positive. Expression over a subset of cells in developing glomeruli of fetal kidney, adult renal tubules, and over "thyroidized" epithelium in end-stage renal disease, low expression in a renal cell carcinoma, probably over the epithelial cells. Low level expression over stromal cells in fetal lung. Expression over stromal cells in the apical portion of gastric glands. High expression in the lamina propria of the fetal small intestinal villi, normal colonic mucosa and over stromal cells in a colonic carcinoma. Strong expression over benign connective tissue cells in the hyalinized stroma of a sarcoma. Expression over stromal cells in the placental villi and the splenic red pulp. In the brain, expression over cortical neurones. Connective tissue surrounding developing bones and over nerve sheath cells in the fetus. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult tissues examined: liver, kidney, adrenal, myocardium, aorta, spleen, lymph node, pancreas, lung, skin, cerebral cortex (rm), hippocampus(rm), eye, stomach, gastric carcinoma, colon, colonic carcinoma, thyroid (chimp), parathyroid (chimp) ovary (chimp) and chondrosarcoma. Acetaminophen induced liver injury and hepatic cirrhosis.

Expression was present in many cells in the outer layers (I and II) of the monkey cerebral cortex. A small subset of cells in the deeper cortical layers also expressed mRNA for this chemokine homolog. Scattered cells within the molecular layers of the hippocampus and bordering the inner edge of the dentate gyrus contained chemokine homolog mRNA. No expression was detected within the cerebellar cortex. Chemokine homolog expression is not observed in infarcted brain, where cell death has occurred in the regions where the chemokine homolog normally is expressed. This probe could possibly serve as a marker of a subset of neurons of outer layers of the cerebral cortex and could possibly reveal neuronal migration disorders. Abnormal neuronal migration is a possible cause of some seizure disorders and schizophrenia. In order to gain a better appreciation of the distribution of this mRNA we will test whether the probe will cross-hybridize with mouse brain tissue.

Also shows intriguing and specific patterns of hybridization within postnatal day (P)10 and adult mouse brains. In one sagittal section of P10 mouse brain, strong signal was observed scattered within the molecular layer of the hippocampus and inner edges of the dentate gyrus. Cells in the presubiculum were moderately labeled; the signal extended in a strong band through outer layers of the retrosplenial cortex to the occipital cortex, where the signal diminished to background levels. A small set of positive neurons were detected in deeper regions of P10 motor cortex; neurons in outer layers of P10 cortex did not exhibit signal above background levels. Moderate hybridization signal was also detected in the inferior colliculus. Chemokine

homolog signal in the adult mouse brain was evaluated in three coronal sections at different levels. Strong signal was detected in the septum and in scattered neurons in the pontine nuclei and motor root of the trigeminal nerve; moderate signal was seen in the molecular layers of the hippocampus and outer layers of the retrosplenial cortex.

(5) DNA39979-1213 (PRO296)

5 Widespread expression in fetal in adult tissues. Expressed in a variety of fetal and adult epithelia, skeletal and cardiac muscle, developing (including retina) and adult CNS, thymic epithelium, placental villi, hepatocytes in cirrhotic and acetaminophen induced toxicity. Highly expressed in hypertrophic chondrocytes in developing skeletal system. The overall expression pattern, while not completely overlapping (not expressed in glomeruli, more widely expressed in CNS), is not dissimilar to VEGF. A possible role in angiogenesis should  
10 therefore be considered. Human fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, great vessels, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis, testis and lower limb. Adult human tissues examined: kidney (normal and end-stage), adrenal, spleen, lymph node, pancreas, lung, eye (inc. retina), bladder, liver (normal, cirrhotic, acute failure). Non-human primate tissues examined: Chimp tissues: adrenal. Rhesus Monkey tissues: cerebral  
15 cortex, hippocampus, cerebellum.

(6) DNA52594-1270 (PRO868)

Expression over neuronal cells in fetal dorsal root ganglia, spinal cord, developing enteric neurons, cortical neurons. Low level expression also seen in placental trophoblast. In adult tissues the only site where  
20 notable expression was observed was the normal adult prostate; as such it may represent a possible prostate cell surface receptor target antigen. Studies to further characterize the expression in adult tissues seem warranted. Low level expression also observed in a liposarcoma. Fetal tissues examined (E12-E16 weeks) include: placenta, umbilical cord, liver, kidney, adrenals, thyroid, lungs, heart, great vessels, oesophagus, stomach, small intestine, spleen, thymus, pancreas, brain, eye, spinal cord, body wall, pelvis and lower limb. Adult human tissues  
25 examined: liver, kidney, adrenal, myocardium, aorta, spleen, lung, skin, chondrosarcoma, eye, stomach, gastric carcinoma, colon, colonic carcinoma, renal cell carcinoma, prostate, bladder mucosa and gall bladder. Acetaminophen induced liver injury and hepatic cirrhosis. Rhesus tissues examined: cerebral cortex (rm), hippocampus(rm), cerebellum. Chimp tissues examined: thyroid, parathyroid, ovary, nerve, tongue, thymus, adrenal, gastric mucosa and salivary gland. WIG-1(WISP-1), WIG-2 (WISP-2) and WIG-5 (WISP-3) expression  
30 in human breast carcinoma and normal breast tissue, Wig-2 in lung carcinoma, and Wig-5 in colon carcinoma.

(7) DNA64907-1163 (PRO1330)

In human fetal tissues there was strong specific expression over arterial, venous, capillary and sinusoidal endothelium in all tissues examined, except for fetal brain. In normal adult tissues expression was  
35 low to absent, but when present appeared expression was confined to the vasculature. Highest expression in adult tissues was observed regionally in vessels running within the white matter of rhesus brain - the significance of this pattern is unclear. Elevated expression observed in vasculature of many inflamed and diseased tissues,

including tumor vasculature. In some of these tissues it was unclear if expression was solely confined to vascular endothelium. In the 15 lung tumors examined no expression was seen over the malignant epithelium, however, vascular expression was observed in many of the tumors and adjacent lung tissue. Moderate, apparently non-specific background, was seen with this probe over hyalinised collagen and sites of tissue necrosis. In the absence of a sense control, however, it is not possible to be absolutely certain that all of this signal is non-specific. Some signal, also thought to be non-specific, was seen over the chimp gastric mucosa, transitional cell epithelium of human adult bladder and fetal retina.

(8) DNA49624-1279 (PRO545)

Expression of the ADAM family molecule, ADAM 12 (DNA49624-1279) observed in normal human lung, lung tumor, normal colon and colon carcinoma.

(9) DNA59294-1381 (PRO1031)

The expression of this IL17 homologue was evaluated in a panel consisting of normal adult and fetal tissues and tissues with inflammation, predominantly chronic lymphocytic inflammation. This panel is designed to specifically evaluate the expression pattern in immune mediated inflammatory disease of novel proteins that modulate T lymphocyte function (stimulatory or inhibitory). This protein when expressed as an Ig-fusion protein was immunostimulatory in a dose dependent fashion in the human mixed lymphocyte reaction (MLR); it caused a 285% and 147% increase above the baseline stimulation index when utilized at two different concentrations (1.0% and 0.1% of a 560 nM stock). Summary: expression was restricted to muscle, certain types of smooth muscle in the adult and in skeletal and smooth muscle in the human fetus. Expression in adult human was in smooth muscle of tubular organs evaluated including colon and gall bladder. There no expression in the smooth muscle of vessels or bronchi. No adult human skeletal muscle was evaluated. In fetal tissues there was moderate to high diffuse expression in skeletal muscle the axial skeleton and limbs. There was weak expression in the smooth muscle of the intestinal wall but no expression in cardiac muscle. Adult human tissues with expression: Colon. there was low level diffuse expression in the smooth muscle (tunica muscularis) in 5 specimens with chronic inflammatory bowel disease. Gall bladder: there was weak to low level expression in the smooth muscle of the gall bladder. Fetal human tissues with expression: there was moderate diffuse expression in skeletal muscle and weak to low expression in smooth muscle; there was no expression in fetal heart or any other fetal organ including liver, spleen, CNS, kidney, gut, lung. Human tissues with no expression: lung with chronic granulomatous inflammation and chronic bronchitis (5 patients), peripheral nerve, prostate, heart, placenta, liver (disease multiblock), brain (cerebrum and cerebellum), tonsil (reactive hyperplasia), peripheral lymph node, thymus.

(10) DNA45416-1251 (PRO362)

The expression of this novel protein was evaluated in a variety of human and non-human primate tissues and was found to be highly restricted. Expression was present only in alveolar macrophages in the lung and in Kupffer cells of the hepatic sinusoids. Expression in these cells was significantly increased when these distinct



cell populations were activated. Though these two subpopulations of tissue macrophages are located in different organs, they have similar biological functions. Both types of these phagocytes act as biological filters to remove material from the blood stream or airways including pathogens, senescent cells and proteins and both are capable of secreting a wide variety of important proinflammatory cytokines. In inflamed lung (7 patient samples) expression was prominent in reactive alveolar macrophage cell populations defined as large, pale often vacuolated cells present singly or in aggregates within alveoli and was weak to negative in normal, non-reactive macrophages (single scattered cells of normal size). Expression in alveolar macrophages was increased during inflammation when these cells were both increased in numbers and size (activated). Despite the presence of histocytes in areas of interstitial inflammation and peribronchial lymphoid hyperplasia in these tissues, expression was restricted to alveolar macrophages. Many of the inflamed lungs also had some degree of suppurative inflammation; expression was not present in neutrophilic granulocytes. In liver, there was strong expression in reactive/activated Kupffer cells in livers with acute centrilobular necrosis (acetaminophen toxicity) or fairly marked periportal inflammation. However there was weak or no expression in Kupffer cells in normal liver or in liver with only mild inflammation or mild to moderate lobular hyperplasia/hypertrophy. Thus, as in the lung, there was increased expression in activated/reactive cells. There was no expression of this molecule in histiocytes/macrophages present in inflamed bowel, hyperplastic/reactive tonsil or normal lymph node. The lack of expression in these tissues which all contained histiocytic inflammation or resident macrophage populations strongly supports restricted expression to the unique macrophage subset populations defined as alveolar macrophage and hepatic Kupffer cells. Spleen or bone marrow was not available for evaluation. Human tissues evaluated which had no detectable expression included: Inflammatory bowel disease (7 patient samples with moderate to severe disease), tonsil with reactive hyperplasia, peripheral lymphnode, psoriatic skin (2 patient samples with mild to moderate disease), heart, peripheral nerve. Chimp tissues evaluated which had no detectable expression included: tongue, stomach, thymus.

(11) DNA52196-1348 (PRO733)

Generalized low level signal in many tissues and in many cell types. While endothelial cell expression was observed it was not a prominent feature in either fetal, normal or diseased tissues. Human tissues: moderate expression over fetal liver (mainly hepatocytes), lung, skin, adrenal and heart. Fetal spleen, small intestine, brain and eye are negative. Adult normal kidney, bladder epithelium, lung, adrenal, pancreas, skin - all negative. Expression in adult human liver (normal and diseased), renal tubules in end-stage renal disease, adipose tissue, sarcoma, colon, renal cell carcinoma, hepatocellular carcinoma, squamous cell carcinoma. Non human primate tissues: chimp salivary gland, vessels, stomach, tongue, peripheral nerve, thymus, lymph node, thyroid and parathyroid. Rhesus spinal cord negative, cortical and hippocampal neurones positive.

EXAMPLE 143: Isolation of cDNA Clones Encoding a Human PRO4993

A consensus DNA sequence was assembled relative to other EST sequences using phrap as described in Example 1 above. This consensus sequence is herein designated DNA85042. In some cases, the DNA85042 consensus sequence derives from an intermediate consensus DNA sequence which was extended using repeated



cycles of BLAST and phrap to extend that intermediate consensus sequence as far as possible using the sources of EST sequences discussed above. Based on the DNA85042 consensus sequence, oligonucleotides were synthesized: 1) to identify by PCR a cDNA library that contained the sequence of interest, and 2) for use as probes to isolate a clone of the full-length coding sequence for PRO4993.

PCR primers (forward and reverse) were synthesized:

- 5 forward PCR primer 5'-AGATGTGAAGGTGCAGGTGTGCCG-3' (SEQ ID NO:619)  
reverse PCR primer 5'-GAACATCAGCGCTCCCGGTAATTCC-3' (SEQ ID NO:620)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA85042 sequence which had the following nucleotide sequence

- hybridization probe  
 10 5'-CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCC-3' (SEQ ID NO:621)

RNA for construction of the cDNA libraries was isolated from human fetal brain tissue.

DNA sequencing of the clones isolated as described above gave the full-length DNA sequence for a full-length PRO4993 polypeptide (designated herein as DNA94832-2659 [Figure 229, SEQ ID NO:611]) and the derived protein sequence for that PRO4993 polypeptide.

- 15 The full length clone identified above contained a single open reading frame with an apparent translational initiation site at nucleotide positions 305-307 and a stop signal at nucleotide positions 1361-1363 (Figure 229, SEQ ID NO:611). The predicted polypeptide precursor is 352 amino acids long, has a calculated molecular weight of approximately 38,429 daltons and an estimated pI of approximately 6.84. Analysis of the full-length PRO4993 sequence shown in Figure 230 (SEQ ID NO:612) evidences the presence of a variety of  
 20 important polypeptide domains as shown in Figure 230, wherein the locations given for those important polypeptide domains are approximate as described above. Clone DNA94832-2659 has been deposited with ATCC on June 15, 1999 and is assigned ATCC deposit no. 240-PTA.

- An analysis of the Dayhoff database (version 35.45 SwissProt 35), using the ALIGN-2 sequence alignment analysis of the full-length sequence shown in Figure 230 (SEQ ID NO:612), evidenced sequence  
 25 identity between the PRO4993 amino acid sequence and the following Dayhoff sequences: P\_W05152; LAMP\_HUMAN; P\_W05157; P\_W05155; I56551; OPCM\_RAT; AMAL\_DROME; DMU78177\_1; I37246; and NCA1\_HUMAN.

#### EXAMPLE 144: Isolation of cDNA Clones Encoding Human PRO1559, PRO725 and PRO739

- 30 A consensus sequence was obtained relative to a variety of EST sequences as described in Example 1 above. Based upon an observed homology between this consensus sequence and an EST sequence contained within Incyte EST clone No. 4242090, Incyte EST clone No. 4242090 was purchased and its insert was obtained and sequenced. It was discovered that the insert sequence encoded a full-length protein designated herein as PRO1559 (Figure 232; SEQ ID NO:614). The DNA sequence of the insert (DNA68886) is shown in Figure  
 35 231 (SEQ ID NO:613).

A cDNA sequence isolated in the amylase screen described in Example 2 above is herein designated DNA43301. The DNA43301 sequence was then compared to a variety of expressed sequence tag (EST)

databases which included public EST databases (e.g., GenBank) and a proprietary EST DNA database (LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA) to identify existing homologies. The homology search was performed using the computer program BLAST or BLAST2 (Altshul et al., *Methods in Enzymology* 266:460-480 (1996)). Those comparisons resulting in a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, Washington). The consensus sequence obtained therefrom is herein designated DNA45458. Based on the DNA45458 consensus sequence, oligonucleotide probes were generated and used to screen a human fetal brain (LIB153) library prepared as described in paragraph 1 of Example 2 above. The cloning vector was pRK5B (pRK5B is a precursor of pRK5D that does not contain the SfiI site; see, Holmes et al., *Science*, 253:1278-1280 (1991)), and the cDNA size cut was less than 2800 bp.

PCR primers (forward and reverse) were synthesized:

forward PCR primer (45458.f1) 5'-CCAAACTCACCCAGTGAGTGTGAGC-3' (SEQ ID NO:619)

reverse PCR primer (45458.r1) 5'-TGGGAAATCAGGAATGGTGTCTCC-3' (SEQ ID NO:620)

Additionally, a synthetic oligonucleotide hybridization probe was constructed from the consensus DNA45458 sequence which had the following nucleotide sequence

hybridization probe (45458.p1)

5'-CTTGTTTTACCATTTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCC-3' (SEQ ID NO:621)

In order to screen several libraries for a source of a full-length clone, DNA from the libraries was screened by PCR amplification with the PCR primer pair identified above. A positive library was then used to isolate clones encoding the PRO725 gene using the probe oligonucleotide and one of the PCR primers.

A full length clone was identified that contained a single open reading frame with an apparent translational initiation site at nucleotide positions 161-163 and ending at the stop codon found at nucleotide positions 455-457 (Figure 233; SEQ ID NO:615). The predicted polypeptide precursor is 98 amino acids long, has a calculated molecular weight of approximately 11,081 daltons and an estimated pI of approximately 6.68. Analysis of the full-length PRO725 sequence shown in Figure 234 (SEQ ID NO:616) evidences the presence of the following: a signal peptide from about amino acid 1 to about amino acid 20, a potential N-glycosylation site from about amino acid 72 to about amino acid 75 and a tyrosine kinase phosphorylation site from about amino acid 63 to about amino acid 70. Clone DNA52758-1399 has been deposited with ATCC on April 14, 1998 and is assigned ATCC deposit no. 209773.

Analysis of the amino acid sequence of the full-length PRO725 polypeptide suggests that it possesses no significant sequence similarity to any known protein. However, an analysis of the Dayhoff database (version 35.45 SwissProt 35) evidenced some degree of homology between the PRO725 amino acid sequence and the following Dayhoff sequences, POL\_BLVAU, PSSP\_RAT, CELC36C5\_7, AF019234\_1, I48862, P\_R12498, P\_P10125, P\_R26861, A64527 and P\_W20495.

DNA52756, as shown in Figure 235 (SEQ ID NO:617) and which encodes native PRO739 polypeptide (Figure 236; SEQ ID NO:618) was obtained from GenBank.

EXAMPLE 145: Identification of Receptor/Ligand Interactions

In this assay, various PRO polypeptides are tested for ability to bind to a panel of potential receptor molecules for the purpose of identifying receptor/ligand interactions. The identification of a ligand for a known receptor, a receptor for a known ligand or a novel receptor/ligand pair is useful for a variety of indications including, for example, targeting bioactive molecules (linked to the ligand or receptor) to a cell known to express the receptor or ligand, use of the receptor or ligand as a reagent to detect the presence of the ligand or receptor in a composition suspected of containing the same, wherein the composition may comprise cells suspected of expressing the ligand or receptor, modulating the growth of or another biological or immunological activity of a cell known to express or respond to the receptor or ligand, modulating the immune response of cells or toward cells that express the receptor or ligand, allowing the preparation of agonists, antagonists and/or antibodies directed against the receptor or ligand which will modulate the growth of or a biological or immunological activity of a cell expressing the receptor or ligand, and various other indications which will be readily apparent to the ordinarily skilled artisan.

The assay is performed as follows. A PRO polypeptide of the present invention suspected of being a ligand for a receptor is expressed as a fusion protein containing the Fc domain of human IgG (an immunoadhesin). Receptor-ligand binding is detected by allowing interaction of the immunoadhesin polypeptide with cells (e.g. Cos cells) expressing candidate PRO polypeptide receptors and visualization of bound immunoadhesin with fluorescent reagents directed toward the Fc fusion domain and examination by microscope. Cells expressing candidate receptors are produced by transient transfection, in parallel, of defined subsets of a library of cDNA expression vectors encoding PRO polypeptides that may function as receptor molecules. Cells are then incubated for 1 hour in the presence of the PRO polypeptide immunoadhesin being tested for possible receptor binding. The cells are then washed and fixed with paraformaldehyde. The cells are then incubated with fluorescent conjugated antibody directed against the Fc portion of the PRO polypeptide immunoadhesin (e.g. FITC conjugated goat anti-human-Fc antibody). The cells are then washed again and examined by microscope. A positive interaction is judged by the presence of fluorescent labeling of cells transfected with cDNA encoding a particular PRO polypeptide receptor or pool of receptors and an absence of similar fluorescent labeling of similarly prepared cells that have been transfected with other cDNA or pools of cDNA. If a defined pool of cDNA expression vectors is judged to be positive for interaction with a PRO polypeptide immunoadhesin, the individual cDNA species that comprise the pool are tested individually (the pool is "broken down") to determine the specific cDNA that encodes a receptor able to interact with the PRO polypeptide immunoadhesin.

In another embodiment of this assay, an epitope-tagged potential ligand PRO polypeptide (e.g. 8 histidine "His" tag) is allowed to interact with a panel of potential receptor PRO polypeptide molecules that have been expressed as fusions with the Fc domain of human IgG (immunoadhesins). Following a 1 hour co-incubation with the epitope tagged PRO polypeptide, the candidate receptors are each immunoprecipitated with protein A beads and the beads are washed. Potential ligand interaction is determined by western blot analysis of the immunoprecipitated complexes with antibody directed towards the epitope tag. An interaction is judged to occur if a band of the anticipated molecular weight of the epitope tagged protein is observed in the western blot analysis with a candidate receptor, but is not observed to occur with the other members of the panel

of potential receptors.

Using these assays, the following receptor/ligand interactions have been herein identified: PRO337 binds to PRO4993, PRO1559 binds to PRO725, PRO1559 binds to PRO700 and PRO1559 binds to PRO739.

#### Deposit of Material

5 The following materials have been deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, MD, USA (ATCC):

	<u>Material</u>	<u>ATCC Dep. No.</u>	<u>Deposit Date</u>
	DNA39987-1184	ATCC 209786	April 21, 1998
	DNA40625-1189	ATCC 209788	April 21, 1998
10	DNA23318-1211	ATCC 209787	April 21, 1998
	DNA39979-1213	ATCC 209789	April 21, 1998
	DNA40594-1233	ATCC 209617	February 5, 1998
	DNA45416-1251	ATCC 209620	February 5, 1998
	DNA45419-1252	ATCC 209616	February 5, 1998
15	DNA52594-1270	ATCC 209679	March 17, 1998
	DNA45234-1277	ATCC 209654	March 5, 1998
	DNA49624-1279	ATCC 209655	March 5, 1998
	DNA48309-1280	ATCC 209656	March 5, 1998
	DNA46776-1284	ATCC 209721	March 31, 1998
20	DNA50980-1286	ATCC 209717	March 31, 1998
	DNA50913-1287	ATCC 209716	March 31, 1998
	DNA50914-1289	ATCC 209722	March 31, 1998
	DNA48296-1292	ATCC 209668	March 11, 1998
	DNA32284-1307	ATCC 209670	March 11, 1998
25	DNA36343-1310	ATCC 209718	March 31, 1998
	DNA40571-1315	ATCC 209784	April 21, 1998
	DNA41386-1316	ATCC 209703	March 26, 1998
	DNA44194-1317	ATCC 209808	April 28, 1998
	DNA45415-1318	ATCC 209810	April 28, 1998
30	DNA44189-1322	ATCC 209699	March 26, 1998
	DNA48304-1323	ATCC 209811	April 28, 1998
	DNA49152-1324	ATCC 209813	April 28, 1998
	DNA49646-1327	ATCC 209705	March 26, 1998
	DNA49631-1328	ATCC 209806	April 28, 1998
35	DNA49645-1347	ATCC 209809	April 28, 1998
	DNA45493-1349	ATCC 209805	April 28, 1998
	DNA48227-1350	ATCC 209812	April 28, 1998
	DNA41404-1352	ATCC 209844	May 6, 1998
	DNA44196-1353	ATCC 209847	May 6, 1998
40	DNA52187-1354	ATCC 209845	May 6, 1998
	DNA48328-1355	ATCC 209843	May 6, 1998
	DNA56352-1358	ATCC 209846	May 6, 1998
	DNA53971-1359	ATCC 209750	April 7, 1998
	DNA50919-1361	ATCC 209848	May 6, 1998
45	DNA44179-1362	ATCC 209851	May 6, 1998
	DNA54002-1367	ATCC 209754	April 7, 1998
	DNA53906-1368	ATCC 209747	April 7, 1998
	DNA52185-1370	ATCC 209861	May 14, 1998
	DNA53977-1371	ATCC 209862	May 14, 1998
50	DNA57253-1382	ATCC 209867	May 14, 1998
	DNA58847-1383	ATCC 209879	May 20, 1998
	DNA58747-1384	ATCC 209868	May 14, 1998



	DNA57689-1385	ATCC 209869	May 14, 1998
	DNA23330-1390	ATCC 209775	April 14, 1998
	DNA26847-1395	ATCC 209772	April 14, 1998
	DNA53974-1401	ATCC 209774	April 14, 1998
	DNA57039-1402	ATCC 209777	April 14, 1998
5	DNA57033-1403	ATCC 209905	May 27, 1998
	DNA34353-1428	ATCC 209855	May 12, 1998
	DNA45417-1432	ATCC 209910	May 27, 1998
	DNA39523-1192	ATCC 209424	October 31, 1997
	DNA44205-1285	ATCC 209720	March 31, 1998
10	DNA50911-1288	ATCC 209714	March 31, 1998
	DNA48329-1290	ATCC 209785	April 21, 1998
	DNA48306-1291	ATCC 209911	May 27, 1998
	DNA48336-1309	ATCC 209669	March 11, 1998
	DNA44184-1319	ATCC 209704	March 26, 1998
15	DNA48314-1320	ATCC 209702	March 26, 1998
	DNA48333-1321	ATCC 209701	March 26, 1998
	DNA50920-1325	ATCC 209700	March 26, 1998
	DNA50988-1326	ATCC 209814	April 28, 1998
	DNA48331-1329	ATCC 209715	March 31, 1998
20	DNA30867-1335	ATCC 209807	April 28, 1998
	DNA55737-1345	ATCC 209753	April 7, 1998
	DNA49829-1346	ATCC 209749	April 7, 1998
	DNA52196-1348	ATCC 209748	April 7, 1998
	DNA56965-1356	ATCC 209842	May 6, 1998
25	DNA56405-1357	ATCC 209849	May 6, 1998
	DNA57530-1375	ATCC 209880	May 20, 1998
	DNA56439-1376	ATCC 209864	May 14, 1998
	DNA56409-1377	ATCC 209882	May 20, 1998
	DNA56112-1379	ATCC 209883	May 20, 1998
30	DNA56045-1380	ATCC 209865	May 14, 1998
	DNA59294-1381	ATCC 209866	May 14, 1998
	DNA56433-1406	ATCC 209857	May 12, 1998
	DNA53912-1457	ATCC 209870	May 14, 1998
	DNA50921-1458	ATCC 209859	May 12, 1998
35	DNA29101-1122	ATCC 209653	March 5, 1998
	DNA40021-1154	ATCC 209389	October 17, 1997
	DNA42663-1154	ATCC 209386	October 17, 1997
	DNA30943-1-1163-1	ATCC 209791	April 21, 1998
	DNA64907-1163-1	ATCC 203242	September 9, 1998
40	DNA64908-1163-1	ATCC 203243	September 9, 1998
	DNA39975-1210	ATCC 209783	April 21, 1998
	DNA43316-1237	ATCC 209487	November 21, 1997
	DNA55800-1263	ATCC 209680	March 17, 1998
	DNA94832-2659	240-PTA	June 15, 1999
45	DNA52758-1399	ATCC 209773	April 14, 1998

These deposit were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny



to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

5 The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in accordance with its patent laws.

10 The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by the construct deposited, since the deposited embodiment is intended as a single illustration of certain aspects of the invention and any constructs that are functionally equivalent are within the scope of this invention. The deposit of material herein does not constitute an admission that the written description herein contained is inadequate to enable the practice of any aspect of the invention, including the best mode thereof, nor is it to be construed as limiting the scope of the claims to the specific illustrations that it represents. Indeed, various modifications of the invention in addition  
15 to those shown and described herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).

30

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID

35

NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253),  
 5 Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263), Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ ID NO:351), Figure 144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441), Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522), Figure 224 (SEQ ID NO:525), Figure 229 (SEQ ID NO:611), Figure 231 (SEQ ID NO:613), Figure 233 (SEQ ID NO:615) and Figure 235 (SEQ ID NO:617).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:6), Figure 8 (SEQ ID NO:18), Figure 10 (SEQ ID NO:27), Figure 14 (SEQ ID NO:35), Figure 19 (SEQ ID NO:44), Figure 21 (SEQ ID NO:51), Figure 23 (SEQ ID NO:58), Figure 25 (SEQ ID NO:63), Figure 27 (SEQ ID NO:68), Figure 29 (SEQ ID NO:73), Figure 32 (SEQ ID NO:84), Figure 34 (SEQ ID NO:89), Figure 36 (SEQ ID NO:96), Figure 38 (SEQ ID NO:101), Figure 40 (SEQ ID NO:108), Figure 42 (SEQ ID NO:113), Figure 44 (SEQ ID NO:118), Figure 46 (SEQ ID NO:123), Figure 48 (SEQ ID NO:131), Figure 50 (SEQ ID NO:136), Figure 52 (SEQ ID NO:144), Figure 54 (SEQ ID NO:149), Figure 58 (SEQ ID NO:156), Figure 60 (SEQ ID NO:161), Figure 62 (SEQ ID NO:168), Figure 65 (SEQ ID NO:177), Figure 67 (SEQ ID NO:182), Figure 69 (SEQ ID NO:189), Figure 72 (SEQ ID NO:195), Figure 74 (SEQ ID NO:205), Figure 76 (SEQ ID NO:210), Figure 78 (SEQ ID NO:215), Figure 80 (SEQ ID NO:220), Figure 82 (SEQ ID NO:225), Figure 84 (SEQ ID NO:230), Figure 86 (SEQ ID NO:235), Figure 88 (SEQ ID NO:244), Figure 90 (SEQ ID NO:253), Figure 92 (SEQ ID NO:258), Figure 94 (SEQ ID NO:263),  
 30 Figure 97 (SEQ ID NO:269), Figure 108 (SEQ ID NO:283), Figure 117 (SEQ ID NO:295), Figure 119 (SEQ ID NO:300), Figure 121 (SEQ ID NO:302), Figure 124 (SEQ ID NO:308), Figure 128 (SEQ ID NO:321), Figure 131 (SEQ ID NO:329), Figure 135 (SEQ ID NO:336), Figure 138 (SEQ ID NO:345), Figure 141 (SEQ

ID NO:351), Figure 144 (SEQ ID NO:357), Figure 146 (SEQ ID NO:362), Figure 148 (SEQ ID NO:369), Figure 150 (SEQ ID NO:374), Figure 152 (SEQ ID NO:379), Figure 154 (SEQ ID NO:384), Figure 156 (SEQ ID NO:389), Figure 158 (SEQ ID NO:394), Figure 160 (SEQ ID NO:399), Figure 162 (SEQ ID NO:404), Figure 164 (SEQ ID NO:409), Figure 166 (SEQ ID NO:414), Figure 168 (SEQ ID NO:419), Figure 170 (SEQ ID NO:424), Figure 172 (SEQ ID NO:429), Figure 176 (SEQ ID NO:436), Figure 178 (SEQ ID NO:441),  
 5 Figure 180 (SEQ ID NO:446), Figure 182 (SEQ ID NO:451), Figure 184 (SEQ ID NO:453), Figure 186 (SEQ ID NO:455), Figure 189 (SEQ ID NO:458), Figure 191 (SEQ ID NO:463), Figure 193 (SEQ ID NO:465), Figure 195 (SEQ ID NO:467), Figure 197 (SEQ ID NO:469), Figure 199 (SEQ ID NO:471), Figure 201 (SEQ ID NO:476), Figure 203 (SEQ ID NO:482), Figure 206 (SEQ ID NO:487), Figure 208 (SEQ ID NO:495), Figure 210 (SEQ ID NO:497), Figure 212 (SEQ ID NO:505), Figure 214 (SEQ ID NO:507), Figure 216 (SEQ ID NO:509), Figure 218 (SEQ ID NO:514), Figure 221 (SEQ ID NO:522), Figure 224 (SEQ ID NO:525),  
 10 Figure 229 (SEQ ID NO:611), Figure 231 (SEQ ID NO:613), Figure 233 (SEQ ID NO:615) and Figure 235 (SEQ ID NO:617).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding  
 15 sequence of the DNA deposited under ATCC accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654, ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812,  
 20 ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772, ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715,  
 25 ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386, ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487, ATCC 209680, 240-PTA or ATCC 209773.

30 5. A vector comprising the nucleic acid of any one of Claims 1 to 4.

6. The vector of Claim 5 operably linked to control sequences recognized by a host cell transformed with the vector.

35 7. A host cell comprising the vector of Claim 5.

8. The host cell of Claim 7, wherein said cell is a CHO cell.



9. The host cell of Claim 7, wherein said cell is an *E. coli*.
10. The host cell of Claim 7, wherein said cell is a yeast cell.
11. A process for producing a PRO polypeptides comprising culturing the host cell of Claim 7  
5 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.
12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2),  
10 Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132),  
15 Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270),  
20 Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375),  
25 Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612),  
30 Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).



13. An isolated polypeptide scoring at least 80% positives when compared to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) and Figure 236 (SEQ ID NO:618).

14. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under ATCC accession number ATCC 209791, ATCC 209786, ATCC 209788, ATCC 209787, ATCC 209789, ATCC 209617, ATCC 209620, ATCC 209616, ATCC 209679, ATCC 209654, ATCC 209655, ATCC 209656, ATCC 209721, ATCC 209717, ATCC 209716, ATCC 209722, ATCC 209668, ATCC 209670, ATCC 209718, ATCC 209784, ATCC 209703, ATCC 209808, ATCC 209810, ATCC 209699, ATCC 209811, ATCC 209813, ATCC 209705, ATCC 209806, ATCC 209809, ATCC 209805, ATCC 209812, ATCC 209844, ATCC 209847, ATCC 209845, ATCC 209843, ATCC 209846, ATCC 209750, ATCC 209848, ATCC 209851, ATCC 209754, ATCC 209747, ATCC 209861, ATCC 209862, ATCC 209867, ATCC 209879, ATCC 209868, ATCC 209869, ATCC 209775, ATCC 209772,

ATCC 209774, ATCC 209777, ATCC 209905, ATCC 209855, ATCC 209910, ATCC 209424, ATCC 209720, ATCC 209714, ATCC 209785, ATCC 209911, ATCC 209669, ATCC 209704, ATCC 209702, ATCC 209701, ATCC 209700, ATCC 209814, ATCC 209715, ATCC 209807, ATCC 209753, ATCC 209749, ATCC 209748, ATCC 209842, ATCC 209849, ATCC 209880, ATCC 209864, ATCC 209882, ATCC 209883, ATCC 209865, ATCC 209866, ATCC 209857, ATCC 209870, ATCC 209859, ATCC 209653, ATCC 209389, ATCC 209386,  
5 ATCC 203242, ATCC 203243, ATCC 209783, ATCC 209487, ATCC 209680, 240-PTA or ATCC 209773.

15. A chimeric molecule comprising a polypeptide according to any one of Claims 12 to 14 fused to a heterologous amino acid sequence.

10 16. The chimeric molecule of Claim 15, wherein said heterologous amino acid sequence is an epitope tag sequence.

17. The chimeric molecule of Claim 15, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

15

18. An antibody which specifically binds to a polypeptide according to any one of Claims 12 to 14.

19. The antibody of Claim 18, wherein said antibody is a monoclonal antibody, a humanized  
20 antibody or a single-chain antibody.

20. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270),  
35 Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ

ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447),  
 5 Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150),  
 20 Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), with its associated signal peptide; or

- (c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide.

21. An isolated polypeptide having at least 80% amino acid sequence identity to:

- (a) the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID



NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;

(b) an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide;



NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), with its associated signal peptide; or

(c) an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:7), Figure 9 (SEQ ID NO:19), Figure 11 (SEQ ID NO:28), Figure 15 (SEQ ID NO:36), Figure 20 (SEQ ID NO:45), Figure 22 (SEQ ID NO:52), Figure 24 (SEQ ID NO:59), Figure 26 (SEQ ID NO:64), Figure 28 (SEQ ID NO:69), Figure 30 (SEQ ID NO:74), Figure 33 (SEQ ID NO:85), Figure 35 (SEQ ID NO:90), Figure 37 (SEQ ID NO:97), Figure 39 (SEQ ID NO:102), Figure 41 (SEQ ID NO:109), Figure 43 (SEQ ID NO:114), Figure 45 (SEQ ID NO:119), Figure 47 (SEQ ID NO:124), Figure 49 (SEQ ID NO:132), Figure 51 (SEQ ID NO:137), Figure 53 (SEQ ID NO:145), Figure 55 (SEQ ID NO:150), Figure 59 (SEQ ID NO:157), Figure 61 (SEQ ID NO:162), Figure 63 (SEQ ID NO:169), Figure 66 (SEQ ID NO:178), Figure 68 (SEQ ID NO:183), Figure 70 (SEQ ID NO:190), Figure 73 (SEQ ID NO:196), Figure 75 (SEQ ID NO:206), Figure 77 (SEQ ID NO:211), Figure 79 (SEQ ID NO:216), Figure 81 (SEQ ID NO:221), Figure 83 (SEQ ID NO:226), Figure 85 (SEQ ID NO:231), Figure 87 (SEQ ID NO:236), Figure 89 (SEQ ID NO:245), Figure 91 (SEQ ID NO:254), Figure 93 (SEQ ID NO:259), Figure 95 (SEQ ID NO:264), Figure 98 (SEQ ID NO:270), Figure 109 (SEQ ID NO:284), Figure 118 (SEQ ID NO:296), Figure 120 (SEQ ID NO:301), Figure 122 (SEQ ID NO:303), Figure 125 (SEQ ID NO:309), Figure 129 (SEQ ID NO:322), Figure 132 (SEQ ID NO:330), Figure 136 (SEQ ID NO:337), Figure 139 (SEQ ID NO:346), Figure 142 (SEQ ID NO:352), Figure 145 (SEQ ID NO:358), Figure 147 (SEQ ID NO:363), Figure 149 (SEQ ID NO:370), Figure 151 (SEQ ID NO:375), Figure 153 (SEQ ID NO:380), Figure 155 (SEQ ID NO:385), Figure 157 (SEQ ID NO:390), Figure 159 (SEQ ID NO:395), Figure 161 (SEQ ID NO:400), Figure 163 (SEQ ID NO:405), Figure 165 (SEQ ID NO:410), Figure 167 (SEQ ID NO:415), Figure 169 (SEQ ID NO:420), Figure 171 (SEQ ID NO:425), Figure 173 (SEQ ID NO:430), Figure 177 (SEQ ID NO:437), Figure 179 (SEQ ID NO:442), Figure 181 (SEQ ID NO:447), Figure 183 (SEQ ID NO:452), Figure 185 (SEQ ID NO:454), Figure 187 (SEQ ID NO:456), Figure 190 (SEQ ID NO:459), Figure 192 (SEQ ID NO:464), Figure 194 (SEQ ID NO:466), Figure 196 (SEQ ID NO:468), Figure 198 (SEQ ID NO:470), Figure 200 (SEQ ID NO:472), Figure 202 (SEQ ID NO:477), Figure 204 (SEQ ID NO:483), Figure 207 (SEQ ID NO:488), Figure 209 (SEQ ID NO:496), Figure 211 (SEQ ID NO:498), Figure 213 (SEQ ID NO:506), Figure 215 (SEQ ID NO:508), Figure 217 (SEQ ID NO:510), Figure 219 (SEQ ID NO:515), Figure 222 (SEQ ID NO:523), Figure 225 (SEQ ID NO:526), Figure 230 (SEQ ID NO:612), Figure 232 (SEQ ID

NO:614), Figure 234 (SEQ ID NO:616) or Figure 236 (SEQ ID NO:618), lacking its associated signal peptide.

22. A method of detecting a PRO4993 polypeptide in a sample suspected of containing a PRO4993 polypeptide, said method comprising contacting said sample with a PRO337 polypeptide and determining the formation of a PRO4993/PRO337 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO4993 polypeptide in said sample.

23. The method according to Claim 22, wherein said sample comprises cells suspected of expressing said PRO4993 polypeptide.

24. The method according to Claim 22, wherein said PRO337 polypeptide is labeled with a detectable label.

25. The method according to Claim 22, wherein said PRO337 polypeptide is attached to a solid support.

26. A method of detecting a PRO337 polypeptide in a sample suspected of containing a PRO337 polypeptide, said method comprising contacting said sample with a PRO4993 polypeptide and determining the formation of a PRO4993/PRO337 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO337 polypeptide in said sample.

27. The method according to Claim 26, wherein said sample comprises cells suspected of expressing said PRO337 polypeptide.

28. The method according to Claim 26, wherein said PRO4993 polypeptide is labeled with a detectable label.

29. The method according to Claim 26, wherein said PRO4993 polypeptide is attached to a solid support.

30. A method of detecting a PRO1559 polypeptide in a sample suspected of containing a PRO1559 polypeptide, said method comprising contacting said sample with a PRO725, PRO700 or PRO739 polypeptide and determining the formation of a PRO1559/PRO725, PRO700 or PRO739 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO1559 polypeptide in said sample.

31. The method according to Claim 30, wherein said sample comprises cells suspected of expressing said PRO1559 polypeptide.

32. The method according to Claim 30, wherein said PRO725, PRO700 or PRO739 polypeptide is labeled with a detectable label.

33. The method according to Claim 30, wherein said PRO725, PRO700 or PRO739 polypeptide is attached to a solid support.

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34. A method of detecting a PRO725, PRO700 or PRO739 polypeptide in a sample suspected of containing a PRO725, PRO700 or PRO739 polypeptide, said method comprising contacting said sample with a PRO1559 polypeptide and determining the formation of a PRO1559/PRO725, PRO700 or PRO739 polypeptide conjugate in said sample, wherein the formation of said conjugate is indicative of the presence of a PRO725, PRO700 or PRO739 polypeptide in said sample.

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35. The method according to Claim 34, wherein said sample comprises cells suspected of expressing said PRO725, PRO700 or PRO739 polypeptide.

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36. The method according to Claim 34, wherein said PRO1559 polypeptide is labeled with a detectable label.

37. The method according to Claim 34, wherein said PRO1559 polypeptide is attached to a solid support.

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38. A method of linking a bioactive molecule to a cell expressing a PRO337 polypeptide, said method comprising contacting said cell with a PRO4993 polypeptide that is bound to said bioactive molecule and allowing said PRO337 and PRO4993 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

25

39. The method according to Claim 38, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

40. The method according to Claim 38, wherein said bioactive molecule causes the death of said cell.

30

41. A method of linking a bioactive molecule to a cell expressing a PRO4993 polypeptide, said method comprising contacting said cell with a PRO337 polypeptide that is bound to said bioactive molecule and allowing said PRO4993 and PRO337 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

35

42. The method according to Claim 41, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

43. The method according to Claim 41, wherein said bioactive molecule causes the death of said cell.

5 44. A method of linking a bioactive molecule to a cell expressing a PRO1559 polypeptide, said method comprising contacting said cell with a PRO725, PRO700 or PRO739 polypeptide that is bound to said bioactive molecule and allowing said PRO1559 and PRO725, PRO700 or PRO739 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

10 45. The method according to Claim 44, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

15 46. The method according to Claim 44, wherein said bioactive molecule causes the death of said cell.

20 47. A method of linking a bioactive molecule to a cell expressing a PRO725, PRO700 or PRO739 polypeptide, said method comprising contacting said cell with a PRO1559 polypeptide that is bound to said bioactive molecule and allowing said PRO1559 and PRO725, PRO700 or PRO739 polypeptides to bind to one another, thereby linking said bioactive molecules to said cell.

48. The method according to Claim 47, wherein said bioactive molecule is a toxin, a radiolabel or an antibody.

25 49. The method according to Claim 47, wherein said bioactive molecule causes the death of said cell.

30 50. A method of modulating at least one biological activity of a cell expressing a PRO337 polypeptide, said method comprising contacting said cell with a PRO4993 polypeptide or an anti-PRO337 antibody, whereby said PRO4993 polypeptide or said anti-PRO337 antibody binds to said PRO337 polypeptide, thereby modulating at least one biological activity of said cell.

51. The method according to Claim 50, wherein said cell is killed.

52. A method of modulating at least one biological activity of a cell expressing a PRO4993 polypeptide, said method comprising contacting said cell with a PRO337 polypeptide or an anti-PRO4993 antibody, whereby said PRO337 polypeptide or said anti-PRO4993 antibody binds to said PRO4993 polypeptide, thereby modulating at least one biological activity of said cell.

5 53. The method according to Claim 52, wherein said cell is killed.

54. A method of modulating at least one biological activity of a cell expressing a PRO1559 polypeptide, said method comprising contacting said cell with a PRO725, PRO700 or PRO739 polypeptide or an anti-PRO1559 antibody, whereby said PRO725, PRO700 or PRO739 polypeptide or said anti-PRO1559  
10 antibody binds to said PRO1559 polypeptide, thereby modulating at least one biological activity of said cell.

55. The method according to Claim 54, wherein said cell is killed.

56. A method of modulating at least one biological activity of a cell expressing a PRO725, PRO700  
15 or PRO739 polypeptide, said method comprising contacting said cell with a PRO1559 polypeptide or an anti-PRO725, anti-PRO700 or anti-PRO739 antibody, whereby said PRO1559 polypeptide or said anti-PRO725, anti-PRO700 or anti-PRO739 antibody binds to said PRO725, PRO700 or PRO739 polypeptide, thereby modulating at least one biological activity of said cell.

20 57. The method according to Claim 56, wherein said cell is killed.



**FIGURE 1**

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGGAGGCACAGGTGGCCCCCACCACCCGGAGG  
AGCAGCTCCTGCCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGA  
AGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCT  
TCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTTAGGGTGTGTGCT  
GTCCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCC  
TCACCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATTATAGGACCGCCTAC  
CGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAG  
GACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAG  
GGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAG  
TCAGATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGC  
CGGCAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTG  
TGCCCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAG  
GAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCT  
GGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCC  
TCCTGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTC  
CTGGAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGG  
CTGGACTGAGCCCCTCACGCCGCCCTGCAGCCCCCATGCCCTGCCCAACATGCTGGGGGTC  
CAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTTTTCCTCCTC  
CCCTTCCCTCGGGAGGGTCCCCAGACCCTGGCATGGGATGGGCTGGGATTTTTTTTGTGAAT  
CCACCCCTGGCTACCCCCACCCTGGTTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCA  
GCTGAGGGAAGGTACGAGTTCCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCC  
CGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAA  
CGTGAAAGGGCGGCCGCGACTCT  
AGAGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGT  
TACAAAT

**FIGURE 2**

MTDSPPPGHPPEEKATPPGGTGHEGLSGGAADVASGVGSGRHRARLPARPLGCVLSRAHGDPV  
SESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGAC  
GAAICQPPCRNGGSCVQPGRRCRCPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCW  
EGHSLSADGTLCVPGKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLAS  
QALEHGLPDPGSLLVHSFQQGLGRIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 93-97, 270-274

**N-myristoylation sites.**

amino acids 19-25, 78-84, 97-103, 100-106, 103-109, 157-163,  
191-197, 265-271

**Amidation site.**

amino acids 26-30

**Aspartic acid and asparagine hydroxylation site.**

amino acids 152-164

**Cell attachment sequence.**

amino acids 130-133

**EGF-like domain cysteine pattern signature.**

amino acids 123-135

**FIGURE 3**

CGCTCGCCCCGTGCCCCCTCGCCTCCCCGCAGAGTCCCCTCGCGGCAGCAGATGTGTGTGGG  
GTCAGCCCACGGCGGGGACT**ATGG**TGAAATTCCCGGCGCTCACGCACTACTGGCCCCCTGATC  
CGGTTCTTGGTGCCCCCTGGGCATCACCAACATAGCCATCGACTTCGGGGAGCAGGCCTTGAA  
CCGGGGCATTGCTGCTGTCAAGGAGGATGCAGTCGAGATGCTGGCCAGCTACGGGCTGGCGT  
ACTCCCTCATGAAGTTCTTCACGGGTCCCATGAGTGACTTCAAAAATGTGGGCCTGGTGTTT  
GTGAACAGCAAGAGAGACAGGACCAAAGCCGTCTGTGTATGGTGGTGGCAGGGGCCATCGC  
TGCCGTCTTTCACACACTGATAGCTTATAGTGATTTAGGATACTACATTATCAATAAACTGC  
ACCATGTGGACGAGTCGGTGGGGAGCAAGACGAGAAGGGCCTTCCTGTACCTCGCCGCCTTT  
CCTTTCATGGACGCAATGGCATGGACCCATGCTGGCATTCTCTTAAACACAAATACAGTTT  
CCTGGTGGGATGTGCCTCAATCTCAGATGTCATAGCTCAGGTTGTTTTTGTAGCCATTTTGC  
TTCACAGTCACCTGGAATGCCGGGAGCCCCCTGCTCATCCCGATCCTCTCCTTGATCATGGGC  
GCACTTGTGCGCTGCACCACCCTGTGCCTGGGCTACTACAAGAACATTCACGACATCATCCC  
TGACAGAAGTGGCCCCGAGCTGGGGGGAGATGCAACAATAAGAAAGATGCTGAGCTTCTGGT  
GGCCTTTGGCTCTAATTCTGGCCACACAGAGAATCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTTCG  
ACAAGAATAACCCCAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCAGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGAGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTCTTGCCCCCAGCTCTGTGCTGCG  
GATCATCGTCTCATCGCCAGCCTCGTGGTCTACCTACCTGGGGGTGCACGGTGCAGCCC  
TGGGCGTGGGCTCCCTCCTGGCGGGCTTTGTGGGAGAATCCACCATGGTCGCCATCGCTGCG  
TGCTATGTCTACCGGAAGCAGAAAAAGAAGATGGAGAATGAGTCGGCCACGGAGGGGGAAGA  
CTCTGCCATGACAGACATGCCTCCGACAGAGGAGGTGACAGACATCGTGGAATGAGAGAGG  
AGAATGAAT**TAA**GGCACGGGACGCCATGGGCACTGCAGGGACGGTCAGTCAGGATGACACTTC  
GGCATCATCTCTTCCCTCTCCCATCGTATTTTGTTCCTTTTTTTTTGTTTTGTTTTGGTAAT  
GAAAGAGGCCTTGATTTAAAGGTTTCGTGTCAATTCTCTAGCATACTGGGTATGCTCACACT  
GACGGGGGGACCTAGTGAATGGTCTTTACTGTTGCTATGTAAAAACAAACGAAACAACTGAC  
TTCATACCCCCTGCCTCACGAAAACCCAAAAGACACAGCTGCCTCACGGTTGACGTTGTGTCC  
TCCTCCCCTGGACAATCTCCTCTTGGAACCAAAGGACTGCAGCTGTGCCATCGCGCCTCGGT  
CACCTGCACAGCAGGCCACAGACTCTCCTGTCCCCCTTCATCGCTCTTAAGAATCAACAGG  
TTAAAACTCGGCTTCCTTTGATTTGCTTCCCAGTCACATGGCCGTACAAAGAGATGGAGCCC  
CGGTGGCCTCTTAAATTTCCCTTCTGCCACGGAGTTCGAAACCATCTACTCCACACATGCAG  
GAGGCGGGTGGCACGCTGCAGCCCGGAGTCCCCGTTTACACTGAGGAACGGAGACCTGTGAC  
CACAGCAGGCTGACAGATGGACAGAATCTCCCGTAGAAAGGTTTGGTTTGAAATGCCCCGGG  
GGCAGCAAACCTGACATGGTTGAATGATAGCATTTCACTCTGCGTTCTCCTAGATCTGAGCAA  
GCTGTCAGTTCTCACCCCCACCGTGTATATACATGAGCTAACTTTTTTAAATTGTCACAAAA  
GCGCATCTCCAGATTCCAGACCCTGCCGCATGACTTTTCCTGAAGGCTTGCTTTTCCCTCGC  
CTTTCCTGAAGGTGCGATTAGAGCGAGTCACATGGAGCATCCTAACTTTGCATTTTAGTTTT  
TACAGTGAAGTGAAGCTTTAAGTCTCATCCAGCATCTAATGCCAGGTTGCTGTAGGGTAAC  
TTTTGAAGTAGATATATTACCTGGTTCTGCTATCCTTAGTCATAACTCTGCGGTACAGGTAA  
TTGAGAATGTACTACGGTACTTCCCTCCCACACCATAACGATAAAGCAAGACATTTTATAACG  
ATACCAGAGTCACTATGTGGTCTCCTGAAATAACGCATTCGAAATCCATGCAGTGCAGTA  
TATTTTTCTAAGTTTTTGGAAAGCAGGTTTTTTCCTTTAAAAAAATTATAGACACGGTTCCT  
AAATTGATTTAGTCAGAATTCCTAGACTGAAAGAACCTAAACAAAAAAATATTTTAAAGATA  
TAAATATATGCTGTATATGTTATGTAATTTATTTTAGGCTATAATACATTTCTATTTTCGC  
ATTTTCAATAAAATGTCTCTAATACAAAAA

**FIGURE 4**

MVKFPAL~~TH~~YWPLIRFLVPLGITNIAIDFGEQALNRGIAAVKEDAVEMLASYGLAYSLMKFF  
TGPMSDFKNVGLVFN~~SK~~RDR~~TK~~AVLCMVVAGAI~~AA~~VFHTLIAYS~~DL~~GY~~YI~~INKLHHVDES~~V~~  
GSKTRRAFLYLA~~AF~~PFMDAMAWTHAGILLKHKYSFLVGCASISDVIAQVVFVAILLHSHLEC  
REPL~~LIP~~ILSLYMGALVRCTTLCLGY~~YK~~NIHDIIPDRSGPELGGDATIRKMLSFWWPLALIL  
ATQ~~RIS~~RPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMPYGWLTEIRAVYPAFDKNNPSN  
KLVSTSN~~TV~~TAAHIKKFTFVCMALSLTLCFVMFWTPNVSEKILIDIIGVDFAF~~AE~~LCVVPLR  
IFSFFPVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYLG~~VH~~GATLGVGSL~~L~~  
AGFVGESTMVAIAACYVYRKQKKK~~MEN~~ESATEGEDSAMTDMPPT~~EE~~VTDIVEMRENE

**Transmembrane domains:**

amino acids 86-106, 163-179, 191-205, 237-253, 327-343, 357-374,  
408-423, 431-445

**FIGURE 5**

CCTGACAGAAGTGCCCCGGAGCTGGGGGAGATNCAACATTAAGAAGATGCTGAGCTTCTGGT  
GCCNTTTGGCTCTAATTCTGGCCACACAGAGAANCAGTCGGCCTATTGTCAACCTCTTTGTT  
TCCCGGGACCTTGGTGGCAGTTCTGCAGCCACAGAGGCAGTGGCGATTTTGACAGCCACATA  
CCCTGTGGGTCACATGCCATACGGCTGGTTGACGGAAATCCGTGCTGTGTATCCTGCTTTCG  
ACAAGAATAACCCCAAGCAACAACTGGTGAGCACGAGCAACACAGTCACGGCGGCCCACATC  
AAGAAGTTCACCTTCGTCTGCATGGCTCTGTCACTCACGCTCTGTTTCGTGATGTTTTGGAC  
ACCCAACGTGTCTGNGAAAATCTTGATAGACATCATCGGAGTGGACTTTGCCTTTGCAGAAC  
TCTGTGTTGTTCCCTTTGCGGATCTTCTCCTTCTTCCCAGTTCCAGTCACAGTGAGGGCGCAT  
CTCACCGGGTGGCTGATGACACTGAAGAAAACCTTCGTC



**FIGURE 6**

TGACGGAATCCCGGGCTGGGTATCCTGGTTTNGACAAGATAAACCCCCAGCAANAAATTGGG  
GAGCAGGGCAAACAGTNACGGGCAGCCCACATCAAGAAGTTCACCTTNGTTTGNATGGNTC  
TGTCAACTCACGCTNTGTTTCGTGATGTTTTGGACACCCAAAGTGTTTGAGAAAATTTTGAT  
AGACATNATCGGAGTGGANTTTGCCTTTGCAGAANTTTGNGNTGTTTCCTTTGCGGATTTTCT  
CCTTTTTCCAGTTCCAGTCACAGNGAGGGCGCATCTCACCGGGNGGNTGATGACANTGAAG  
AAAACCTTTGTCCTTGCCCCCAGCTNTTTGGTGCGGATCATTTGTCCTNATNGCCAGCCTTGT  
GGTCCTACCCTACCTGGGGGTGCACGGTGCGACCCTGGGCGTGGGTTCCTCCTGGCGGGCA

FIGURE 7

-TATTCCCAGTTCCGGTCACGGGGAGGGCGCATNTCACCGGGTGGCTGANGACACTGAAGAAA  
ACCTTNGTCCTTGCCCCCAGNTTTGTGNTGCGGATNATCGTCCTCATCGCCAGCCTNGTGGT  
CCTACCCTACCTGGGGGTGCACGGTGAGAC

**FIGURE 8**

GCCCCGCGCCCGGCGCCGGGCGCCCGAAGCCGGGAGCCACCGCCATGGGGGCCTGCCTGGGA  
GCCTGCTCCCTGCTCAGCTGCGCGTCCTGCCTCTGCGGCTCTGCCCCCTGCATCCTGTGCAG  
CTGCTGCCCCGCCAGCCGCAACTCCACCGTGAGCCGCCTCATCTTCACGTTCTTCCTCTTCC  
TGGGGGTGCTGGTGTCCATCATTATGCTGAGCCCCGGGCGTGGAGAGTCAGCTCTACAAGCTG  
CCCTGGGTGTGTGAGGAGGGGGCGGGATCCCCACCGTCCTGCAGGGCCACATCGACTGTGG  
CTCCCTGCTTGGCTACCGCGCTGTCTACCGCATGTGCTTCGCCACGGCGGCCTTCTTCTTCT  
TCTTTTTTACCCTGCTCATGCTCTGCGTGAGCAGCAGCCGGGACCCCCGGGCTGCCATCCAG  
AATGGGTTTTGGTTCTTTAAGTTCCTGATCCTGGTGGGCCTCACCGTGGGTGCCTTCTACAT  
CCCTGACGGCTCCTTCACCAACATCTGGTTCTACTTCGGCGTCGTGGGCTCCTTCCTCTTCA  
TCCTCATCCAGCTGGTGCTGCTCATCGACTTTGCGCACTCCTGGAACCAGCGGTGGCTGGGC  
AAGGCCGAGGAGTGCGATTCCCGTGCTGGTACGCAGGCCTCTTCTTCTTCACTCTCCTCTT  
CTACTTGCTGTGATCGCGGCCGTGGCGCTGATGTTTCATGTACTACACTGAGCCCAGCGGCT  
GCCACGAGGGCAAGGTCTTCATCAGCCTCAACCTCACCTTCTGTGTCTGCGTGTCCATCGCT  
GCTGTCCTGCCCAAGGTCCAGGACGCCCAGCCCAACTCGGGTCTGCTGCAGGCCTCGGTCTAT  
CACCTCTACACCATGTTTGTACCTGGTCAGCCCTATCCAGTATCCCTGAACAGAAATGCA  
ACCCCCATTTGCCAACCAGCTGGGCAACGAGACAGTTGTGGCAGGCCCCGAGGGCTATGAG  
ACCCAGTGGTGGGATGCCCCGAGCATTGTGGGCCTCATCATCTTCCTCCTGTGCACCCTCTT  
CATCAGTCTGCGCTCCTCAGACCACCGGCAGGTGAACAGCCTGATGCAGACCGAGGAGTGCC  
CACCTATGCTAGACGCCACACAGCAGCAGCAGCAGCAGGTGGCAGCCTGTGAGGGCCGGGCC  
TTTGACAACGAGCAGGACGGCGTCACCTACAGCTACTCCTTCTTCCACTTCTGCCTGGTGCT  
GGCCTCACTGCACGTCATGATGACGCTCACCAACTGGTACAAGCCCGGTGAGACCCGGAAGA  
TGATCAGCACGTGGACCGCCGTGTGGGTGAAGATCTGTGCCAGCTGGGCAGGGCTGCTCCTC  
TACCTGTGGACCCTGGTAGCCCCACTCCTCCTGCGCAACCGCGACTTCAGCTTGAGGCAGCCT  
CACAGCCTGCCATCTGGTGCTCCTGCCACCTGGTGCCTCTCGGCTCGGTGACAGCCAACCT  
GCCCCCTCCCCACACCAATCAGCCAGGCTGAGCCCCCACCCTGCCCCAGCTCCAGGACCTG  
CCCCTGAGCCGGGCCTTCTAGTCGTAGTGCCCTTCAGGGTCCGAGGAGCATCAGGCTCCTGCA  
GAGCCCCATCCCCCGCCACACCCACACGGTGGAGCTGCCTCTTCCCTTCCCCTCCTCCCTGT  
TGCCATACTCAGCATCTCGGATGAAAGGGCTCCCTTGTCCTCAGGCTCCACGGGAGCGGGG  
CTGCTGGAGAGAGCGGGGAACTCCCACCACAGTGGGGCATCCGGCACTGAAGCCCTGGTGT  
CCTGGTCACGTCCCCCAGGGGACCCTGCCCCCTTCCCTGGACTTCGTGCCTTACTGAGTCTCT  
AAGACTTTTTCTAATAACAAGCCAGTGCGTGTAATAAAAAA.

**FIGURE 9**

MGACLGACSLLSASCCLCGSAPCILCSCCPASRNSTVSRLIFTFFLFLGVLVSIIMLSPGVE  
SOLYKLPWVCEEAGAGIPTVLQGHIDCGSLLGYRAVYRMCFATAAFFFFFFFTLLMLCVSSSRD  
PRAAIQNGFWFFKFLILVGLTVGAFYIPDGSFTNIWFYFGVVGSEFLFILIQLVLLIDFAHSW  
NQRWLGKAEECDSRAWYAGLFFFTLLFYLLSIAAVALMFMYYTEPSGCHEGKVFISLNLTF  
VCVSIAAVLPKVQDAQPNSGLLQASVITLYTMFVTWSALSSIQKCNPHLPTQLGNETVVA  
GPEGYETQWWDAPSIVGLIIFLLCTLFISLRSSDHRQVNSLMQTEECPPMLDATQQQQQQVA  
ACEGRAFDNEQDGVITYSYFFHFCLVLASLHVMMTLTNWYKPGETRKMISTWTAVWVKICAS  
WAGLLLYLWTLVAPLLLRNRDFS

**Signal sequence:**

amino acids 1-20

**Transmembrane domains:**

amino acids 40-58, 101-116, 134-150, 162-178, 206-223, 240-257,  
272-283, 324-340, 391-406, 428-444

**FIGURE 10**

GAGCGAGGCCGGGGACTGAAGGTGTGGGTGTCGAGCCCTCTGGCAGAGGGTTAACCTGGGTC  
AAATGCACGGATTCTCACCTCGTACAGTTACGCTCTCCCGCGGCACGTCCGCGAGGACTTGA  
AGTCCTGAGCGCTCAAGTTTGTCCGTAGGTGAGAGAAAGGCCATGGAGGTGCCGCCACCGGC  
ACCGCGGAGCTTTCTCTGTAGAGCATTGTGCCTATTTCCCCGAGTCTTTGCTGCCGAAGCTG  
TGA CTGCCGATTTCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCC  
TATTACCCGGAATCTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAG  
AATTTCAAAGGACCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGG  
TGTATGGGGGAATACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCA  
GAAATTTATCATAACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTT  
CATTCGTTATGGCTGGCGCTGGGGTTGGAGAACTGCAGTGTTTGTGACTATATTCAACACAG  
TGAACACTAGTCTGAATGTATACCGAAATAAAGATGCCTTAAGCCATTTTGTAATTGCAGGA  
GCTGTCACGGGAAGTCTTTT TAGGATAAACGTAGGCCTGCGTGGCCTGGTGGCTGGTGGCAT  
AATTGGAGCCTTGCTGGGCACTCCTGTAGGAGGCCTGCTGATGGCATTTCAGAAGTACGCTG  
GTGAGACTGTT CAGGAAAGAAAACAGAAGGATCGAAAGGCACTCCATGAGCTAAAACTGGAA  
GAGTGGAAGGCAGACTACAAGTTACTGAGCACCTCCCTGAGAAAATTGAAAGTAGTTTACG  
GGAAGATGAACCTGAGAATGATGCTAAGAAAATTGAAGCACTGCTAAACCTTCCTAGAAACC  
CTTCAGTAATAGATAAACAAGACAAGGACTGAAAGTGCTCTGAACTTGAACTCACTGGAGA  
GCTGAAGGGAGCTGCCATGTCCGATGAATGCCAACAGACAGGCCACTCTTTGGTCAGCCTGC  
TGACAAATTTAAGTGCTGGTACCTGTGGTGGCAGTGGCTTGCTCTTGTCTTTTCTTTTCTT  
TTTAACTAAGAATGGGGCTGTTGTACTCTCACTTTACTTATCCTTAAATTTAAATACATACT  
TATGTTTGTATTAATCTATCAATATATGCATACATGGATATATCCACCCACCTAGATTTTAA  
GCAGTAAATAAAACATTT CGCAAAGATTAAAGTTGAATTTTACAGTTT



**FIGURE 11**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23318

><subunit 1 of 1, 285 aa, 1 stop

><MW: 32190, pI: 9.03, NX(S/T): 2

MEVPPPAPRSFLCRALCLFPRVFAAEAVTADSEVLEERQKRLPYVPEPYYPESGWDRLRELF  
GKDEQQRISKDLANICKTAATAGIIGWVYGGIPAFIHAKQQYIEQSQAIEYHNRFDVQSAH  
RAATRGFIRYGWRWGWRTAVFVTIFNTVNTSLNVYRNKDALSHFVIAGAVTGSLFRINVGLR  
GLVAGGIIGALLGTPVGGLLMAFQKYAGETVQERKQKDRKALHELKLEEWKGRLQVTEHLPE  
KIESSLREDEPENDAKKIEALLNLPRNPSVIDKQDKD

**Important Features:****Signal Peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 76-96 and 171-195

**N-glycosylation site:**

amino acids 153-156

77/237

**FIGURE 12**

CGGAAGTCCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATCTGGATGGGACCGCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGGA  
CCTTGCTAATATCTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGAA  
TACCAGCTTTTATTCATGCTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATCAT  
AACCGGTTTGATGCTGTGCAATCTGCACATCGTGCTGCCACACGAGGCTTCATTCGTTTCATG  
GCTGGCGCCGAACC

**FIGURE 13**

TCAAGTTTGTCCGTAGGTCGAGAGAAGGCCATGGAGGTGCCGCCACCGGCACCGCGGAGCTT  
TTTTCTGTAGAGCATTGTGCCTATTTCCCCGAGTTTTTGCTGCCGAAGCTGTGACTGCCGAT  
TCGGAAGTCCTTGAGGAGCGTCAGAAGCGGCTTCCCTACGTCCCAGAGCCCTATTACCCGGA  
ATTTGGATGGGACCGCCTCCGGGAGCTGTTTGGCAAAGATGAACAGCAGAGAATTTCAAAGG  
ACCTTGCTGATATNTGTAAGACGGCAGCTACAGCAGGCATCATTGGCTGGGTGTATGGGGGA  
ATACCAGCTTTTATTCATGNTAAACAACAATACATTGAGCAGAGCCAGGCAGAAATTTATNA  
TAACC

FIGURE 14

GAGCCGCCGCCGCGCGCGCGCGCGCACTGCAGCCCCAGGCCCGGCCCGCCACCCACGTCT  
GCGTTGCTGCCCCGCCTGGGCCAGGCCCCAAAGGCAAGGACAAAGCAGCTGTCAGGGAACCT  
CCGCCGGAGTCGAATTTACGTGCAGCTGCCGGCAACCACAGGTTCCAAGATGGTTTGCGGGG  
GCTTCGCGTGTTCCAAGAACTGCCTGTGCGCCCTCAACCTGCTTTACACCTTGGTTAGTCTG  
CTGCTAATTGGAATTGCTGCGTGGGGCATTGGCTTCGGGCTGATTTCCAGTCTCCGAGTGGT  
CGGCGTGGTCATTGCAGTGGGCATCTTCTTGTTCCCTGATTGCTTTAGTGGGTCTGATTGGAG  
CTGTAAACATCATCAGGTGTTGCTATTTTTTTTATATGATTATTCTGTTACTTGTATTTATT  
GTTCAAGTTTTCTGTATCTTGCGCTTGTTTAGCCCTGAACCAGGAGCAACAGGGTCAGCTTCT  
GGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAATCTAAACTGCT  
GTGGGTTCCGAAGTGTTAACCCTAATGACACCTGTCTGGCTAGCTGTGTTAAAAGTGACCAC  
TCGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGAGATTTGTTGG  
TGGCATTGGCCTGTTCTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACCTACAGATACA  
GGAACCAGAAAGACCCCCGCGCGAATCCTAGTGCATTCCTTTGATGAGAAAACAAGGAAGAT  
TTCCTTTCGTATTATGATCTTGTTCACTTTCTGTAATTTTCTGTAAAGCTCCATTTGCCAGT  
TTAAGGAAGGAAACACTATCTGGAAAAGTACCTTATTGATAGTGGAATTATATATTTTTTACT  
CTATGTTTCTCTACATGTTTTTTTTCTTTCCGTTGCTGAAAAATATTTGAAACTTGTGGTCTC  
TGAAGCTCGGTGGCACCTGGAATTTACTGTATTCATTGTCGGGCACTGTCCACTGTGGCCTT  
TCTTAGCATTTTTTACCTGCAGAAAACTTTGTATGGTACCCTGTGTTGGTTATATGGTGAA  
TCTGAACGTACATCTCACTGGTATAATTATATGTAGCACTGTGCTGTGTAGATAGTTCCTAC  
TGGA AAAAGAGTGGAATTTATTAAAATCAGAAAGTATGAGATCCTGTTATGTTAAGGGAAA  
TCCAAATTCCCAATTTTTTTTTGGTCTTTTTTAGGAAAGATTGTTGTGGTAAAAAGTGTTAGTA  
TAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAAATAGTTAT  
GTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTGGTTT  
CATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCATCAGAATGGAACGAGTTT  
TGAGTAATCAGGAAGTATATCTATATGATCTTGATATTGTTTTATAATAATTTGAAGTCTAA  
AAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCACGTAGCAAAAAGATATTTG  
ATTATCTTAAAAAATTGTTAAATACCGTTTTTCATGAAATTTCTCAGTATTGTAACAGCAACTT  
GTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATTGTGTG  
GCTCTGTATATTCTGTTA AAAAATTAAGGACAGAAACCTTTCTTTGTGTATGCATGTTTGA  
ATTA AAAAGAAAGTAATGGAAG

74/237

**FIGURE 15**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA39979

><subunit 1 of 1, 204 aa, 1 stop

><MW: 22147, pI: 8.37, NX(S/T): 3

MVCGGFACSKNCLCALNLLYTLVSLLLIGIAAWGIGFGLISSLRVVGVVIAVGIFLFLIALV  
GLIGAVKHHQVLLFFYMIILLLVFIVQFSVSCACLALNQEQQGQLLEVGVNNTASARNDIQR  
NLNCCGFRSVNPNDTCLASCVKSDHSCSPCAPIIGEYAGEVLRVFGGIGLFFSFTEILGVWL  
TYRYRNQKDPRANPSAFL

**Signal Peptide:**

amino acids 1-34

**Transmembrane domains:**

amino acids 47-63, 72-95 and 162-182

15/237



**FIGURE 16**

TGATTGGAGCTGTAAAAAANTCTTCAGGTGTTGTNATTTTTTTTATATGATTATTCTGTAANT  
TGTATTTATTGTTTCAGTTTTNTGTATCTTGCGCTTGTTTAGCCNTGAACCAGGAGCAACAGG  
GTCAGNTTNTGGAGGTTGGTTGGAACAATACGGCAAGTGCTCGAAATGACATCCAGAGAAAT  
NTAAACTGCTGTGGGTTCGGAAGTGTTAACCCTAAATGACACCTGTNTGGCTAGCTGTGTAA  
AAGTGACCACTNGTGCTCGCCATGTGCTCCAATCATAGGAGAATATGCTGGAGAGGTTTTGA  
GATTTGTTGGTGGCATTGGCCTGTTNTTCAGTTTTACAGAGATCCTGGGTGTTTGGCTGACC  
TACAGATACAGGAACCAG

**FIGURE 17**

AATCCCAAATTCCCCAATTTTTTTGGNCTTTTTAGGGAAAGATGTGTTGTGGTAAAAAGTGT  
TAGTATAAAAATGATAATTTACTTGTAGTCTTTTATGATTACACCAATGTATTCTAGAATAG  
TTATGTCTTAGGAAATTGTGGTTTAATTTTTGACTTTTACAGGTAAGTGCAAAGGAGAAGTG  
GTTTCATGAAATGTTCTAATGTATAATAACATTTACCTTCAGCCTCCCATCAGAATGGAACG  
AGTTTTGAGTAATCCAGGAAGTATATCTATATGATCTTGATATTGTTTTATATAATTTGAAG  
TCTAAAAGACTGCATTTTTTAAACAAGTTAGTATTAATGCGTTGGCCCACGTAGCAAAAAGAT  
ATTTGATTATCTTAAAAATTGTTAAATACCGTTTTTCATGAAAGTTCTCAGTATTGTAACAGC  
AACTTGTCAAACCTAAGCATATTTGAATATGATCTCCCATAAATTTGAAATTGAAATCGTATT  
GTGTGGAGGAAATGGCAATCTTATGTGTGCTGAAGGACACAGTAAGAGCACCAAGTTGTGCC  
CCACTTGC

**FIGURE 18**

ATGATTATTCTGTTACTTGTATTTATTG TTCAGTTTTATGGTATCTTGCGCTTGTTTAGCCC  
CTGAAACCAGGAGCAACAGGGNNCAGCTTCCTGGAGGTTGGTTGGCAACAATCACGGCCAAG  
TGACTCCGCAAATGACATCCCAGAGAAATCCTAAACTGCTGTGGGTTCCGAAGTGTTAACCC  
AAATGACACCTGTCTGGCTNGCTGTGTTAAAAGTGACCACTCGTGCTCGCCATGTGCTCCAA  
TCATAGGAGAATATGC

**FIGURE 19**

CAGTCACCAATGAAAGCTGGGCTGTGTCCTCATGGCCTGGGCCCTCTACCTTTCCCTTGGTGTG  
CTCTGGGTGGCCCAGATGCTACTGGCTGCCAGTTTTTGAGACGCTGCAGTGTGAGGGACCTGT  
CTGCACTGAGGAGAGCAGCTGCCACACGGAGGATGACTTGACTGATGCAAGGGAAGCTGGCT  
TCCAGGTCAAGGCCTACACTTTCAGTGAACCCTTCCACCTGATTGTGTCCTATGACTGGCTG  
ATCCTCCAAGGTCCAGCCAAGCCAGTTTTTTGAAGGGGACCTGCTGGTTCTGCGCTGCCAGGC  
CTGGCAAGACTGGCCACTGACTCAGGTGACCTTCTACCGAGATGGCTCAGCTCTGGGTCCCC  
CCGGGCCTAACAGGGAATTCTCCATCACCGTGGTACAAAAGGCAGACAGCGGGCACTACCAC  
TGCAGTGGCATCTTCCAGAGCCCTGGTCCTGGGATCCCAGAAACAGCATCTGTTGTGGCTAT  
CACAGTCCAAGAACTGTTTCCAGCGCCAATTCTCAGAGCTGTACCCTCAGCTGAACCCCAAG  
CAGGAAGCCCCATGACCCTGAGTTGTCAGACAAAGTTGCCCTGCAGAGGTGAGCTGCCCGC  
CTCCTCTTCTCCTTCTACAAGGATGGAAGGATAGTGCAAAGCAGGGGGCTCTCCTCAGAATT  
CCAGATCCCCACAGCTTCAGAAGATCACTCCGGGTCATACTGGTGTGAGGCAGCCACTGAGG  
ACAACCAAGTTTGGAAACAGAGCCCCCAGCTAGAGATCAGAGTGCAGGGTGCTTCCAGCTCT  
GCTGCACCTCCCACATTGAATCCAGCTCCTCAGAAATCAGCTGCTCCAGGAACTGCTCCTGA  
GGAGGGCCCCTGGGCCTCTGCCTCCGCCGCCAACCCCATCTTCTGAGGATCCAGGCTTTTCTT  
CTCCTCTGGGGATGCCAGATCCTCATCTGTATCACCAGATGGGCCTTCTTCTCAAACACATG  
CAGGATGTGAGAGTCCTCCTCGGTCACTGCTCATGGAGTTGAGGGAATTATCTGGCCACCA  
GAAGCCTGGGACCACAAAGGCTACTGCTGAATAGAAAGTAAACAGTTCATCCATGATCTCACT  
TAACCACCCCAATAAATCTGATTCTTTATTTTCTCTTCTGCTGCTGCACATATGCATAAGTA  
CTTTTACAAGTTGTCCCAGTGTTTTGTTAGAATAATGTAGTTAGGTGAGTGTAATAAATTT  
ATATAAAGTGAGAATTAGAGTTTAGCTATAATTGTGTATTCTCTCTTAACACAACAGAATTC  
TGCTGTCTAGATCAGGAATTTCTATCTGTTATATCGACCAGAATGTTGTGATTTAAAGAGAA  
CTAATGGAAGTGGATTGAATACAGCAGTCTCAACTGGGGGCAATTTTGCCCCCAGAGGACA  
TTGGGCAATGTTTGGAGACATTTTGGTCATTATACTTGGGGGGTTGGGGGATGGTGGGATGT  
GTGTCTACTGGCATCCAGTAAATAGAAGCCAGGGGTGCCGCTAAACATCCTATAATGCACAG  
GGCAGTACCCCAACAACGAAAAATAATCTGGCCCAAAATGTCAGTTGTACTGAGTTTGAGAAA  
CCCCAGCCTAATGAAACCCTAGGTGTTGGGCTCTGGAATGGGACTTTGTCCCTTCTAATTAT  
TATCTCTTTCCAGCCTCATTCAGCTATTCTTACTGACATAACCAGTCTTTAGCTGGTGCTATG  
GTCTGTTCTTTAGTTCTAGTTTGTATCCCCCTCAAAGCCATTATGTTGAAATCCTAATCCCC  
AAGGTGATGGCATTAAAGAAGTGGGCCTTTGGGAAGTGATTAGATCAGGAGTGCAGAGCCCTC  
ATGATTAGGATTAGTGCCCTTATTTAAAAAGGCCCCAGAGAGCTAACTCACCTTCCACCAT  
ATGAGGACGTGGCAAGAAGATGACATGTATGAGAACCACAAAAACAGCTGTCGCCAAACACCG  
ACTCTGTCGTTGCCTTGATCTTGAACCTCCAGCCTCCAGAACTATGAGAAATAAAATTCTGG  
TTGTTTGTAGCCTAA

**FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40594

><subunit 1 of 1, 359 aa, 1 stop

><MW: 38899, pI: 5.21, NX(S/T): 0

MKLGCVLMAWALYLSLGVLWVAQMLLAASFETLQCEGPVCTEESSCHTEDDLTDAREAGFQV  
KAYTFSEPFHLIVSYDWLILQGPAKPVFEGDLLVLRCQAWQDWPLTQVTFYRDGSALGPPGP  
NREFSITVVQKADSGHYHCSGIFQSPGPGIPETASVVAITVQELFPAPILRAVPSAEPQAGS  
PMTLSCQTKLPLQRSAARLLFSFYKDGRIVQSRGLSSEFQIPTASEDHSGSYWCEAATEDNQ  
VWKQSPQLEIRVQGASSAAPPTLNPAPQKSAAPGTAPEEAPGPLPPPPTPSSDPGFSSPL  
GMPDPHLYHQMGLLLKHMQDVRVLLGHLLMELRELSGHQKPGTTKATAE

**Signal sequence:**

amino acids 1-17

**Leucine zipper pattern sequence:**

amino acids 12-33

**Protein kinase C phosphorylation site:**

amino acids 353-355



**FIGURE 21**

CCCACGCGTCCGCCCCACGCGTCCGCCCCACGGGTCCGCCCCACGCGTCCGGGCCACCAGAAGTT  
TGAGCCTCTTTGGTAGCAGGAGGCTGGAAGAAAGGACAGAAGTAGCTCTGGCTGTGATGGGG  
ATCTTACTGGGCCTGCTACTCCTGGGGCACCTAACAGTGGACACTTATGGCCGTCCCATCCT  
GGAAGTGCCAGAGAGTGTAACAGGACCTTGGAAGGGGGATGTGAATCTTCCCTGCACCTATG  
ACCCCTGCAAGGCTACACCCAAGTCTTGGTGAAGTGGCTGGTACAACGTGGCTCAGACCCT  
GTCACCATCTTTCTACGTGACTCTTCTGGAGACCATATCCAGCAGGCAAAGTACCAGGGCCG  
CCTGCATGTGAGCCACAAGGTTCCAGGAGATGTATCCCTCCAATTGAGCACCTTGAGATGG  
ATGACCGGAGCCACTACACGTGTGAAGTCACCTGGCAGACTCCTGATGGCAACCAAGTCGTG  
AGAGATAAGATTACTGAGCTCCGTGTCCAGAACTCTCTGTCTCCAAGCCCACAGTGACAAC  
TGGCAGCGGTTATGGCTTCACGGTGCCCCAGGGAATGAGGATTAGCCTTCAATGCCAGGCTC  
GGGGTTCTCCTCCCATCAGTTATATTGGTATAAGCAACAGACTAATAACCAGGAACCCATC  
AAAGTAGCAACCCTAAGTACCTTACTCTTCAAGCCTGCGGTGATAGCCGACTCAGGCTCCTA  
TTTCTGCACTGCCAAGGGCCAGGTTGGCTCTGAGCAGCACAGCGACATTGTGAAGTTTGTGG  
TCAAAGACTCCTCAAAGCTACTCAAGACCAAGACTGAGGCACCTACAACCATGACATACCCC  
TTGAAAGCAACATCTACAGTGAAGCAGTCCTGGGACTGGACCACTGACATGGATGGCTACCT  
TGGAGAGACCAGTGCTGGGCCAGGAAAGAGCCTGCCTGTCTTTGCCATCATCCTCATCATCT  
CCTTGTGCTGTATGGTGGTTTTTACCATGGCCTATATCATGCTCTGTCTCGGAAGACATCCCAA  
CAAGAGCATGTCTACGAAGCAGCCAGGTAAGAAAGTCTCTCCTCTTCCATTTTTGACCCCGT  
CCCTGCCCTCAATTTTGATTACTGGCAGGAAATGTGGAGGAAGGGGGGTGTGGCACAGACCC  
AATCCTAAGGCCGGAGGCCTTCAGGGTCAGGACATAGCTGCCTTCCCTCTCTCAGGCACCTT  
CTGAGGTTGTTTTGGCCCTCTGAACACAAAGGATAATTTAGATCCATCTGCCTTCTGCTTCC  
AGAATCCCTGGGTGGTAGGATCCTGATAATTAATTGGCAAGAATTGAGGCAGAAGGGTGGGA  
AACCAGGACCACAGCCCCAAGTCCCTTCTTATGGGTGGTGGGCTCTTGGGCCATAGGGCACA  
TGCCAGAGAGGCCAACGACTCTGGAGAAACCATGAGGGTGGCCATCTTCGCAAGTGGCTGCT  
CCAGTGATGAGCCAACTTCCCAGAATCTGGGCAACAACACTACTCTGATGAGCCCTGCATAGGA  
CAGGAGTACCAGATCATCGCCAGATCAATGGCAACTACGCCCCGCTGCTGGACACAGTTCC  
TCTGGATTATGAGTTTCTGGCCACTGAGGGCAAAGTGTCTGTAAATAATGCCCCATTAGGC  
CAGGATCTGCTGACATAATTGCCTAGTCAGTCCTTGCCTTCTGCATGGCCTTCTTCCCTGCT  
ACCTCTCTTCCCTGGATAGCCCAAAGTGTCCGCCTACCAACACTGGAGCCGCTGGGAGTCACT  
GGCTTTGCCCTGGAATTTGCCAGATGCATCTCAAGTAAGCCAGCTGCTGGATTTGGCTCTGG  
GCCCTTCTAGTATCTCTGCCGGGGGCTTCTGGTACTCCTCTCTAAATAACCAGAGGGAAGATG  
CCCATAGCACTAGGACTTGGTCATCATGCCTACAGACACTATTCAACTTTGGCATCTTGCCA  
CCAGAAGACCCGAGGGAGGCTCAGCTCTGCCAGCTCAGAGGACCAGCTATATCCAGGATCAT  
TTCTCTTTCTTCAGGGCCAGACAGCTTTTAATTGAAATTGTTATTTACAGGCCAGGGTTCA  
GTTCTGCTCCTCCACTATAAGTCTAATGTTCTGACTCTCTCCTGGTGCTCAATAAATATCTA  
ATCATAACAGC

**FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45416

><subunit 1 of 1, 321 aa, 1 stop

><MW: 35544, pI: 8.51, NX(S/T): 0

MGILLGLLLLLGHILTVDITYGRPILEVPESVTGPWKGDVNLPCITYDPLQGYTQVLVKWLVQRGS  
DPVTIFLRDSSGDHIQQAKYQGRHLVSHKVPGDVSLQLSTLEMDDRSHYTCEVTWQTPDGNQ  
VVRDKITELRVQKLSVSKPTVTTGSGYGFTVPQGMRISLQCQARGSPPISYIWKQQTNNQE  
PIKVATLSTLLFKPAVIADSGSYFCTAKGQVGSEQHSDIVKFVVKDSSKLLKTKTEAPTMT  
YPLKATSTVKQSWDWTDDMDGYLGETSAGPGKSLPVFAIILIIISLCCMVVFTMAYIMLCRKT  
SQQEHVYEAAAR

**Signal Sequence:**

amino acids 1-19

**Glycosaminoglycan attachment site:**

amino acids 149-152

**Transmembrane domain:**

amino acids 282-300

**FIGURE 23**

GCGCCGGGAGCCCATCTGCCCCCAGGGGCACGGGGCGCGGGGGCCGGCTCCCGCCCCGGCACAT  
GGCTGCAGCCACCTCGCGCGCACCCCGAGGCGCCGCGCCAGCTCGCCCGAGGTCCGTCCGA  
GGCGCCCCGGCCGCCCCGGAGCCAAGCAGCAACTGAGCGGGGAAGCGCCCCGCGTCCGGGGATC  
GGGATGTCCCTCCTCCTTCTCCTCTTGCTAGTTTCCTACTATGTTGGAACCTTGGGGACTCA  
CACTGAGATCAAGAGAGTGGCAGAGGAAAAGGTCACTTTGCCCTGCCACCATCAACTGGGGC  
TTCCAGAAAAAGACACTCTGGATATTGAATGGCTGCTCACCGATAATGAAGGGAACCAAAAA  
GTGGTGATCACTTACTCCAGTCGTCATGTCTACAATAACTTGACTGAGGAACAGAAGGGCCG  
AGTGGCCTTTGCTTCCAATTTCTTGGCAGGAGATGCCTCCTTGCAGATTGAACCTCTGAAGC  
CCAGTGATGAGGGCCGGTACACCTGTAAGGTTAAGAATTCAGGGCGCTACGTGTGGAGCCAT  
GTCATCTTAAAAGTCTTAGTGAGACCATCCAAGCCCAAGTGTGAGTTGGAAGGAGAGCTGAC  
AGAAGGAAGTGACCTGACTTTGCAGTGTGAGTCATCCTCTGGCACAGAGCCCATTTGTGTATT  
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGGATGAACGTCTGCCCTCCCAAATCTAGGATT  
GACTACAACCACCCTGGACGAGTTCTGCTGCAGAATCTTACCATGTCCTACTCTGGACTGTA  
CCAGTGACACAGCAGGCAACGAAGCTGGGAAGGAAAGCTGTGTGGTGCGAGTAACTGTACAGT  
ATGTACAAAGCATCGGCATGGTTGCAGGAGCAGTGACAGGCATAGTGGCTGGAGCCCTGCTG  
ATTTTCCTCTTGGTGTGGCTGCTAATCCGAAGGAAAGACAAAGAAAGATATGAGGAAGAAGA  
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAAGCCCGTCTTGTGAAACCCAGCT  
CCTCTTCCTCAGGCTCTCGGAGCTCACGCTCTGGTTCTTCCTCCACTCGCTCCACAGCAAAT  
AGTGCCTCACGCAGCCAGCGGACACTGTCAACTGACGCAGCACCCCCAGCCAGGGCTGGCCAC  
CCAGGCATACAGCCTAGTGGGGCCAGAGGTGAGAGGTTCTGAACCAAAGAAAGTCCACCATG  
CTAATCTGACCAAAGCAGAAACCACACCCAGCATGATCCCCAGCCAGAGCAGAGCCTTCCAA  
ACGGTCTTGAATTACAATGGACTTGACTCCCACGCTTTCCTAGGAGTCAGGGTCTTTGGACTC  
TTCTCGTCATTGGAGCTCAAGTCACCAGCCACACAACCAGATGAGAGGTCATCTAAGTAGCA  
GTGAGCATTGCACGGAACAGATTCAGATGAGCATTTCCTTATACAATACCAAACAAGCAAA  
AGGATGTAAGCTGATTCATCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGAGTAAGGG  
AAAGCAGGAGTCCAAATCTATTTGTTGACCAGGACCTGTGGTGAGAAGGTTGGGGAAAGGTG  
AGGTGAATATACCTAAAACCTTTTAATGTGGGATATTTTGTATCAGTGCTTTGATTCACAATT  
TTCAAGAGGAAATGGGATGCTGTTTGTAAATTTTCTATGCATTTCTGCAAACCTTATTGGATT  
ATTAGTTATTCAGACAGTCAAGCAGAACCCACAGCCTTATTACACCTGTCTACACCATGTAC  
TGAGCTAACCACCTTCTAAGAACTCCAAAAAAGGAAACATGTGTCTTCTATTCTGACTTAAC  
TTCATTTGTCATAAGGTTTGGATATTAATTTCAAGGGGAGTTGAAATAGTGGGAGATGGAGA  
AGAGTGAATGAGTTTCTCCCACTCTATACTAATCTCACTATTTGTATTGAGCCCCAAAATAAC  
TATGAAAGGAGACAAAAATTTGTGACAAAGGATTGTGAAGAGCTTTCCATCTTCATGATGTT  
ATGAGGATTGTTGACAAACATTAGAAATATATAATGGAGCAATTGTGGATTTCCCCTCAAAT  
CAGATGCCTCTAAGGACTTTCCTGCTAGATATTTCTGGAAGGAGAAAATACAACATGTCATT  
TATCAACGTCCTTAGAAAGAATTCTTCTAGAGAAAAAGGGATCTAGGAATGCTGAAAGATTA  
CCCAACATAACATTATAGTCTCTTCTTTCTGAGAAAATGTGAAACCAGAATTGCAAGACTGG  
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGGCA  
TGGTGCCAGGCACCTGTAGGAAAATCCAGCAGGTGGAGGTTGCAGTGAGCCGAGATTATGCC  
ATTGCACTCCAGCCTGGGTGACAGAGCGGGACTCCGTCTC

**FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV  
VITYSSRHVYNNLTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV  
ILKVLVRPSKPKCELEGELTEGSDLTLOCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID  
YNHPGRVLLQNLTMSSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI  
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSGSSSTRSTANS  
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

**Signal sequence:**

amino acids 1-16

**Transmembrane domain:**

amino acids 232-251

**FIGURE 25**

GTGTTTCTTTGCTCTCTCGCGCCAGTCCTCCTCCCTGGTTCTCCTCAGCCGCTGTGGAGGAGAGCACCCGGA  
GACGCGGGCTGCAGTCGCGGGCGGCTTCTCCCCGCTGGGCGGCTCGCCGCTGGGCAGGTGCTGAGCGCCCTAG  
AGCCTCCCTTGGCGCTCCCTCCTCTGCCCCGGCGCAGCAGTGCACATGGGGTGTGGAGGTAGATGGGCTCCCG  
GCCCCGGAGGGCGGCGGTGGATGCGGCGCTGGGCAGAAGCAGCCGCGATTCCAGCTGCCCCGCGCGCCCCGGGCG  
CCCCTGCGAGTCCCCGGTTCAGCCATGGGGACCTCTCCGAGCAGCAGCACCGCCCTCGCCTCCTGCAGCCGCATC  
GCCCCGGAGCCACAGCCACGATGATCGCGGGCTCCCTTCTCCTGCTTGGATTCCCTTAGCACCACCACAGCTCAG  
CCAGAACAGAAGGCCTCGAATCTCATTGGCACATAACGCCATGTTGACCGTGCCACCGGCCAGGTGCTAACCTGT  
GACAAGTGTCCAGCAGGAACCTATGTCTCTGAGCATTGTACCAACACAAGCCTGCGCGTCTGCAGCAGTTGCCCT  
GTGGGGACCTTTACCAGGCATGAGAATGGCATAGAGAAATGCCATGACTGTAGTCAGCCATGCCCATGGCCAATG  
ATTGAGAAATTACCTTGTGCTGCCTTGACTGACCGAGAATGCACTTGCCACCTGGCATGTTCCAGTCTAACGCT  
ACCTGTGCCCCCATAACGGTGTGCTGCTGGGGTGGGGTGTGCGGAAGAAAGGGACAGAGACTGAGGATGTGCGG  
TGTAAGCAGTGTGCTCGGGGTACCTTCTCAGATGTGCCTTCTAGTGTGATGAAATGCAAAGCATAACAGACTGT  
CTGAGTCAGAACCTGGTGGTGATCAAGCCGGGGACCAAGGAGACAGACAACGTCTGTGGCACACTCCCGTCTTC  
TCCAGCTCCACCTCACCTTCCCCTGGCACAGCCATCTTCCACGCCCTGAGCACATGGAAACCCATGAAGTCCCT  
TCCTCCACTTATGTTCCCAAAGGCATGAACCTCAACAGAATCCAACCTCTTCTGCCTCTGTTAGACCAAAGGTACTG  
AGTAGCATCCAGGAAGGGACAGTCCCTGACAACACAAGCTCAGCAAGGGGGAAGGAAGACGTGAACAAGACCCTC  
CCAAACCTTCAGGTAGTCAACCACCAGCAAGGCCCCACCACAGACACATCCTGAAGCTGCTGCCGTCCATGGAG  
GCCACTGGGGGCGAGAAGTCCAGCACGCCCATCAAGGGCCCCAAGAGGGGACATCCTAGACAGAACCTACACAAG  
CATTTTGACATCAATGAGCATTGTCCTGGATGATTGTGCTTTCTCTGCTGCTGGTGCTTGTGGTGATTGTGGTG  
TGCAGTATCCGGAAAAGCTCGAGGACTCTGAAAAAGGGGCCCCGGCAGGATCCAGTGCCATTGTGGAAAAGGCA  
GGGCTGAAGAAATCCATGACTCCAACCCAGAACCGGGAGAAATGGATCTACTACTGCAATGGCCATGGTATCGAT  
ATCCTGAAGCTTGTAGCAGCCCAAGTGGGAAGCCAGTGGAAGATATCTATCAGTTTCTTTGCAATGCCAGTGAG  
AGGGAGGTTGCTGCTTTCTCCAATGGGTACACAGCCGACCACGAGCGGGCTACGCAGCTCTGCAGCACTGGACC  
ATCCGGGGCCCCGAGGCCAGCCTCGCCAGCTAATTAGCGCCCTGCGCCAGCACCGGAGAAACGATGTTGTGGAG  
AAGATTCTGTTGGGCTGATGGAAGACACCACCCAGCTGGAACTGACAACTAGCTCTCCCGATGAGCCCCAGCCCG  
CTTAGCCCCGAGCCCCATCCCCAGCCCCAACGCGAAACTTGAGAATTCCGCTCTCCTGACGGTGGAGCCTTCCCCA  
CAGGACAAGAACAAGGGCTTCTTCGTGGATGAGTCGGAGCCCCCTTCTCCGCTGTGACTCTACATCCAGCGGCTCC  
TCCGCGCTGAGCAGGAACGGTTCTTTATTACCAAAGAAAAGAAGGACACAGTGTGCGGCAGGTACGCCTGGAC  
CCCTGTGACTTGACGCTATCTTTGATGACATGCTCCACTTTCTAAATCCTGAGGAGCTGCGGGTGATTGAAGAG  
ATTCCCCAGGCTGAGGACAACTAGACCGGCTATTCGAAATTATTGGAGTCAAGAGCCAGGAAGCCAGCCAGACC  
CTCCTGGACTCTGTTTATAGCCATCTTCTGACCTGCTGTAGAACATAGGGATACTGCATTCTGGAAATTACTCA  
ATTTAGTGGCAGGGTGGTTTTTTAAATTTCTTCTGTTTCTGATTTTGTGTTTGGGGTGTGTGTGTGTGTGTGT  
GT  
TCTCTCTCTTTTTTTTTTTAAATAACTCTTCTGGGAAGTTGGTTTATAAGCCTTTGCCAGGTGTAACGTGTGTGAA  
ATACCCACCACTAAAGTTTTTTAAGTTCCATATTTCTCCATTTTGCTTCTTATGTATTTTCAAGATTATTCTG  
TGCACTTTAAATTTACTTAACTTACCATAAATGCAGTGTGACTTTTCCACACACTGGATTGTGAGGCTCTTAAC  
TTCTTAAAGTATAATGGCATCTTGTGAATCCTATAAGCAGTCTTTATGTCTCTTAACATTACACCTACTTTTT  
AAAAACAAATATTATTACTATTTTTATTATTGTTTGTCTTTATAAATTTCTTAAAGATTAAGAAAATTTAAGA  
CCCCATTGAGTTACTGTAATGCAATTCAACTTTGAGTTATCTTTAAATATGTCTTGTATAGTTCATATTCATGG  
CTGAAACTTGACCACACTATTGCTGATTGTATGGTTTTTACCTGGACACCGTGTAGAATGCTTGATTACTTGTA  
TCTTCTTATGCTAATATGCTCTGGGCTGGAGAAATGAAATCCTCAAGCCATCAGGATTTGCTATTTAAGTGGCTT  
GACAACTGGGCCACCAAAGAACTTGAACCTTACCTTTTAGGATTTGAGCTGTTCTGGAACACATTGCTGCACTTT  
GGAAAGTCAAAATCAAGTGCCAGTGGCGCCCTTTCCATAGAGAATTTGCCAGCTTTGCTTTAAAGATGTCTTG  
TTTTTTATATACACATAATCAATAGGTCCAATCTGCTCTCAAGGCCTTGGTCTGGTGGGATTCTTCAACCAAT  
ACTTTAATTAATAATGGCTGCAACTGTAAGAACCTTGTCTGATATATTTGCAACTATGCTCCCATTTACAAATG  
TACCTTCTAATGCTCAGTTGCCAGGTTCCAATGCAAAGGTGGCGTGGACTCCCTTTGTGTGGGTGGGGTTGTGG  
GTAGTGGTGAAGGACCGATATCAGAAAAATGCCTTCAAGTGTACTAATTTATTAATAAACATTAGGTGTTGTGA  
AAAAA



**FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52594  
><subunit 1 of 1, 655 aa, 1 stop  
><MW: 71845, pI: 8.22, NX(S/T): 8  
MGTSPSSSTALASCSRIARRATATMIAGSLLLLGFLSTTTAQPEQKASNLIQTYRHVDRATG  
QVLTCDKCPAGTYVSEHCTNTSLRVCSSCPVGTFTTRHENGIEKCHDCSQPCPWPMIEKLPCA  
ALTDRECTCPPGMFQSNATCAPHTVCPVGWGVRRKGTETEDVRCKQCARGTFSDVPSSVMKC  
KAYTDCLSQNLVVIKPGTKETDNVCGTLPSSFSSSTSPSPGTAFPRPEHMETHEVPSSTYVP  
KGMNSTESNSSASVRPKVLSSIQEGTVPDNTSSARGKEDVNKTLPNLQVVNHQQGPHHRHIL  
KLLPSMEATGGEKSSTPIKGPGRGHPRQNLHKHFDINEHLPWMIVLFLLLVLVVIIVVCSIRK  
SSRTLKKGPRQDPSAIVEKAGLKKSMPTPTQNREKWIYYCNGHGIDILKLVAQVGSQWKDIY  
QFLCNASEREVAAFSNGYTADHERAYAALQHWTIRGPEASLAQLISALRQHRNDVVEKIRG  
LMEDTTQLETDKLALPMSPSPSPSPSPNAKLENSALLTVEPSPQDKNKGFFVDESEPLL  
RCDSTSSGSSALSRNGSFITKEKKDTVLRQVRLDPCDLQPIFDDMLHFLNPEELRVIEEIPQ  
AEDKLDRLFEEIIGVKSQEASQTLLDSVYSHLPDLL

**Signal sequence:**

amino acids 1-41

**Transmembrane domain:**

amino acids 350-370

**FIGURE 27**

ATGGGAAGCCAGTAACACTGTGGCCTACTATCTCTTCCGTGGTGCCATCTACATTTTTTGGGA  
CTCGGGAATTATGAGGTAGAGGTGGAGGCGGAGCCGGATGTCAGAGGTCCTGAAATAGTCAC  
**CATG**GGGGGAAAATGATCCGCCTGCTGTTGAAGCCCCCTTCTCATTCCGATCGCTTTTTTGGCC  
TTGATGATTTGAAAATAAGTCCTGTTGCACCAGATGCAGATGCTGTTGCTGCACAGATCCTG  
TCACTGCTGCCATTGAAGTTTTTTTCCAATCATCGTCATTGGGATCATTGCATTGATATTAGC  
ACTGGCCATTGGTCTGGGCATCCACTTCGACTGCTCAGGGAAGTACAGATGTCGCTCATCCT  
TTAAGTGTATCGAGCTGATAGCTCGATGTGACGGAGTCTCGGATTGCAAAGACGGGGAGGAC  
GAGTACCGCTGTGTCCGGGTGGGTGGTCAGAATGCCGTGCTCCAGGTGTTACAGCTGCTTC  
GTGGAAGACCATGTGCTCCGATGACTGGAAGGGTCACTACGCAAATGTTGCCTGTGCCCAAC  
TGGGTTTTCCCAAGCTATGTGAGTTCAGATAACCTCAGAGTGAGCTCGCTGGAGGGGCAGTTC  
CGGGAGGAGTTTGTGTCCATCGATCACCTCTTGCCAGATGACAAGGTGACTGCATTACACCA  
CTCAGTATATGTGAGGGAGGGATGTGCCTCTGGCCACGTGGTTACCTTGCAGTGCACAGCCT  
GTGGTCATAGAAGGGGGCTACAGCTCACGCATCGTGGGTGGAAACATGTCCTTGCTCTCGCAG  
TGGCCCTGGCAGGCCAGCCTTCAGTTCCAGGGCTACCACCTGTGCGGGGGCTCTGTCTATCAC  
GCCCCTGTGGATCATCACTGCTGCACACTGTGTTTATGACTTGTACCTCCCCAAGTCATGGA  
CCATCCAGGTGGGTCTAGTTTTCCCTGTTGGACAATCCAGCCCCATCCCACCTTGGTGGAGAAG  
ATTGTCTACCACAGCAAGTACAAGCCAAAGAGGCTGGGCAATGACATCGCCCTTATGAAGCT  
GGCCGGGCCACTCACGTTCAATGAAATGATCCAGCCTGTGTGCCTGCCCAACTCTGAAGAGA  
ACTTCCCCGATGGAAAAGTGTGCTGGACGTCAGGATGGGGGGCCACAGAGGATGGAGGTGAC  
GCCTCCCCCTGTCCTGAACCACGCGGCCGTCCCTTTGATTTCCAACAAGATCTGCAACCACAG  
GGACGTGTACGGTGGCATCATCTCCCCCTCCATGCTCTGCGCGGGCTACCTGACGGGTGGCG  
TGGACAGCTGCCAGGGGGACAGCGGGGGGGCCCCCTGGTGTGTCAAGAGAGGAGGCTGTGGAAG  
TTAGTGGGAGCGACCAGCTTTGGCATCGGCTGCGCAGAGGTGAACAAGCCTGGGGTGTACAC  
CCGTGTACCTCCTTCCCTGGACTGGATCCACGAGCAGATGGAGAGAGACCTAAAAACCT**TGAA**  
GAGGAAGGGGACAAGTAGCCACCTGAGTTCCTGAGGTGATGAAGACAGCCCGATCCTCCCCT  
GGACTCCCGTGTAGGAACCTGCACACGAGCAGACACCCTTGAGCTCTGAGTTCGGGCACCA  
GTAGCAGGCCCCGAAAGAGGCACCCTTCCATCTGATTCCAGCACAACTTCAAGCTGCTTTTTT  
GTTTTTTGTTTTTTTGGAGTGGAGTCTCGCTCTGTTGCCAGGCTGGAGTGCAGTGGCGAAA  
TCCCTGCTCACTGCAGCCTCCGCTTCCCTGGTTCAAGCGATTCTCTTGCCCTCAGCTTCCCCA  
GTAGCTGGGACCACAGGTGCCCGCCACCACACCCAACTAATTTTTGTATTTTTTAGTAGAGAC  
AGGGTTTCACCATGTTGGCCAGGCTGCTCTCAAACCCCTGACCTCAAATGATGTGCCTGCTT  
CAGCCTCCCACAGTGCTGGGATTACAGGCATGGGCCACCACGCCTAGCCTCAGCTCCTTTC  
TGATCTTCACTAAGAACAAAAGAAGCAGCAACTTGCAAGGGCGGCCTTTCCCACTGGTCCAT  
CTGGTTTTCTCTCCAGGGTCTTGCAAAATTCCTGACGAGATAAGCAGTTATGTGACCTCACG  
TGCAAAGCCACCAACAGCCACTCAGAAAAGACGCACCAGCCCAGAAGTGCAGAACTGCAGTC  
ACTGCACGTTTTTCATCTCTAGGGACCAGAACCAAAACCCACCCTTTCTACTTCCAAGACTTAT  
TTTCACATGTGGGGAGGTTAATCTAGGAATGACTCGTTTAAGGCCTATTTTCATGATTTCTT  
TGTAGCATTTGGTGCTTGACGTATTATTGTCCTTTGATTCCAAATAATATGTTTCCTTCCCT  
CATGTCTGGCGTGTCTGCGTGGACTGGTGACGTGAATCAAATCATCCACTGAAA

**FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45234

><subunit 1 of 1, 453 aa, 1 stop

><MW: 49334, pI: 6.32, NX(S/T): 1

MGENDPPAVEAPFSFRSLFGLDDLKISPVAPDADAVAAQILSLLPLKFFPIIVIGIIALILA  
LAIGLGIHFDCSGKYRCRSSFKCIELIARCDGVSDCKDGEDEYRCVRVGGQNAVQLQVFTAAS  
WKTMCSDDWKGHYANVACAQLGFPSYVSSDNLRVSSLEGQFREEFVSIHLLPDDKV TALHH  
SVYVREGCASGHVVTLQCTACGHRRGYSSRIVGGNMSLLSQWPWQASLQFQGYHLCGGSVIT  
PLWIIITAAHCVYDLYLPKSWTIQVGLVSLLDNPAPSHLVEKIVYHISKYKPKRLGNDIALMKL  
AGPLTFNEMIQPVCLPNSEENFPDGKVCWTSGWGATEDGGDASPVLNHAAPLISNKICNHR  
DVGGIISPSMLCAGYLTGGVDSCQGDSSGGLVCQERRLWKLVGATSFQIGCAEVNKPVGVT  
RVTSFLDWIHEQMERDLKT

**Signal Peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 240-284

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**FIGURE 29**

CCCACGCGTCCGTCTAGTCCCCGGGCCAACTCGGACAGTTTGCTCATTTATTGCAACGGTCAAGGCTGGCTTGT  
GCCAGAACGGCGCGCGCGCGCGCACGCACGCACACACAGGGGGGAACTTTTTTAAAAATGAAAGGCTAGAAGA  
GCTCAGCGGCGGCGCGGCGCTGCGCGAGGGCTCCGGAGCTGACTCGCCGAGGCAGGAAATCCCTCCGGTCGCGA  
CGCCCGGCCCCGGCTCGGCGCCCGCGTGGGATGGTGCAGCGCTCGCCGCGGGGCCCCGAGAGCTGCTGCACTGAAG  
GCCGGCGACGATGGCAGCGCGCCCGCTGCCCGTGTCCCCCGCCGCGCCCTCCTGCTCGCCCTGGCCGGTGCTCT  
GCTCGCGCCCTGCGAGGCCCGAGGGGTGAGCTTATGGAACCAAGGAAGAGCTGATGAAGTTGTCACTGCCTCTGT  
TCGGAGTGGGGACCTCTGGATCCAGTGAAGAGCTTCGACTCCAAGAATCATCCAGAAGTGCTGAATATTCGACT  
ACAACGGGAAAGCAAAGAAGTATCATATAATCTGGAAAGAAATGAAGGTCTCATTGCCAGCAGTTTCACGGAAAC  
CCACTATCTGCAAGACGGTACTGATGTCTCCCTCGCTCGAAATTACACGGGTCACTGTTACTACCATGGACATGT  
ACGGGGATATTCTGATTTCAGCAGTCAGTCTCAGCACGTGTTCTGGTCTCAGGGGACTTATTGTGTTTGAAAATGA  
AAGCTATGTCTTAGAACCAATGAAAAGTGCAACCAACAGATACAACTCTTCCCAGCGAAGAAGCTGAAAAGCGT  
CCGGGGATCATGTGGATCACATCACAAACACACCAACCTCGCTGCAAAGAATGTGTTTCCACCACCCTCTCAGAC  
ATGGGCAAGAAGGCATAAAAGAGAGACCCTCAAGGCAACTAAGTATGTGGAGCTGGTGATCGTGGCAGACAACCG  
AGAGTTTCAGAGGCAAGGAAAAGATCTGGAAAAGTTAAGCAGCGATTAATAGAGATTGCTAATCACGTTGACAA  
GTTTTACAGACCACTGAACATTCGGATCGTGTGGTAGGCGTGGAAGTGGAATGACATGGACAAATGCTCTGT  
AAGTCAGGACCCATTACACAGCCTCCATGAATTTCTGGACTGGAGGAAGATGAAGCTTCTACCTCGCAAATCCCA  
TGACAATGCGCAGCTTGTCACTGGGGTTTATTTCCAAGGGACCACCATCGGCATGGCCCCAATCATGAGCATGTG  
CACGGCAGACCAGTCTGGGGGAATTGTCATGGACCATTTCAGACAATCCCTTGGTGACGCCGTGACCCCTGGCACA  
TGAGCTGGGCCACAATTTCCGGATGAATCATGACACACTGGACAGGGGCTGTAGCTGTCAAATGGCGGTTGAGAA  
AGGAGGCTGCATCATGAACGCTTCCACCGGGTACCCATTTCCCATGGTGTTTCAGCAGTTGCAGCAGGAAGGACTT  
GGAGACCAGCCTGGAGAAAGGAATGGGGGTGTGCTGTGTTAACCTGCCGGAAGTCAGGGAGTCTTTCGGGGGCCA  
GAAGTGTTGGGAACAGATTTGTGGAAGAAGGAGAGGAGTGACTGTGGGGAGCCAGAGGAATGTATGAATCGCTC  
CTGCAATGCCACCACCTGTACCCTGAAGCCGGACGCTGTGTGCGCACATGGGCTGTGCTGTGAAGACTGCCAGCT  
GAAGCCTGCAGGAACAGCGTGCAGGGACTCCAGCAACTCCTGTGACCTCCAGAGTTCTGCACAGGGGCCAGCCC  
TCACTGCCCAGCCAATGTGTACCTGCACGATGGGCACTCATGTGAGGATGTGGACGGCTACTGCTACAATGGCAT  
CTGCCAGACTCACGAGCAGCAGTGTGTACGCTCTGGGGACCAGGTGCTAAACCTGCCCTGGGATCTGCTTTGA  
GAGAGTCAATTCTGCAGGTGATCCTTATGGCAACTGTGGCAAAGTCTCGAAGAGTTCTTTGCCAAATGCGAGAT  
GAGAGATGCTAAATGTGGAAAATCCAGTGTCAAGGAGGTGCCAGCCGGCCAGTCATTGGTACCAATGCCGTTTC  
CATAGAAACAAACATCCCTCTGCAGCAAGGAGGCCGATTCTGTGCCGGGGGACCCACGTGTACTTGGGCGATGA  
CATGCCGGACCCAGGGCTTGTGCTTGCAGGCACAAAGTGTGCAGATGGAAAAATCTGCCTGAATCGTCAATGTCA  
AAATATTAGTGTCTTTGGGGTTTACGAGTGTGCAATGCAGTGCCACGGCAGAGGGGTGTGCAACACAGGAAGAA  
CTGCCACTGCGAGGCCCACTGGGCACCTCCCTTCTGTGACAAGTTTGGCTTTGGAGGAAGCACAGACAGCGGCC  
CATCCGGCAAGCAGAAGCAAGGCAGGAAGCTGCAGAGTCCAACAGGGAGCGCGGCCAGGGCCAGGAGCCCGTGGG  
ATCGCAGGAGCATGCGTCTACTGCCTCACTGACACTCATCTGAGCCCTCCCATGACATGGAGACCGTGACCACTG  
CTGCTGCAGAGGAGGTACGCGTCCCCAAGGCCTCCTGTGACTGGCAGCATTGACTCTGTGGCTTTGCCATCGTT  
TCCATGACAACAGACACAACACAGTTCTCGGGGCTCAGGAGGGGAAGTCCAGCCTACCAGGCACGTCTGCAGAAA  
CAGTGCAAGGAAGGGCAGCGACTTCTGGTTGAGCTTCTGCTAAACATGGACATGCTTCAGTGCTGCTCCTGAG  
AGAGTAGCAGGTTACCACTCTGGCAGGCCCCAGCCCTGCAGCAAGGAGGAAGAGGACTCAAAGTCTGGCCTTTC  
ACTGAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTTGGGGCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCT  
TGGCAGCCCTGATGACTGGTCTCTGGCTGCAACTTAATGCTCTGATATGGCTTTTAGCATTTATTATATGAAAT  
AGCAGGGTTTTAGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATCTCCATCCAAGCAAACCTGAATGGCAA  
TGAAACAACTGGAGAAGAAGGTAGGAGAAAGGGCGGTGAACTCTGGCTCTTTGCTGTGGACATGCGTGACCAGC  
AGTACTCAGGTTTGGAGGTTTGCAGAAAGCCAGGGAAACCCACAGAGTCAACCAACCCTTCATTTAACAAGTAAGAA  
TGTTAAAAAGTGAAAACAATGTAAGAGCCTAACTCCATCCCCCGTGGCCATTACTGCATAAAATAGAGTGCATTT  
GAAAT

**FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49624

><subunit 1 of 1, 735 aa, 1 stop

><MW: 80177, pI: 7.08, NX(S/T): 5

MAARPLPVSPARALLLAGALLAPCEARGVSLWNQGRADEVVSASVRSGDLWIPVKSFDSK  
NHPEVLNIRLQRESKELIINLERNEGLIASSFTETHYLQDGTDVSLARNYTGHCIYHGHVVRG  
YSDSAVSLSTCSGLRGLIVFENESYVLEPMKSATNRYKLFPAKKLKSVRGSCGSHHNTPNLA  
AKNVFPPPSQTWARRHKRETLKATKYVELVIVADNREFQRQGDLEKVKQRLIEIANHVDFK  
YRPLNIRIVLVGVEVWNDMDKCSVSQDPFTSLHEFLDWRKMKLLPRKSHDNAQLVSGVYFQG  
TTIGMAPIMSMCTADQSGGIVMDHSDNPLGAAVTLAHELGHNFNMHDTLDRGCSCQMAVEK  
GGCIMNASTGYPFPMVFSSCSRKDLETSLEKGMGVCLFNLPEVRESFGGQKCGNRFVEEGEE  
CDCGEPEECMNRCCNATTCTLKPDVCAHGLCCEDCQLKPAGTACRDSSNSCDLPEFCTGAS  
PHCPANVYLHDGHSCQDVDGYCYNGICQTHEQQCVTLWGPGAKPAPGICFERVNSAGDPYGN  
CGKVS KSSFAKCEMRDAKCGKIQCGGASRPVIGTNAVSIETNIPLOQGGRI LCRGTHVYLG  
DDMPDPGLVLAGTKCADGKICLNRQCQNISVFGVHECAMQCHGRGVCNNRKNCHCEAHWAPP  
FCDKFGFGGSTDGPIRQAEARQEA AESNRERGQGQEPVGSQEHASTASLTLI

**Signal peptide:**

amino acids 1-28

30/237



**FIGURE 31**

TCCCAAGGCTTCTTGGATGGCAGATGATTNTGGGGTTTTGCATTGTTTCCCTGACAACGAAA  
ACAAAACAGTTTTTGGGGGTT CAGGAGGGGAANTCCAGCCTACCCAGGAAGTTTGCAGAAACA  
GTGCAAGGAAGGGCAGGANTTCCTGGTTGAGNTTTTTGNTAAAACATGGACATGNTTCAGTG  
CTGCTCNTGAGAGAGTAGCAGGTTACCACTTTTGGCAGGCCCCAGCCCTGCAGCAAGGAGGA  
AGAGGACTCAAAAGTTTGGCCTTTCAGT GAGCCTCCACAGCAGTGGGGGAGAAGCAAGGGTT  
GGGCCAGTGTCCCCTTTCCCCAGTGACACCTCAGCCTTGGCAGCCCTGATAACTGGTNTNT  
GGCTGCAANTTAATGCTNTGATATGGCTTTTAGCATTTATTATATGAAAATAGCAGGGTTTT  
AGTTTTTAATTTATCAGAGACCCTGCCACCCATTCCATNTCCATCCAAG

**FIGURE 32**

CATCCTGCAACATGGTGAAACCACGCCTGGCTAATTTTGTGTATTTTGGTAGAGATGGGA  
TTTCACCGTGTTAGCCAGGATTGTCTCAATCTGACCTCATGATCTGCCCGCCTCGGCCTCCC  
AAAGTGCTGGGATTACAGGCGAGTGCAACCACACCCGGCCACAAACTTTTAAAGAAGTTAAT  
GAAACCATACCTTTTACATTTTAAATGACAGGAAAATGCTCACAATAATTGTTAACCCAAAA  
TTCTGGATACAAAAGTACAATCTTTACTGTGTAAATACATGTATATGTACTATATGAAAATA  
TACCAAATATCAATAATACTTATCTCTGGGTAAAAACCTCTTCTCATACCCTGTGCTAACAA  
CTTTTAACAAAAAATTTGCATCACTTTTAAGAATCAAGAAAAATTTCTGAAGGTCATATGGG  
ACAGAAAAAAAACCAAGGGAAAAATCACGCCACTTGGGAAAAAAGATTTCGAAATCTGCCT  
TTTTATAGATTTGTAATTAATAAGGTCCAGGCTTTCTAAGCAACTTAAATGTTTTGTTTCGA  
AACAAAGTACTTGTCTGGATGTAGGAGGAAAGGGAGTGATGTCACTGCCATTATGATGCCCC  
TTGAATATAAGACCCTACTTGCTATCTCCCCCTGCACCAGCCAGGAGCCACCCATCCTCCAGC  
ACACTGAGCAGCAAGCTGGACACACGGCACACTGATCCAAATGGGTAAGGGGATGGTGGCGA  
TGCTCATTCTGGGTCTGCTACTTCTGGCGCTGCTCCTACCCGTGCAGGTTTCTTCATTTGTT  
CCTTTAACCAGTATGCCGGAAGCTACTGCAGCCGAAACCACAAAGCCCTCCAACAGTGCCCT  
ACAGCCTACAGCCGGTCTCCTTGTGGTCTTGCTTGCCCTTCTACATCTCTACCATTAAGAGG  
CAGGTCAAGAAACAGCTACAGTTCTCCAACCCATACACTAAAACCGAATCCAAATGGTGCCT  
AGAAGTTCAATGTGGCAAGGAAAAAAACCAGGTCTTCATCAAATCTACTAATTTCACTCCTT  
ATTAACAGAGAAACGCTTGAGAGTCTCAAACCTGGACTGGTTTAAAGAGCATCTGAAGGATTT  
GACTAGATGATAAATGCCTGTACTCCCAGTACTTTGGGAGGCCTAGGCCGGCGGATCACCTG  
AGGTCAGGAGTTTGAGACTAACCTGGCCAAAATGGTGAAACCCCATCTGTACTAAAAATACA  
AATATTGACTGGGCGTGGTGGTGAGTGCCTGTGATCCCAGCTACTCAGGTGGCTGAAGCAGG  
ACAATCACTTGAACCTCAGGAGGCAGAGGTTGCAGTGAGCTGAGATCGCGCTACTGCACTCTA  
GCCTAGCCTGGGCAACAGAGTGAGACTTCGTCTCAAAAAAAAAAAGCCAAGTGCAGTGGCT  
CACGCCTGTAATCCCGGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGGAGATCA  
AGACCATCCTGGCTAATACAGTGAAACCCTGTCTCTACTAAAAATACAAAAAATTAGCCGGG  
GATGGTGGCAGGCACCTGGAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATAGCGTGAA  
CTCAGGAGGCGGAGCTTGCAGTGAGCCGAGATTGCGCTACTGCACTCCAGCCTGGGCGACAG  
CGCGAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 33**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48309

><subunit 1 of 1, 67 aa, 1 stop

><MW: 6981, pI: 7.47, NX(S/T): 0

MGKGMVAMLILGLLLLALLLPVQVSSFVPLTSMPEATAAETTKPSNSALQPTAGLLVLLAL  
LHLYH

**Signal peptide:**

amino acids 15-27

33/237

**FIGURE 34**

GCCGCGGCGAGAGCGCGCCAGCCCCGCGCGATGCCGCGCGCCAGGACGCCTCCTCCCGCTGCTGGCCCCGGC  
CGGCGGCCCTGACTGCGCTGCTGCTGCTGCTGCTGGGCCATGGCGGCGGCGGGCGCTGGGGCGCCCGGGCCAGG  
AGGCGGCGGCGGCGGCGGCGGACGGGCCCCCGCGGCAGACGGCGAGGACGGACAGGACCCGCACAGCAAGCACC  
TGTACACGGCCGACATGTTACGCACGGGATCCAGAGCGCCGCGCACTTCGTTCATGTTCTTCGCGCCCTGGTGTG  
GACACTGCCAGCGGCTGCAGCCGACTTGGAATGACCTGGGAGACAAATACAACAGCATGGAAGATGCCAAAGTCT  
ATGTGGCTAAAGTGGACTGCACGGCCCACTCCGACGTGTGCTCCGCCAGGGGGTGGGAGGATACCCACCTTAA  
AGCTTTTCAAGCCAGGCCAAGAAGCTGTGAAGTACCAGGGTCTCGGGACTTCAGACACTGGAAAAGTGGATGC  
TGCAGACACTGAACGAGGAGCCAGTGACACCAGAGCCGGAAGTGAACCGCCAGTGCCCCGAGCTCAAGCAAG  
GGCTGTATGAGCTCTCAGCAAGCAACTTTGAGCTGCACGTTGCACAAGGCGACCACTTTATCAAGTTCTTCGCTC  
CGTGGTGTGGTCACTGCAAAGCCCTGGCTCCAACCTGGGAGCAGCTGGCTCTGGGCCCTTGAACATTCCGAAACTG  
TCAAGATTGGCAAGGTTGATTGTACACAGCACTATGAACCTCTGCTCCGGAACAGGTTTCGTGGCTATCCCACTC  
TTCTCTGTTCCGAGATGGGAAAAGGTGGATCAGTACAAGGGAAAGCGGGATTTGGAGTCACTGAGGGAGTACG  
TGGAGTCGCAGCTGCAGCGCACAGAGACTGGAGCGACGGAGACCGTCACGCCCTCAGAGGCCCGGTGCTGGCAG  
CTGAGCCCCAGGCTGACAAGGGCACTGTGTTGGCACTCACTGAAAATAACTTCGATGACACCATTGCAGAAGGAA  
TAACCTTCATCAAGTTTATGCTCCATGGTGTGGTCATTGTAAGACTCTGGCTCCTACTTGGGAGGAACTCTCTA  
AAAAGGAATTCCCTGGTCTGGCGGGGGTCAAGATCGCCGAAGTAGACTGCACTGCTGAACGGAATATCTGCAGCA  
AGTATTCGGTACGAGGCTACCCACGTTATTGCTTTTCCGAGGAGGGAAGAAAGTCAGTGAGCACAGTGGAGGCA  
GAGACCTTGACTCGTTACACCGCTTTGTCTGAGCCAAGCGAAAGACGAACCTTAGGAACACAGTTGGAGGTCAC  
CTCTCCTGCCAGCTCCCGCACCCTGCGTTTAGGAGTTCAGTCCACAGAGGCCACTGGGTCCCAGTGGTGGCT  
GTTCAAGAAAGCAGAACATACTAAGCGTGAGGTATCTTCTTTGTGTGTGTGTTTCCAAGCCAACACACTCTACAG  
ATTCTTTATTAAGTTAAGTTTCTCTAAGTAAATGTGTAACCTCATGGTCACTGTGTAAACATTTTCAGTGGCGATA  
TATCCCCCTTTGACCTTCTCTTGATGAAATTTACATGGTTTCTTTGAGACTAAAATAGCGTTGAGGGAAATGAAA  
TTGCTGGACTATTTGTGGCTCCTGAGTTGAGTGATTTTGGTGAAAGAAAGCACATCCAAAGCATAGTTTACCTGC  
CCACGAGTTCTGGAAAGGTGGCCTTGTGGCAGTATTGACGTTCTCTGATCTTAAGGTCACAGTTGACTCAATAC  
TGTGTTGGTCCGTAGCATGGAGCAGATTGAAATGCAAAAACCCACACCTCTGGAAGATACCTTCACGGCCGCTGC  
TGGAGCTTCTGTTGCTGTGAATACTTCTCTCAGTGTGAGAGGTTAGCCGTGATGAAAGCAGCGTTACTTCTGACC  
GTGCCTGAGTAAGAGAATGCTGATGCCATAACTTTATGTGTGATACTTGTCAAATCAGTTACTGTTTCAGGGGAT  
CCTTCTGTTTCTCACGGGGTGAAACATGTCTTTAGTTCTCATGTTAACACGAAGCCAGAGCCACATGAACTGT  
TGGATGTCTTCTTAGAAAGGGTAGGCATGGAAAATTCACAGAGGCTCATTCTCAGTATCTCATTAACTCATTGA  
AAGATTCCAGTTGTATTTGTCACCTGGGGTGACAAGACCAGACAGGCTTTCCAGGCCTGGGTATCCAGGGAGGC  
TCTGCAGCCCTGCTGAAGGGCCCTAACTAGAGTTCTAGAGTTTCTGATTCTGTTTCTCAGTAGTCCTTTTAGAGG  
CTTGCTATACTTGGTCTGCTTCAAGGAGGTCGACCTTCTAATGTATGAAGAATGGGATGCATTTGATCTCAAGAC  
CAAAGACAGATGTCAGTGGGCTGCTCTGGCCCTGGTGTGCACGGCTGTGGCAGCTGTTGATGCCAGTGTCTCTA  
ACTCATGCTGTCTTGTGATTAAACACCTCTATCTCCCTTGGGAATAAGCACATACAGGCTTAAGCTCTAAGATA  
GATAGGTGTTTGTCTTTTACCATCGAGCTACTTCCCATAATAACCACTTTGCATCCAACACTCTTCACCCACCT  
CCCATAACGCAAGGGGATGTGGATACTTGGCCCAAAGTAACCTGGTGGTAGGAATCTTAGAAACAGACCACTTATA  
CTGTCTGTCTGAGGCAGAAGATAACAGCAGCATCTCGACCAGCCTCTGCCTTAAAGGAAATCTTTATTAATCAG  
TATGGTTCACAGATAATTCTTTTTTAAAAAACCCAACCTCCTAGAGAAGCACAACTGTCAAGAGTCTTGTACA  
CACAACCTTCAGCTTTGCATCACGAGTCTTGTATTCCAAGAAAATCAAAGTGGTACAATTTGTTTGTTTACACTAT  
GATACTTTCTAAATAAACTCTTTTTTTTTTAA

**FIGURE 35**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46776

><subunit 1 of 1, 432 aa, 1 stop

><MW: 47629, pI: 5.90, NX(S/T): 0

MPARPGRLLPLLARPAALTALLLLLGHGGGGRWGARAQEAAAAAADGPPAADGEDGQDPHS  
KHLYTADMFTHTGIQSAAHFVMFFAPWCGHCQRLQPTWNDLGDKYNSMEDAKVYVAKVDCTAH  
SDVCSAQGVRYPTLKLFKPGQEAVKYQGPRDFQTLNWMQLTLNEEPVTPEPEVEPPSAPE  
LKQGLYELSASNFEHLHVAQGDHFIKFFAPWCGHCKALAPTWEQLALGLEHSETVKIGKVDCT  
QHYELCSGNQVRGYPTLLWFRDGKKVDQYKGKRDLESLREYVESQLQRTETGATETVTPSEA  
PVLAAEPEADKGTVLALTENNFDDTIAEGITFIKFYAPWCGHCKTLAPTWEELSKKEFPGLA  
GVKIAEVDCTAERNICSKYSVRGYPTLLLFRGGKKVSEHSGGRDLDSLHRFVLSQAKDEL

**Signal sequence:**

amino acids 1-32

35/237



**FIGURE 36**

CTTTTCTGAGGAACCAACAGCAATGAATGGCTTTGCATCCTTGCTTCGAAGAAACCAATTTAT  
CCTCCTGGTACTATTTCTTTTGCAAATTCAGAGTCTGGGTCTGGATATTGATAGCCGTCCTA  
CCGCTGAAGTCTGTGCCACACACACAATTTACCAGGACCCAAAGGAGATGATGGTGAAAAA  
GGAGATCCAGGAGAAGAGGGGAAAGCATGGCAAAGTGGGACGCATGGGGCCGAAAGGAATTAA  
AGGAGAACTGGGTGATATGGGAGATCAGGGCAATATTGGCAAGACTGGGCCCATTGGGAAGA  
AGGGTGACAAAGGGGAAAAAGGTTTGCTTGGAATACCTGGAGAAAAAGGCAAAGCAGGTACT  
GTCTGTGATTGTGGAAGATACCGGAAATTTGTTGGACAACCTGGATATTAGTATTGCTCGGCT  
CAAGACATCTATGAAGTTTGTCAAGAATGTGATAGCAGGGATTAGGGAACTGAAGAGAAAT  
TCTACTACATCGTGCAGGAAGAGAAGAACTACAGGGAATCCCTAACCCACTGCAGGATTCGG  
GGTGGAATGCTAGCCATGCCCAAGGATGAAGCTGCCAACACACTCATCGCTGACTATGTTGC  
CAAGAGTGGCTTCTTTCGGGTGTTTCATTGGCGTGAATGACCTTGAAAGGGAGGGACAGTACA  
TGTCCACAGACAACACTCCACTGCAGAACTATAGCAACTGGAATGAGGGGGGAACCCAGCGAC  
CCCTATGGTCATGAGGACTGTGTGGAGATGCTGAGCTCTGGCAGATGGAATGACACAGAGTG  
CCATCTTACCATGTACTTTGTCTGTGAGTTCATCAAGAAGAAAAAGTAACTTCCCTCATCCT  
ACGTATTTGCTATTTTCCTGTGACCGTCATTACAGTTATTGTTATCCATCCTTTTTTTCCTG  
ATTGTACTACATTTGATCTGAGTCAACATAGCTAGAAAATGCTAAACTGAGGTATGGAGCCT  
CCATCATCAAAAAAAAAAAAAAAAAA

**FIGURE 37**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50980

><subunit 1 of 1, 277 aa, 1 stop

><MW: 30645, pI: 7.47, NX(S/T): 2

MNGFASLLRRNQFILLVLFLLQIQSLGLDIDSRPTAEVCATHHTISPGPKGDDGEKGDPEGEEG  
KHGKVGRMGPKGIKGELGDMGDQGNIGKTGPIGKKGDKGEKGLLGIPGEKKGAGTVCDGCRY  
RKFBVGQLDISIARLKTSMKFVKNVIAGIRETEEFYIYVQEEKNYRESLTHCRIRGGMLAMP  
KDEAANTLIADYVAKSGFFRVFIGVNDLEREGQYMSTDNTPLQNYSNWNEGEPSDPYGHEDC  
VEMLSSGRWNDTECHLTMYFVCEFIKKKK

**Signal peptide:**

amino acids 1-25

**FIGURE 38**

GGTTCTATCGATTCTGAATTCGGCCACACTGGCCGGATCCTCTAGAGATCCCTCGACCTCGAC  
CCACGCGTCCGCTGCTCTCCGCCCCGTGTGGAGTGGTGGGGGCTGGGTGGGAATGGGCGTGT  
GCCAGCGCACGCGCGCTCCCTGGAAGGAGAAGTCTCAGCTAGAACGAGCGGCCCTAGGTTTT  
CGGAAGGGAGGATCAGGGATGTTTGCGAGCGGCTGGAACCAGACGGTGCCGATAGAGGAAGC  
GGGCTCCATGGCTGCCCTCCTGCTGCTGCCCCCTGCTGCTGTTGCTACCGCTGCTGCTGCTGA  
AGCTACACCTCTGGCCGCGAGTTGCGCTGGCTTCCGGCGGACTTGCCCTTTGCGGTGCGAGCT  
CTGTGCTGCAAAAGGGCTCTTCGAGCTCGCGCCCTGGCCGCGGCTGCCGCCGACCCGGAAGG  
TCCCGAGGGGGGCTGCAGCCTGGCCTGGCGCCTCGCGGAACTGGCCCAGCAGCGCGCCGCGC  
ACACCTTTCTCATTACGGCTCGCGGCGCTTTAGCTACTCAGAGGCGGAGCGCGAGAGTAAC  
AGGGCTGCACGCGCCTTCCCTACGTGCGCTAGGCTGGGACTGGGGACCCGACGGCGGGCGACAG  
CGGCGAGGGGAGCGCTGGAGAAGGCGAGCGGGCAGCGCCGGGAGCCGGAGATGCAGCGGCCG  
GAAGCGGCGCGGAGTTTGCCGGAGGGGACGGTGCCGCCAGAGGTGGAGGAGCCGCCGCCCT  
CTGTCACCTGGAGCAACTGTGGCGCTGCTCCTCCCCGCTGGCCCAGAGTTTCTGTGGCTCTG  
GTTCCGGGCTGGCCAAGGCCGGCCTGCGCACTGCCTTTGTGCCACCGCCCTGCGCCGGGGCC  
CCCTGCTGCACTGCCTCCGCGAGCTGCGGCGCGCGCGCGCTGGTGCTGGCGCCAGAGTTTCTG  
GAGTCCCTGGAGCCGGACCTGCCCGCCCTGAGAGCCATGGGGCTCCACCTGTGGGCTGCAGG  
CCCAGGAACCCACCCTGCTGGAATTAGCGATTTGCTGGCTGAAGTGTCCGCTGAAGTGGATG  
GGCCAGTGCCAGGATACCTCTCTCCCCCAGAGCATAACAGACACGTGCCTGTACATCTTC  
ACCTCTGGCACCACGGGCTCCCCAAGGCTGCTCGGATCAGTCATCTGAAGATCCTGCAATG  
CCAGGGCTTCTATCAGCTGTGTGGTGTCCACCAGGAAGATGTGATCTACCTCGCCCTCCAC  
TCTACCACATGTCCGGTTCCCTGCTGGGCATCGTGGGCTGCATGGGCATTGGGGCCACAGTG  
GTGCTGAAATCCAAGTTCTCGGCTGGTCAGTTCTGGGAAGATTGCCAGCAGCACAGGGTGAC  
GGTGTTCAGTACATTGGGGAGCTGTGCCGATACTTGTCAACCAGCCCCCGAGCAAGGCAG  
AACGTGGCCATAAGGTCCGGCTGGCAGTGGGCAGCGGGCTGCGCCCAGATACCTGGGAGCGT  
TTTGTGCGGCGCTTCGGGGCCCTGCAGGTGCTGGAGACATATGGACTGACAGAGGGCAACGT  
GGCCACCATCAACTACACAGGACAGCGGGGCGCTGTGGGGCGTGCTTCCTGGCTTTACAAGC  
ATATCTTCCCCTTCTCCTTGATTGCTATGATGTCAACCACAGGAGAGCCAATTCGGGACCCC  
CAGGGGCACTGTATGGCCACATCTCCAGGTGAGCCAGGGCTGCTGGTGGCCCCGGTAAGCCA  
GCAGTCCCCATTCTTGGGCTATGCTGGCGGGCCAGAGCTGGCCCAGGGGAAGTTGCTAAAGG  
ATGTCTTCCGGCCTGGGGATGTTTTCTTCAACACTGGGGACCTGCTGGTCTGCGATGACCAA  
GGTTTTCTCCGCTTCCATGATCGTACTGGAGACACCTTCAGGTGGAAGGGGGAGAATGTGGC  
CACAACCGAGGTGGCAGAGGTCTTCGAGGCCCTAGATTTTCTTCAGGAGGTGAACGTCTATG  
GAGTCACTGTGCCAGGGCATGAAGGCAGGGCTGGAATGGCAGCCCTAGTTCTGCGTCCCCC  
CACGCTTTGGACCTTATGCAGCTCTACACCCACGTGTCTGAGAACTTGCCACCTTATGCCCG  
GCCCCGATTCTCAGGCTCCAGGAGTCTTTGGCCACCACAGAGACCTTCAAACAGCAGAAAG  
TTCGGATGGCAAATGAGGGCTTCGACCCCAGCACCTGTCTGACCCACTGTACGTTCTGGAC  
CAGGCTGTAGGTGCCTACCTGCCCCCTCACAACCTGCCCGGTACAGCGCCCTCCTGGCAGGAAA  
CCTTCGAATCTGAGAACTTCCACACCTGAGGCACCTGAGAGAGGAACTCTGTGGGGTGGGGG  
CCGTTGCAGGTGTACTGGGCTGTCAGGGATCTTTTCTATAACAGAACTGCGGTCACTATTTT  
GTAATAAATGTGGCTGGAGCTGATCCAGCTGTCTCTGACCTAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGTAGGGATAACAGGGTAATAAGC  
TTGGCCGCCATGGCCCAACTTGTTTATTGCAG

**FIGURE 39**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50913  
><subunit 1 of 1, 730 aa, 1 stop  
><MW: 78644, pI: 7.65, NX(S/T): 2  
MGVCQRTAPWKEKSQLERAALGFRKGGSGMFASGWNQTVPIEEAGSMAALLLLPLLLLLPL  
LLLKLHLWPQLRWLPADLAFVRLCCCKRALRARALAAAAADPEGPEGGCSLAWRLAELAQQ  
RAAHTFLIHGSRFRFSYSEAERESNRAARAFLRALGWDWGPDGGDSGEGSAGEGERAAPGAGD  
AAAGSGAEFAGGDGAARGGGAAAPLSPGATVALLLPAGPEFLWLWFGGLAKAGLRTAFVPTAL  
RRGPLLHCLRSCGARALVLAPEFLESLEPDLPALRAMGLHLWAAGPGTHPAGISDLLAEVSA  
EVDGPVPGYLSSPQSITDTCLYIFTSGTTGLPKAARISHLKILQCQGFYQLCGVHQEDVIYL  
ALPLYHMSGSLLGIVGCMGIGATVVLKSKFSAGQFWEDCQQHRVTVFQYIGELCRYLVNQPP  
SKAERGHKVRLAVGSGLRPDTWERFVRRFGPLQVLETYGLTEGNVATINYTGQRGAVGRASW  
LYKHIFPFSLIRYDVTTGEPIRDPOGHCMATSPGEPGLLVAPVSQQSPFLGYAGGPPELAQ GK  
LLKDVFRPGDVFFNTGDLLVCDDQGFLRFHVRTGDTERWKGENVATTEVAEVFEALDFLQEV  
NVYGVTVPGHEGRAGMAALVLRPPHALDLMQLYTHVSENLPYARPRFLRLQESLATTETFK  
QQKVRMANEGFDPSTLSDPLYVLDQAVGAYLPLTTARYSALLAGNLRI

**Type II transmembrane domain:**

amino acids 45-65

**Other transmembrane domain:**

amino acids 379-398

**cAMP- and cGMP-dependent protein kinase phosphorylation site**  
starting at amino acid 136

**CUB domain protein motif**

amino acids 254-261

**putative AMP-binding domain signature**

amino acids 332-343

**N-glycosylation sites**

amino acids 37-40 and 483-486

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**FIGURE 40**

CCTGTGTTAAGCTGAGGTTTCCCCTAGATCTCGTATATCCCCAACACATACCTCCACGCACA  
CACATCCCCAAGAACCTCGAGCTCACACCAACAGACACACGCGCGCATACACACTCGCTCTC  
GCTTGTCCATCTCCCTCCCGGGGGAGCCGGCGCGCGCTCCACCTTTGCCGCACACTCCGGC  
GAGCCGAGCCCGCAGCGCTCCAGGATTCTGCGGCTCGGAACTCGGATTGCAGCTCTGAACCC  
CCATGGTGGTTTTTTTAAACACTTCTTTTCCTTCTCTTCCTCGTTTTTGATTGCACCGTTTCCA  
TCTGGGGGCTAGAGGAGCAAGGCAGCAGCCTTCCCAGCCAGCCCTTGTTGGCTTGCCATCGT  
CCATCTGGCTTATAAAAGTTTGCTGAGCGCAGTCCAGAGGGCTGCGCTGCTCGTCCCCTCGG  
CTGGCAGAAGGGGGTGACGCTGGGCAGCGGCGAGGAGCGCGCCGCTGCCTCTGGCGGGCTTT  
CGGCTTGAGGGGCAAGGTGAAGAGCGCACCGGCCGTGGGGTTTACCGAGCTGGATTTGTATG  
TTGCACCAATGCCTTCTTGATCGGGGCTGTGATTCTTCCCCTCTTGGGGCTGCTGCTCTCCC  
TCCCCGCCGGGGCGGATGTGAAGGCTCGGAGCTGCGGAGAGGTCCGCCAGGCGTACGGTGCC  
AAGGGATTTCAGCCTGGCGGACATCCCCTACCAGGAGATCGCAGGGGAACACTTAAGAATCTG  
TCCTCAGGAATATACATGCTGCACCACAGAAATGGAAGACAAGTTAAGCCAACAAGCAAAC  
TCGAATTTGAAAACCTTGTGGAAGAGACAAGCCATTTTGTGCGCACCACTTTTGTGTCCAGG  
CATAAGAAATTTGACGAATTTTTCGAGAGCTCCTGGAGAATGCAGAAAAGTCACTAAATGA  
TATGTTTGTACGGACCTATGGCATGCTGTACATGCAGAATTCAGAAGTCTTCCAGGACCTCT  
TCACAGAGCTGAAAAGGTACTACACTGGGGGTAATGTGAATCTGGAGGAAATGCTCAATGAC  
TTTTGGGCTCGGCTCCTGGAACGGATGTTTCAGCTGATAAACCTCAGTATCACTTCAGTGA  
AGACTACCTGGAATGTGTGAGCAAATACACTGACCAGCTCAAGCCATTTGGAGACGTGCCCC  
GGAAACTGAAGATTTCAGGTTACCCGCGCCTTCATTGCTGCCAGGACCTTTGTCCAGGGGCTG  
ACTGTGGGCAGAGAAGTTGCAAACCGAGTTTCCAAGGTCAGCCCAACCCCAAGGTGTATCCG  
TGCCCTCATGAAGATGCTGTACTGCCCATACTGTGCGGGGCTTCCCCTGTGAGGCCCTGCA  
ACAATACTGTCTCAACGTCATGAAGGGCTGCTTGGCAAATCAGGCTGACCTCGACACAGAG  
TGGAATCTGTTTATAGATGCAATGCTCTTGGTGGCAGAGCGACTGGAGGGGCCATTCAACAT  
TGAGTCGGTCATGGACCCGATAGATGTCAAGATTTCTGAAGCCATTATGAACATGCAAGAAA  
ACAGCATGCAGGTGTCTGCAAAGGTCTTTCAGGGATGTGGTCAGCCCAAACCTGCTCCAGCC  
CTCAGATCTGCCCGCTCAGCTCCTGAAAATTTTAATACACGTTTCAGGCCCTACAATCCTGA  
GGAAAGACCAACAACCTGCTGCAGGCACAAGCTTGGACCGGCTGGTCACAGACATAAAAGAGA  
AATTGAAGCTCTCTAAAAAGGTCTGGTCAGCATTACCCTACACTATCTGCAAGGACGAGAGC  
GTGACAGCGGGCACGTCCAACGAGGAGGAATGCTGGAACGGGCACAGCAAAGCCAGATACTT  
GCCTGAGATCATGAATGATGGGCTCACCAACCAGATCAACAATCCCGAGGTGGATGTGGACA  
TCACTCGGCCTGACACTTTCATCAGACAGCAGATTATGGCTCTCCGTGTGATGACCAACAAA  
CTAAAAAACGCCTACAATGGCAATGATGTCAATTTCCAGGACACAAGTGATGAATCCAGTGG  
CTCAGGGAGTGGCAGTGGGTGCATGGATGACGTGTGTCCCACGGAGTTTGAGTTTGTACCA  
CAGAGGCCCCCGCAGTGGATCCCGACCGGAGAGAGGTGGACTCTTCTGCAGCCCAGCGTGGC  
CACTCCCTGCTCTCCTGGTCTCTCACCTGCATTGTCCTGGCACTGCAGAGACTGTGCAGATA  
ATCTTGGGTTTTTTGGTCAGATGAAACTGCATTTTAGCTATCTGAATGGCCAACTCACTTCTT  
TTCTTACACTCTTGGACAATGGACCATGCCACAAAACTTACCGTTTTCTATGAGAAGAGAG  
CAGTAATGCAATCTGCCTCCCTTTTTGTTTTTCCCAAAGAGTACCGGGTGCCAGACTGAACTG  
CTTCCTCTTTCCTTCAGCTATCTGTGGGGACCTTGTTTATTCTAGAGAGAATTCTTACTCAA  
ATTTTTCGTACCAGGAGATTTTCTTACCTTCATTTGCTTTTATGCTGCAGAAGTAAAGGAAT  
CTCACGTTGTGAGGGTTTTTTTTTTCTCATTAAAT



**FIGURE 41**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50914

><subunit 1 of 1, 555 aa, 1 stop

><MW: 62736, pI: 5.36, NX(S/T): 0

MPSWIGAVILPLLGLLLSLPAGADV KARS CGEVRQAYGAKGFS LADIPYQEIAGEHLRICPQ  
EYTCCTTEMEDKLSQQSKLEFENLVEETSHFVRTTFVSRHKKFDEFFRELLEN A EKSLNDMF  
VRTYGMLYMQNSEVFQDLFTTELKRYYTGGNVNLEEMLNDFWARLLERMFQLINPQYHFSE DY  
LECVSKYTDQLKPFQDVPRKLKIQVTRAFIAARTFVQGLTVGREVANRVSKVSPTPGCIRAL  
MKMLYCPYCRGLPTVRPCNNYCLNVMKGCLANQADLDTEWNL FIDAMLLVAERLEGPFNIES  
VMDPIDVKISEAIMNMQENSMQVSAKV FQ GCGQPKPAPALRSARSAPENFNTFRPYNPEER  
PTTAAGTSLDRLVTDIKEKLKLSKKVWSALPYTICKDES VTAGTSNEEECWNGH SKARYLPE  
IMNDGLTNQINNPEVDVDITRPDTFIRQQIMALRVMTNKLKNAYNGNDVNFQDTSDESSGSG  
SGSGCMDDVCPTEFEFVTTEAPAVDPDRREVDSSAAQRGHSLLSWSLTCIVLALQRLCR

**Signal peptide:**

amino acids 1-23

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**FIGURE 42A**

CGGACGCGTGGGCGGACGCGTGGGCAAAGAACTCGGAGTGCCAAAGCTAAATAAGTTAGCTGAGAAAACGCACG  
CAGTTTGCAGCGCCTGCGCCGGGTGCGCCAACTACGCAAAGACCAAGCGGGCTCCGCGCGGACCGGCCGCGGGG  
TAGGGACCCGGCTTTGGCCTTCAGGCTCCCTAGCAGCGGGGAAAAGGAATTGCTGCCCGGAGTTTCTGCGGAGGT  
GGAGGGAGATCAGGAAACGGCTTCTTCCTCACTTCGCCGCCTGGTGAGTGTGCGGGGAGATTGGCAAACGCCTAGG  
AAAGGACTGGGGAAAATAGCCCTGGGAAAGTGGAGAAGGTGATCAGGAGGCCGGTCCACTACGGCAGTTTATCTG  
TCTGATCAGAGCCAGACGCGACGCGTCCACTTCGCAGTTCTTTCCAGGTGTGGGGACCGCAGGACAGACGGCCGA  
TCCCGCCGCCCTCCGTACCAGCACTCCAGGAGAGTCAGCCTCGCTCCCCAACGTCGAGGGCGCTCTGGCCACGA  
AAAGTTCCTGTCCACTGTGATTCTCAATTCCTTGCTTGTTTTTTTTCTCCAGAGAACTTTTGGGTGGAGATATTA  
ACTTTTTTCTTTTTTTTTTCTTGCTGGTGGAAAGCTGCTCTAGGGAGGGGGGAGGAGGAGGAGAAAGTGAAATGTGC  
TGGAGAAGAGCGAGCCCTCCTTGTTCTTCGGGAGTCCCATCCATTAAGCCATCACTTCTGGAAGATTAAAGTTGT  
CGGACATGGTGACAGCTGAGAGGAGAGGAGGATTTCTTGCCAGGTGGAGAGTCTTCACCGTCTGTTGGGTGCATG  
TGTGCGCCCGCAGCGGCGCGGGGCGCGTGGTTCTCCGCGTGGAGTCTCACCTGGGACCTGAGTGAATGGCTCCCA  
GGGGCTGTGCGGGGCATCCGCCTCCGCCTTCTCCACAGGCCTGTGTCTGTCTGGAAAGATGCTAGCAATGGGGG  
CGCTGGCAGGATTTCTGGATCCTCTGCCTCCTCACTTATGGTTACCTGTCTGGGGCCAGGCCTTAGAAGAGGAGG  
AAGAAGGGGCTTACTAGCTCAAGCTGGAGAGAACTAGAGCCCAGCACAACTTCCACCTCCCAGCCCCATCTCA  
TTTTCATCCTAGCGGATGATCAGGGATTTAGAGATGTGGGTACCACGGATCTGAGATTAAAACACCTACTCTTG  
ACAAGCTCGCTGCCGAAGGAGTTAAACTGGAGAACTACTATGTCCAGCCTATTTGCACACCATCCAGGAGTCAGT  
TTATTACTGGAAAGTATCAGATACACACCGGACTTCAACATTCTATCATAAGACCTACCCAACCAACTGTTTAC  
CTCTGGACAATGCCACCCTACCTCAGAACTGAAGGAGGTGGATATTCAACGCATATGGTCGGAAAATGGCACT  
TGGGTTTTAACAGAAAAGAATGCATGCCACCAGAAGAGGATTTGATACCTTTTTTGGTTCCCTTTTGGGAAGTG  
GGGATTACTATACACTACAAATGTGACAGTCTGGGATGTGTGGCTATGACTTGTATGAAAACGACAATGCTG  
CCTGGGACTATGACAATGGCATATACTCCACACAGATGTACACTCAGAGAGTACAGCAAATCTTAGCTTCCATA  
ACCCACAAAGCCTATATTTTTATATACTGCCTATCAAGCTGTTCACTCACCCTGCAAGCTCCTGGCAGGTATT  
TCGAACACTACCGATCCATTATCAACATAAACAGGAGAAGATATGCTGCCATGCTTTCCTGCTTAGATGAAGCAA  
TCAACAACGTGACATTGGCTCTAAAGACTTATGGTTTCTATAACAACAGCATTATCATTTACTCTTCAGATAATG  
GTGGCCAGCCTACGGCAGGAGGGAGTAAGTGGCCTCTCAGAGGTAGCAAAGGAACATATTGGGAAGGAGGGATCC  
GGGCTGTAGGCTTTGTGCATAGCCCACTTCTGAAAAACAAGGGAACAGTGTGTAAGGAACTTGTGCACATCACTG  
ACTGGTACCCCACTCTCATTTCACTGGCTGAAGGACAGATTGATGAGGACATTCAACTAGATGGCTATGATATCT  
GGGAGACCATAAGTGAGGGTCTTCGCTCACCCCGAGTAGATATTTTGCATAACATTGACCCCTATACACCAAGGC  
AAAAAATGGCTCCTGGGCAGCAGGCTATGGGATCTGGAACACTGCAATCCAGTCAGCCATCAGAGTGCAGCACTG  
GAAATTGCTTACAGGAAATCCTGGCTACAGCGACTGGGTCCCCCTCAGTCTTTCAGCAACCTGGGACCGAACCG  
GTGGCACAATGAACGGATCACCTTGTCAACTGGCAAAAGTGTATGGCTTTTCAACATCACAGCCGACCCATATGA  
GAGGGTGGACCTATCTAACAGGTATCCAGGAATCGTGAAGAAGCTCCTACGGAGGCTCTCACAGTTCAACAAAAC  
TGCAGTGCCGGTCAGGTATCCCCCAAAGACCCCAAGTAACCTAGGCTCAATGGAGGGGTCTGGGGACCATG  
GTATAAAGAGGAAACCAAGAAAAGAAGCCAAGCAAAAATCAGGCTGAGAAAAAGCAAAAGAAAAGCAAAAAAA  
GAAGAAGAAACAGCAGAAAGCAGTCTCAGGTAAACCAGCAAATTTGGCTCGATAATATCGCTGGCCTAAGCGTCA  
GGCTTGTTTTCATGCTGTGCCACTCCAGAGACTTCTGCCACCTGGCCGCCCACTGAAAACCTGTCCTGCTCAGTG  
CCAAGGTGCTACTCTTGCAAGCCACACTTAGAGAGAGTGGAGATGTTTATTTCTCTCGCTCCTTTAGAAAACGTG  
GTGAGTCTGAGTTCACCTGCTGTGCTTCACTCAACTGACCAACACTGCTTTGAATTATAGGAGGAGAACAATA  
ACCTACCATCCGCAAGCATGCTAATTTGATGGAAGTTACAGGGTAGCATGATTAAACTACCTTTGATAAATTAC

**FIGURE 42B**

AGTCAAAGATTGTGTCACCTCAAAGGCCTTGAAGAATATATTTTCTTGGTGAATTTTGTATGTCTGTCATATGA  
CACTTGGGTTTTTTAATTAATTCTATTTTATATATATAAATATATGTTTCTTTTCCTGTGAAAAGCTGTTTTCT  
CACATGTGAACAGCTTGCACCTCATTTTACCATGCGTGAGGGAATGGCAAAT'AGAATGTTTGAGCACACTGCCC  
ACAATGAATGTAACATTTTCTAAACACTTTACTAGAAGAACATTTTCAGTATAAAAAACCTAATTTATTTTACA  
GAAAAATATTTTGTGTTTTTATAAAAAGTTATGCAAATGACTTTTATTTTATTTTCTGCATACCATTAGAAGA  
ATTTTATTTTCAATTTCTTCAAATTATCAAGCACTGTAATACTATAAATTAATGTAATACTGTGTGAATTCAGACTA  
TAAAAACATCATTTCAGAAAACCTTTATAATCGTCATTGTTCAATCAAGATTTTGAATGTAATAAGATGAATATAT  
ATTACTTGGAAATTCAATGTTTGTGCAGAGTTGAGACAACCTTTATTGTTTCTATCATAAACTATTTATGTATCTT  
AATTATTAAATGATTTACTTTATGGCACTAGAAAATTTACTGTGGCTTTTCTGATCTAACTTCTAGCTAAAATT  
GTATCATTGGTCCTAAAAAATAAAAAATCTTTACTAATAGGCAATTGAAGGAATGGTTTGCTAACAACCACAGTAA  
TATAATATGATTTTACAGATAGATGCTTCCCCTTGGCTATGACATGGAGAAAGATTTTCCCATATAATAACTAA  
TATTTATATTAGGTTGGTGCAAACTAGTTGCGGTTTTTCCCATTAAGTAATAACCTTACTCTTATACAAAGT  
GGACACTGTGGGGAGATACAGAGAAATGGAAGATACGGATCCTGCCTGGAGTAGGTAACCTTGCTTGGAACCCC  
ACATGCAAACGTCATGAGGAGAATTAAAGGAGTATTATCAGTAATGAAGTTTATCATGGGTCATCAATGAGCATA  
GATTGGTGTGGATCCTGTAGACCCTGGTGTTTTCTTTGAAGTGCCCTCTCCTAATGCAGAGGCCCTGAAGCTTAC  
AGTATACACTTGAAAAGTCACAGATAGCTAGAATTATGATCTTTGAAGTTATAACTGTGATCTGAAAATGTGTGT  
GGTGGTATGACAGCATAACCATTAAATACATTTACATCACAGCTCAAAGGACTGTGATATAATCCATTTATATCAC  
AACTCAAAGGACTGTGATATAATCCATTTATATCACAGCTCACAGTTTCTGAAAATGTATAAAGAATCTATAAT  
CTAGTACTGAAATTACTAAATTGGGTAAGATGATTTAAATGATTTTAATTTTAACATTTTATTTCTAGAATATAT  
GGCTCCATTTTATTTTATAGTGTAAGTTGTATTTCTTAAAGTTTGTGTTTTGTGCGACAGTATCTTTTAAATGAG  
TCTTAAAAATAAAGGCATATTGTTTCATGTTTAAA  
AAA

**FIGURE 43**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48296  
><subunit 1 of 1, 515 aa, 1 stop  
><MW: 56885, pI: 6.49, NX(S/T): 5  
MAPRGCAGHPPPPSPQACVCPGKMLAMGALAGFWILCLLTGYLSWGQALEEEEEEGALLAQA  
GEKLEPSTTSTSQPHLIFILADDQGFRDVGYHGSEIKTPTLDKLAAEGVKLENYYVQPICTP  
SRSQFITGKYQIHTGLQHSIIRPTQPNCLPLDNATLPQKLKEVGYSTHMGVKGWHLGFNRKEC  
MPTRRGFDTFFGSLLGSGDYTHYKCDSPGMCGYDLYENDNAAWDYDNGIYSTQMYTQRVQQ  
ILASHNPTKPIFLYTAYQAVHSPLQAPGRYFEHYRSIININRRRYAAMLSCLEAINNVTLA  
LKTYGFYNNNSIIYSSDNGGQPTAGGSNWPLRGSKGTYWEGGIRAVGVHSPLLKNKGTVCK  
ELVHITDWYPTLISLAEGQIDEDIQLDGYDIWETISEGLRSPRVDILHNIDPYTPRQKMAPG  
QQAMGSGTLQSSQPSECSTGNCLQEILATATGSPLSLSATWDRTGGTMNGSPCQLAKVYGFS  
TSQPTHMRGWYLTG IQES

**Important Features:****Signal Peptide:**

amino acids 1-37

**Sulfatases signature 1.**

amino acids 120-132

**Sulfatases signature 2.**

amino acids 168-177

**Tyrosine kinase phosphorylation site.**

amino acids 163-169

**N-glycosylation sites.**

amino acids 157-160, 306-309 and 318-321

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**FIGURE 44**

CGGACGCGTGGGTGCGAGTGGAGCGGAGGACCCGAGCGGCTGAGGAGAGAGGAGGGCGGCGGC  
TTAGCTGCTACGGGGTCCGGCCGGCGCCCTCCCGAGGGGGGGCTCAGGAGGAGGAAGGAGGAC  
CCGTGCGAGAATGCCCTCTGCCCTGGAGCCTTGCGCTCCCGCTGCTGCTCTCCTGGGTGGCAG  
GTGGTTTCGGGAACGCGGCCAGTGCAAGGCATCACGGGTTGTTAGCATCGGCACGTCAGCCT  
GGGGTCTGTCACTATGGAACATAACTGGCCTGCTGCTACGGCTGGAGAAGAAACAGCAAGGG  
AGTCTGTGAAGCTACATGCGAACCTGGATGTAAGTTTGGTGAGTGCGTGGGACCAAACAAAT  
GCAGATGCTTTCCAGGATACACCGGGAAAACCTGCAGTCAAGATGTGAATGAGTGTGGAATG  
AAACCCCGGCCATGCCAACACAGATGTGTGAATACACACGGAAGCTACAAGTGCTTTTGCCT  
CAGTGGCCACATGCTCATGCCAGATGCTACGTGTGTGAACCTCTAGGACATGTGCCATGATAA  
ACTGTCAGTACAGCTGTGAAGACACAGAAGAAGGGCCACAGTGCTGTGTCCATCCTCAGGA  
CTCCGCCTGGCCCCAAATGGAAGAGACTGTCTAGATATTGATGAATGTGCCTCTGGTAAAGT  
CATCTGTCCCTACAATCGAAGATGTGTGAACACATTTGGAAGCTACTACTGCAAATGTCACA  
TTGGTTTCGAACTGCAATATATCAGTGGACGATATGACTGTATAGATATAAATGAATGTACT  
ATGGATAGCCATACGTGCAGCCACCATGCCAATTGCTTCAATACCCAAGGGTCCTTCAAGTG  
TAAATGCAAGCAGGGATATAAAGGCAATGGACTTCGGTGTCTGCTATCCCTGAAAATTCTG  
TGAAGGAAGTCCTCAGAGCACCTGGTACCATCAAAGACAGAATCAAGAAGTTGCTTGCTCAC  
AAAAACAGCATGAAAAAGAAGGCAAAAATTAATAATGTTACCCCAAGAACCCACCAGGACTCC  
TACCCCTAAGGTGAACTTGCAGCCCTTCAACTATGAAGAGATAGTTTCCAGAGGCGGGAACT  
CTCATGGAGGTAAAAAAGGGAATGAAGAGAAATGAAGAGGGGGCTTGAGGATGAGAAAAGAG  
AAGAGAAAGCCCTGAAGAATGACATAGAGGAGCGAAGCCTGCGAGGAGATGTGTTTTTCCCT  
AAGGTGAATGAAGCAGGTGAATTCGGCCTGATTCTGGTCCAAAGGAAAGCGCTAACTTCCAA  
ACTGGAACATAAAGATTTAAATATCTCGGTTGACTGCAGCTTCAATCATGGGATCTGTGACT  
GGAAACAGGATAGAGAAGATGATTTTGACTGGAATCCTGCTGATCGAGATAATGCTATTGGC  
TTCTATATGGCAGTTCCGGCCTTGGCAGGTCACAAGAAAGACATTGGCCGATTGAACTTCT  
CCTACCTGACCTGCAACCCCAAAGCAACTTCTGTTTTGCTCTTTGATTACCGGCTGGCCGGAG  
ACAAAGTCGGGAAACTTCGAGTGTTTGTGAAAAACAGTAACAATGCCCTGGCATGGGAGAAG  
ACCACGAGTGAGGATGAAAAGTGGAAGACAGGGAAAATTCAGTTGTATCAAGGAACTGATGC  
TACCAAAGCATCATTTTTGAAGCAGAACGTGGCAAGGGCAAACCGGCGAAATCGCAGTGG  
ATGGCGTCTTGCTTGTTTCAGGCTTATGTCCAGATAGCCTTTTATCTGTGGATGACTGAATG  
TTACTATCTTTATATTTGACTTTGTATGTCAGTTCCCTGGTTTTTTTGATATTGCATCATAG  
GACCTCTGGCATTTTAGAACTTAGCTGAAAAATTGTAATGTACCAACAGAAATATTATTG  
TAAGATGCCTTTCTTGATAAGATATGCCAATATTTGCTTTAAATATCATATCACTGTATCT  
TCTCAGTCATTTCTGAATCTTTCCNCATTATATTATAAAATNTGGAAANGTCAGTTTATCTC  
CCCTCCTCNGTATATCTGATTTGTATANGTANGTTGATGNGCTTCTCTCTACAACATTTCTA  
GAAAATAGAAAAAAAAGCACAGAGAAATGTTTAACTGTTTGACTCTTATGATACTTCTTGGA  
AACTATGACATCAAAGATAGACTTTTGCCTAAGTGGCTTAGCTGGGTCTTTCATAGCCAAAC  
TTGTATATTTAATTCTTTGTAATAATAA



**FIGURE 45**

MPLPWSLALPLLLSWVAGGFGNAASARHHGLLASARQPGVCHYGTKLACCYGWRNSKGVCE  
ATCEPGCKFGECVGPNNKCRCPGYTGKTCSDVNECGMKPRPCQHRVNTHGSKCFCLSGH  
MLMPDATCVNSRTCAMINCQYSCDTEEGPQCLCPSSGLRLAPNGRDCLDIDECASGKVICP  
YNRRCVNTFGSYCKCHIGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKCK  
QGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKLLAHKNSMKKKAKIKNVTPEPTRTPPK  
VNLQPFNYEEIVSRGGNSHGGKKGNEEK

**Signal peptide:**

amino acids 1-21

**EGF-like domain cysteine pattern signature.**

amino acids 80-91

**Calcium-binding EGF-like domains**

amino acids 103-124, 230-251 and 185-206

**FIGURE 46**

GGGAGCTGCTGCTGTGGCTGCTGGTGCTGTGCGCGCTGCTCCTGCTCTTGGTGCAGCTGCTG  
CGCTTCCTGAGGGCTGACGGCGACCTGACGCTACTATGGGCCGAGTGGCAGGGACGACGCCC  
AGAATGGGAGCTGACTGATATGGTGGTGTGGGTGACTGGAGCCTCGAGTGGAATTGGTGAGG  
AGCTGGCTTACCAGTTGTCTAAACTAGGAGTTTCTCTTGTGCTGTCAGCCAGAAGAGTGCAT  
GAGCTGGAAAGGGTGAAAAGAAGATGCCTAGAGAATGGCAATTTAAAAGAAAAGATATACT  
TGTTTTGCCCCCTTGACCTGACCGACACTGGTTCCCATGAAGCGGCTACCAAAGCTGTTCTCC  
AGGAGTTTGGTAGAATCGACATTCTGGTCAACAATGGTGGAATGTCCCAGCGTTCTCTGTGC  
ATGGATAACCAGCTTGGATGTCTACAGAAAGCTAATAGAGCTTAACTACTTAGGGACGGTGTG  
CTTGACAAAATGTGTTCTGCCTCACATGATCGAGAGGAAGCAAGGAAAGATTGTTACTGTGA  
ATAGCATCCTGGGTATCATATCTGTACCTCTTTCCATTGGATACTGTGCTAGCAAGCATGCT  
CTCCGGGGTTTTTTTAAATGGCCTTCGAACAGAACTTGCCACATACCCAGGTATAATAGTTTC  
TAACATTTGCCCAGGACCTGTGCAATCAAATATTGTGGAGAATTCCCTAGCTGGAGAAGTCA  
CAAAGACTATAGGCAATAATGGAGACCAGTCCCACAAGATGACAACCAGTCGTTGTGTGCGG  
CTGATGTTAATCAGCATGGCCAATGATTTGAAAGAAGTTTGGATCTCAGAACAACCTTTCTT  
GTTAGTAACATATTTGTGGCAATACATGCCAACCTGGGCCTGGTGGATAACCAACAAGATGG  
GGAAGAAAAGGATTGAGAACTTTAAGAGTGGTGTGGATGCAGACTCTTCTTATTTTAAATC  
TTTAAGACAAAACATGACTGAAAAGAGCACCTGTACTTTTCAAGCCACTGGAGGGAGAAATG  
GAAAACATGAAAACAGCAATCTTCTTATGCTTCTGAATAATCAAAGACTAATTTGTGATTTT  
ACTTTTTAATAGATATGACTTTGCTTCCAACATGGAATGAAATAAAAAATAATAATAAAG  
ATTGCCATGAATCTTGCAAAA

**FIGURE 47**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA36343  
><subunit 1 of 1, 289 aa, 1 stop  
><MW: 32268, pI: 9.21, NX(S/T): 0  
MVVWVTGASSGIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDL  
TDTGSHEAATKAVLQEFGRIDILVNNGGMSQSRSLCMDTSLDVYRKLIELNYLGTVSLTKCVL  
PHMIERKQGKIIVTVNSILGIISVPLSIGYCASKHALRGFFENGLRTELATYPGIIVSNICPGP  
VQSNIVENSLAGEVTKTIGNNGDQSHKMTTSRCVRLMLISMANDLKEVWISEQPFLLVTYLW  
QYMPTWAWWITNKMGGKRIENFKSGVDADSSYFKIEFKTKHD

**Important Features:****Signal Peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 136-157

**Tyrosine kinase phosphorylation site.**

106-113 and 107-114

**Homologous region to Short-chain alcohol dehydrogenase**

amino acids 80-90, 131-168, 1-13 and 176-185

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**FIGURE 48**

GCGACGTGGGCACCGCCATCAGCTGTTGCGCGCTCTTCTCCTCCAGGTGGGGCAGGGGTTTC  
GGGCTGGTGGAGCATGTGCTGGGACAGGACAGCATCCTCAATCAATCCAACAGCATATTCGG  
TTGCATCTTCTACACACTACAGCTATTGTTAGGTTGCCTGCGGACACGCTGGGCCTCTGTCC  
TGATGCTGCTGAGCTCCCTGGTGTCTCTCGCTGGTTCTGTCTACCTGGCCTGGATCCTGTTT  
TTCGTGCTCTATGATTTCTGCATTGTTTGTATCACCACCTATGCTATCAACGTGAGCCTGAT  
GTGGCTCAGTTTCCGGAAGGTCCAAGAACCCCAAGGCAAGGCTAAGAGGCACTGAGCCCTCA  
ACCCAAGCCAGGCTGACCTCATCTGCTTTGCTTTGGTCTTCAAGCCGCTCAGCGTGCCTGTG  
GACAGCGTGGCCCCGGCCCCCCCCAAGCCTCAGGAGGGCAACACAGTCCCTGGCGAGTGGCCC  
TGGCAGGCCAGTGTGAGGAGGCAAGGAGCCCACATCTGCAGCGGCTCCCTGGTGGCAGACAC  
CTGGGTCTCTCACTGCTGCCCACTGCTTTGAAAAGGCAGCAGCAACAGAACTGAATTCCTGGT  
CAGTGGTCTTGGGTTCTCTGCAGCGTGAGGGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTG  
GCTGCCCTGCAGTTGCCAGGGGCTATAACCACTACAGCCAGGGCTCAGACCTGGCCCTGCT  
GCAGCTCGCCACCCACGACCCACACACCCCTCTGCCTGCCCCAGCCCGCCCATCGCTTCC  
CCTTTGGAGCCTCCTGCTGGGCCACTGGCTGGGATCAGGACACCAGTGATGCTCCTGGGACC  
CTACGCAATCTGCGCCTGCGTCTCATCAGTCGCCCCACATGTAACGTATCTACAACCAGCT  
GCACCAGCGACACCTGTCCAACCCGGCCCCGGCCTGGGATGCTATGTGGGGGGCCCCAGCCTG  
GGGTGCAGGGCCCCCTGTCAGGGAGATTCCGGGGGGCCCTGTGCTGTGCCTCGAGCCTGACGGA  
CACTGGGTTCAGGCTGGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGT  
GCTGCTGACCAACACAGCTGCTCACAGTTCTGGCTGCAGGCTCGAGTTCAGGGGGCAGCTT  
TCCTGGCCCCAGAGCCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGA  
TCCTTGAGGACAGCAGGTCCCCAGGCAGGAGCACCTCCCCATGGCCCTGGGAGGCCAGGCT  
GATGCACCAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGAGAGGAGGCGGTGCTAACTG  
CTGCCCACTGCTTCATTGGGCGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGGACCAGA  
CCGGAGGAGTGGGGCCTGAAGCAGCTCATCCTGCATGGAGCCTACACCCACCCTGAGGGGGG  
CTACGACATGGCCCTCCTGCTGCTGGCCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCCCC  
TCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGGAGCGTGGCTGGGTTCTGGGACGG  
GCCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGCCCGTGACCCTCCTGGGGCCTAG  
GGCCTGCAGCCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCGGGGATGG  
TGTGTACCAGTGCTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCACCCTGGTG  
CATGAGGTGAGGGGCACATGGTTCTGGCCGGGCTGCACAGCTTCGGAGATGCTTGCCAAGG  
CCCCGCCAGGCCGGCGGTCTTCACCGCGCTCCCTGCCTATGAGGACTGGGTGAGCAGTTTGG  
ACTGGCAGGTCTACTTCGCCGAGGAACCAGAGCCCCGAGGCTGAGCCTGGAAGCTGCCTGGCC  
AACATAAGCCAACCAACCAGCTGCTGACAGGGGACCTGGCCATTCTCAGGACAAGAGAATGC  
AGGCAGGCAAATGGCATTACTGCCCTGTCTCCCCACCCTGTCATGTGTGATTCCAGGCAC  
CAGGGCAGGCCCAGAAGCCCAGCAGCTGTGGGAAGGAACCTGCCTGGGGCCACAGGTGCCCA  
CTCCCCACCCTGCAGGACAGGGGTGTCTGTGGACACTCCACACCCAACTCTGCTACCAAGC  
AGGCGTCTCAGCTTTCCTCCTCCTTTACTCTTTCAGATACAATCACGCCAGCCACGTTGTTT  
TGAAAATTTCTTTTTTTGGGGGGCAGCAGTTTTCTTTTTTTAACTTAAATAAATTGTTAC  
AAAATAAAA

**FIGURE 49**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40571

MLLSSLVSLAGSVYLAWILFFVLYDFCIVCITTYAINVSLMWLSFRKVQEPQGKAKRHGNTV  
PGEWPWQASVRRQGAHICSGSLVADTWVLTAAHCFEKAATELNSWSVVLGSLQREGLSPGA  
EEVGVAALQLPRAYNHYSQGSDDLALLQLAHPTTHTPLCLPQPAHRFPFGASCWATGWDQDTS  
DAPGTLRNLRLRLISRPTCNCIYNQLHQRHLSNPARPGMLCGGPQPGVQGPCQGDSSGGPVLC  
LEPDGHWVQAGIISFASSCAQEDAPVLLTNTAAHSSWLQARVQGAAFLAQSPETPEMSDEDS  
CVACGSLRTAGPQAGAPSPWPWEARLMHQGQLACGGALVSEEAVLTAAHCFIGRQAPEEWSV  
GLGTRPEEWGLKQLILHGAYTHPEGGYDMALLLAQPVTLGASLRPLCLPYPDHHLPDGERG  
WVLGRARPGAGISSLQTVPVTLTGPRACSRHLHAAPGGDGSPILPGMVCTSAVGELPSCEGLS  
GAPLVHEVRGTWFLAGLHSFGDACQGPAPPAVFTALPAYEDWVSSLDWQVYFAEEPEPEAEP  
GSCLANISQPTSC

**Important features:****Signal peptide:**

amino acids 1-15

**Homologous region to Serine proteases, trypsin family**

amino acids 79-95, 343-359 and 237-247

**N-glycosylation sites.**

amino acids 37-40 and 564-567

**Kringle domains**

amino acids 79-96, 343-360 and 235-247



**FIGURE 50**

CGGGCCGCCCCCGGCCCCCATTCGGGCCGGGCCTCGCTGCGGCGGCGACTGAGCCAGGCTGG  
GCCGCGTCCCTGAGTCCCAGAGTCGGCGCGGCGCGGCAGGGGCAGCCTTCCACCACGGGGAG  
CCCAGCTGTCAGCCGCCTCACAGGAAGATGCTGCGTCGGCGGGGCAGCCCTGGCATGGGTGT  
GCATGTGGGTGCAGCCCTGGGAGCACTGTGGTTCTGCCTCACAGGAGCCCTGGAGGTCCAGG  
TCCCTGAAGACCCAGTGGTGGCACTGGTGGGCACCGATGCCACCCTGTGCTGCTCCTTCTCC  
CCTGAGCCTGGCTTCAGCCTGGCACAGCTCAACCTCATCTGGCAGCTGACAGATAACCAAACA  
GCTGGTGCACAGCTTTGCTGAGGGCCAGGACCAGGGCAGCGCCTATGCCAACCGCACGGCCC  
TCTTCCCGGACCTGCTGGCACAGGGCAACGCATCCCTGAGGCTGCAGCGCGTGCCTGTGGCG  
GACGAGGGCAGCTTCACCTGCTTCGTGAGCATCCGGGATTTCGGCAGCGCTGCCGTGAGCCT  
GCAGGTGGCCGCTCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTGCGGC  
CAGGGGACACGGTGACCATCACGTGCTCCAGCTACCAGGGCTACCCTGAGGCTGAGGTGTTT  
TGGCAGGATGGGCAGGGTGTGCCCCCTGACTGGCAACGTGACCACGTGCGAGATGGCCAACGA  
GCAGGGCTTGTTTGATGTGCACAGCGTCCTGCGGGTGGTGGTGGGTGCGAATGGCACCTACA  
GCTGCCTGGTGCAGCAACCCCGTGCTGCAGCAGGATGCGCACRGCTCTGTCAACCATCACAGGG  
CAGCCTATGACATTCCCCCCAGAGGCCCTGTGGGTGACCGTGGGGCTGTCTGTCTGTCTCAT  
TGCACTGCTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAACAGAGCTGTGAGGAGG  
AGAATGCAGGAGCTGAGGACCAGGATGGGGAGGGAGAAGGCTCCAAGACAGCCCTGCAGCCT  
CTGAAACACTCTGACAGCAAAGAAGATGATGGACAAGAAATAGCCTTGACCATGAGGACCAGG  
GAGCTGCTACCCCTCCCTACAGCTCCTACCCTCTGGCTGCAATGGGGCTGCACTGTGAGCCC  
TGCCCCCAACAGATGCATCCTGCTCTGACAGGTGGGCTCCTTCTCCAAAGGATGCGATACAC  
AGACCACTGTGCAGCCTTATTTCTCCAATGGACATGATTCCCAAGTCATCCTGCTGCCTTTT  
TTCTTATAGACACAATGAACAGACCACCCACAACCTTAGTTCTCTAAGTCATCCTGCCTGCT  
GCCTTATTTACAGTACATACATTTCTTAGGGACACAGTACACTGACCACATCACCACCCTC  
TTCTTCCAGTGCTGCGTGGACCATCTGGCTGCCTTTTTTCTCCAAAAGATGCAATATTCAGA  
CTGACTGACCCCTGCCTTATTTACCAAAGACACGATGCATAGTCACCCCGGCCTTGTTTC  
TCCAATGGCCGTGATACACTAGTGATCATGTTTCAGCCCTGCTTCCACCTGCATAGAATCTTT  
TCTTCTCAGACAGGGACAGTGCGGCCTCAACATCTCCTGGAGTCTAGAAGCTGTTTCCTTTC  
CCCTCCTTCCTCCCTGCCCCAAGTGAAGACAGGGCAGGGCCAGGAATGCTTTGGGGACACCG  
AGGGGACTGCCCCCCCACCCCAACCATGGTGCTATTCTGGGGCTGGGGCAGTCTTTTCCTGGC  
TTGCCTCTGGCCAGCTCCTGGCCTCTGGTAGAGTGAGACTTCAGACGTTCTGATGCCTTCCG  
GATGTCATCTCTCCCTGCCCCAGGAATGGAAGATGTGAGGACTTCTAATTTAAATGTGGGAC  
TCGGAGGGATTTTGTAACCTGGGGGTATATTTTGGGGAAAATAAATGTCTTTGTAAAAAAA  
AAAAAAAAAAAAAAAA

**FIGURE 51**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41386

><subunit 1 of 1, 316 aa, 1 stop, 1 unknown

><MW: -1, pI: 4.62, NX(S/T): 4

MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATLCCSFSPEPGFSLAQ  
LNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPDLLAQGNASLRLQRVRVADEGSFTCFV  
SIRDFGSAAVSLQVAAPYSKPSMTLEPNKDLRPGDTVTTITCSSYQGYPEAEVFWQDGQGVPL  
TGNVTTSQMANEQGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHXSVTITGQPMTFPPEA  
LWVTVGLSVCLIALLLVALAFVCWRKIKQSCEEENAGAEDQDGEGESESKTALQPLKHSDSKED  
DGQEIA

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 251-270

**N-glycosylation site.**

amino acids 91-94, 104-107, 189-192 and 215-218

**Homologous region to Immunoglobulins and MHC**

amino acids 217-234

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**FIGURE 52**

TTCGTGACCCTTGAGAAAAGAGTTGGTGGTAAATGTGCCACGTCTTCTAAGAAGGGGGAGTC  
CTGAACTTGTCTGAAGCCCTTGTCGGTAAGCCTTGAACCTACGTTCTTAAATCTATGAAGTCG  
AGGGACCTTTCGCTGCTTTTGTAGGGACTTCTTTCCTTGCTTCAGCAACATGAGGCTTTTCT  
TGTGGAACGCGGTCTTGACTCTGTTTCGTCACCTTCTTTGATTGGGGCTTTGATCCCTGAACCA  
GAAGTGAAAATTGAAGTTCTCCAGAAGCCATTCATCTGCCATCGCAAGACCAAAGGAGGGGA  
TTTGATGTTGGTCCACTATGAAGGCTACTTAGAAAAGGACGGCTCCTTATTTCACTCCACTC  
ACAAACATAACAATGGTCAGCCCATTGTTTACCCTGGGCATCCTGGAGGCTCTCAAAGGT  
TGGGACCAGGGCTTGAAAGGAATGTGTGTAGGAGAGAAGAGAAAGCTCATCATTCCTCCTGC  
TCTGGGCTATGGAAAAGAAGGAAAAGGTAAAATTCCCCCAGAAAGTACACTGATATTTAATA  
TTGATCTCCTGGAGATTCGAAATGGACCAAGATCCCATGAATCATTCCAAGAAATGGATCTT  
AATGATGACTGGAACTCTCTAAAGATGAGGTTAAAGCATATTTAAAGAAGGAGTTTGAAAA  
ACATGGTGCGGTGGTGAATGAAAGTCATCATGATGCTTTGGTGGAGGATATTTTTTGATAAAG  
AAGATGAAGACAAAGATGGGTTTATATCTGCCAGAGAATTTACATATAAACACGATGAGTTA  
TAGAGATACATCTACCCTTTTAAATATAGCACTCATCTTCAAGAGAGGGCAGTCATCTTTAA  
AGAACATTTTATTTTTATACAATGTTCTTTCTTGCTTTGTTTTTTATTTTTATATATTTTTT  
CTGACTCCTATTTAAAGAACCCCTTAGGTTTCTAAGTACCCATTTCTTTCTGATAAGTTATT  
GGGAAGAAAAAGCTAATTGGTCTTTGAATAGAAGACTTCTGGACAATTTTTCACCTTTCACAG  
ATATGAAGCTTTGTTTTACTTTCTCACTTATAAATTTAAATGTTGCAACTGGGAATATACC  
ACGACATGAGACCAGGTTATAGCACAAATTAGCACCCCTATATTTCTGCTTCCCTCTATTTTC  
TCCAAGTTAGAGGTCAACATTTGAAAAGCCTTTTGCAATAGCCCAAGGCTTGCTATTTTCAT  
GTTATAATGAAATAGTTTATGTGTAAGTGGCTCTGAGTCTCTGCTTGAGGACCAGAGGAAAA  
TGGTTGTTGGACCTGACTTGTTAATGGCTACTGCTTTACTAAGGAGATGTGCAATGCTGAAG  
TTAGAAACAAGGTTAATAGCCAGGCATGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAG  
GCTGAGGCGGGCGGATCACCTGAGGTTGGGAGTTCGAGACCAGCCTGACCAACACGGAGAAA  
CCCTATCTCTACTAAAAATACAAAGTAGCCCGGCGTGGTGATGCGTGCTGTAATCCCAGCT  
ACCCAGGAAGGCTGAGGCGGCAGAATCACTTGAACCCGAGGCCGAGGTTGCGGTAAGCCGAG  
ATCACCTNCAGCCTGGACACTCTGTCTCGAAAAAAGAAAAGAACACGGTTAATACCATATNA  
ATATGTATGCATTGAGACATGCTACCTAGGACTTAAGCTGATGAAGCTTGGCTCCTAGTGAT  
TGGTGGCCTATTATGATAAATAGGACAAATCATTTATGTGTGAGTTTCTTTGTAATAAAATG  
TATCAATATGTTATAGATGAGGTAGAAAGTTATATTTATATTCAATATTTACTTCTTAAGGC  
TAGCGGAATATCCTTCCTGGTTCTTTAATGGGTAGTCTATAGTATATTATACTACAATAACA  
TTGTATCATAAGATAAAGTAGTAAACCAGTCTACATTTTCCCATTTCTGTCTCATCAAAAAC  
TGAAGTTAGCTGGGTGTGGTGGCTCATGCCTGTAATCCCAGCACTTTGGGGGCCAAGGAGGG  
TGGATCACTTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGTCTCTA  
CTAAAAATACAAAATTAGCCAGGCGTGGTGGTGCACACCTGTAGTCCCAGCTACTCGGGAG  
GCTGAGACAGGAGATTTGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCAAGATTGTGCC  
ACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCCATCTCAAAAAAAAAAAAAAGAAGCAGA  
CCTACAGCAGCTACTATTGAATAAATACCTATCCTGGATTTT

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**FIGURE 53**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44194  
><subunit 1 of 1, 211 aa, 1 stop  
><MW: 24172, pI: 5.99, NX(S/T): 1  
MRLFLWNAVLTLFVTSLLIGALIPPEVKIEVLQKPFICHRKTKGGDLMLVHYEGYLEKDGSL  
FHSTHKHNNNGQPIWFTLGILEALKGWDQGLKGMVCVGEKRKLIIPPALGYGKEGKGKIPPEST  
LIFNIDLLLEIRNGPRSHESFQEMDLNDDWKLSKDEVKAYLKKEFEKHGAVVNESHHDALVED  
IFDKEDDKDGFISAREFTYKHDEL

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 176-179

**Casein kinase II phosphorylation site.**

amino acids 143-146, 156-159, 178-181 and 200-203

**Endoplasmic reticulum targeting sequence.**

amino acids 208-211

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 78-114 and 118-131

**EF-hand calcium-binding domain.**

amino acids 191-203, 184-203 and 140-159

**S-100/ICaBP type calcium binding domain**

amino acids 183-203

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**FIGURE 54**

AATAAAGCTTCCTTAATGTTGTATATGTCTTTGAAGTACATCCGTGCATTTTTTTTTTAGCAT  
CCAACCATTCCTCCCTTGTAGTTCTCGCCCCCTCAAATCACCTCTCCCGTAGCCCACCCGA  
CTAACATCTCAGTCTCTGAAAATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCT  
CACGGGGCTCAGTCTCTTTTTCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCACAGTAC  
CTGCCACCCTCAACGTCCTCAATGGCTCTGACGCCCGCCTGCCCTGCACCTTCAACTCCTGC  
TACACAGTGAACCACAAACAGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTC  
TGAGGAGATGTTCCCTCCAGTTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAG  
ACCGCGTGGAGTTCTCAGGGAACCCAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTG  
CAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCCTGACCGCCACCGTGG  
CCATGGCAAGATCCATCTGCAGGTCCTCATGGAAGAGCCCCCTGAGCGGGACTCCACGGTGG  
CCGTGATTGTGGGTGCCTCCGTGCGGGGGCTTCCTGGCTGTGGTCATCTTGGTGCTGATGGTG  
GTCAAGTGTGTGAGGAGAAAAAAGAGCAGAAGCTGAGCACAGATGACCTGAAGACCGAGGA  
GGAGGGCAAGACGGACGGTGAAGGCAACCCGGATGATGGCGCCAAGTAGTGGGTGGCCGGCC  
CTGCAGCCTCCCGTGTCCCGTCTCCTCCCCTCTCCGCCCTGTACAGTGACCCTGCCTGCTCG  
CTCTTGGTGTGCTTCCCGTGACCTAGGACCCAGGGGCCACCTGGGGCCTCCTGAACCCCCG  
ACTTCGTATCTCCCACCCTGCACCAAGAGTGACCACTCTCTTCCATCCGAGAAACCTGCCA  
TGCTCTGGGACGTGTGGGCCCTGGGGAGAGGAGAGAAAGGGCTCCCACCTGCCAGTCCCTGG  
GGGAGGCAGGAGGCACATGTGAGGGTCCCCAGAGAGAAGGGAGTGGGTGGGCAGGGGTAGA  
GGAGGGGCCGCTGTCACCTGCCCAGTGCTTGCCTGGCAGTGGCTTCAGAGAGGACCTGGTGG  
GGAGGGAGGGCTTTCCTGTGCTGACAGCGCTCCCTCAGGAGGGCCTTGGCCTGGCACGGCTG  
TGCTCCTCCCCTGCTCCCAGCCCAGAGCAGCCATCAGGCTGGAGGTGACGATGAGTTCCTGA  
AACTTGGAGGGGCATGTTAAAGGGATGACTGTGCATTCCAGGGCACTGACGGAAAGCCAGGG  
CTGCAGGCAAAGCTGGACATGTGCCCTGGCCCAGGAGGCCATGTTGGGGCCCTCGTTTCCATT  
GCTAGTGGCCTCCTTGGGGCTCCTGTTGGCTCCTAATCCCTTAGGACTGTGGATGAGGCCAG  
ACTGGAAGAGCAGCTCCAGGTAGGGGGCCATGTTTCCCAGCGGGGACCCACCAACAGAGGCC  
AGTTTCAAAGTCAGCTGAGGGGCTGAGGGGTGGGGCTCCATGGTGAATGCAGGTTGCTGCAG  
GCTCTGCCTTCTCCATGGGGTAACCAACCTCGCCTGGGCAGGGGCAGCCAAGGCTGGGAAAT  
GAGGAGGCCATGCACAGGGTGGGGCAGCTTTCCTTGGGGCTTCAGTGAGAACTCTCCCAGTT  
GCCCTTGGTGGGGTTTCCACCTGGCTTTTGGCTACAGAGAGGGGAAGGGAAAGCCTGAGGCCG  
GCATAAGGGGAGGCCTTGGAACCTGAGCTGCCAATGCCAGCCCTGTCCCCTCTGCGGCCACG  
CTACTCGCTCCTCTCCCAACAACCTCCCTTCGTGGGGACAAAAGTGACAATTGTAGGCCAGGC  
ACAGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCAAGGCGGGTGGATTACCTCCAT  
CTGTTTAGTAGAAATGGGCAAAACCCCATCTCTACTAAAAATACAAGAATTAGCTGGGCGTG  
GTGGCGTGTGCCTGTAATCCCAGCTATTTGGGAGGCTGAGGCAGGAGAATCGCTTGAGCCCG  
GGAAGCAGAGGTTGCAGTGAACCTGAGATAGTGATAGTGCCACTGCAATTCAGCCTGGGTGAC  
ATAGAGAGACTCCATCTCAAAAAAAA

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**FIGURE 55**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45415

<subunit 1 of 1, 215 aa, 1 stop

<MW: 24326, pI: 6.32, NX(S/T): 4

MHRDAWLPRPAFSLTGLSLFFSLVPPGRSMEVTVPATLNVLNGSDARLPCTFNSCYTVNHKQ  
FSLNWTYQECNNCSEEMFLQFRMKIINLKLERFQDRVEFSGNPSKYDVSVMRLRNVQPEDEGI  
YNCYIMNPPDRHRGHGKIHQLQVLMEEPPERDSTVAVIVGASVGGFLAVVILVLMVVKCVRRK  
KEQKLSTDDLKTEEEGKTDGEGNPDDGAK

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 161-179

**Immunoglobulin-like fold:**

amino acids 83-127

**N-glycosylation sites.**

amino acids 42-45, 66-69 and 74-77

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**FIGURE 56**

GTTGTATATGTCCTGAAGTACATCCGTGCATTTTTTTTAGCATCCAACCATCCTCCCTTGTA  
GTTCTCGCCCCCTCAAATCACCTTCTCCCTTAGCCCCACCCNACTAACATCTCAGTCTCTGAA  
AATGCACAGAGATGCCTGGCTACCTCGCCCTGCCTTCAGCCTCACGGGGCTCAGTCTCTTTT  
TCTCTTTGGTGCCACCAGGACGGAGCATGGAGGTCCACAGTACCTGNCCACCCTCAACGTCC  
TCAATGGCTCTGACGCCCCGCCTGCCCTGCCCTTCAACTCCTGCTACACAGTGAACCACAAAC  
AGTTCTCCCTGAACTGGACTTACCAGGAGTGCAACAACCTGCTCTGAGGAGATGTTCCCTCCAG  
TTCCGCATGAAGATCATTAACCTGAAGCTGGAGCGGTTTCAAGACCGCGTGGAGTTCTCAGG  
GAACCCCAAGCAAGTACGATGTGTGCGGTGATGCTGAGAAACGTGCAGCCGGAGGATGAGGGGA  
TTTACAACCTGCTACATCATGAACCCCCC

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**FIGURE 57**

TCACGGGGCTCATCTCTTTTTCTCTTTGGTGCCCACCAGGACGGAGCATGGAGGTNCACATA  
CCTGCCACCCTCAACGTCCTCAATGGCTTTGACGCCCCGCCTGCCCTGCACCTTCAACTCCNG  
CTACACAGTGAACCACAAACAGTTCTCCCTGAACTGGATTTACCAGGAGTGCAACAACCTGGC  
TCTGAGGAGATGTTCTCCAGTTCCCGCATGGAAGATCATTTAACCTGAAAGCTGGAAGCGG  
TTTTCAAGAACCGCGTGGAAGTTTCTCAGGGAACCCCAGCAAGTACGATGTGTCGGTGATGC  
TGAGAAACGTGCAGCCGGAGGATGAGGGGATTTACAACCTGCTACATCATGAACCCCCC

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**FIGURE 58**

TGCGGCGACCGTCGTACACCATGGGCCTCCACCTCCGCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGT  
TCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGGACGTCACCCCCAGTGGTGCTGGTCC  
CTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGA  
CCGAAAGCTACTTCACAATCTGGCTGAACCTGGAAGCTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATA  
TCAGGCTGGTTTACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCTTTG  
GGAAGACCTTCTCACTGGAGTTCTTGGACCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGA  
GCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATG  
AAAACGGGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGC  
TGGTTGCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGAGGCCTGGAAGGACAAGT  
ATATCCGGGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCTGGCTTCAGGAG  
ACAACAACCGGATCCCAGTCATCGGGCCCTGAAGATCCGGGAGCAGCAGCGGTCAGCTGTCTCCACAGCTGGC  
TGCTGCCCTACAACATACACATGGTCACCTGAGAAGGTGTTCTGTCAGACACCCACAATCAACTACACACTGCGGG  
ACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGG  
AAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACT  
ATGAGAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAAGTTGAAGAGTGCCC  
TGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCG  
AGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACGTGTGCTCCTTGGGGCCCTTGACTCCTGTGCCACAGGA  
CTCCTGTGGCTCGGGCGTGGACCTGCTGTTGGCCTCTGGGGCTGTGATGGCCACGCGTTTTGCAAAGTTTGTGA  
CTCACCATTCAAGGCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGTGTTTGTATCCTTTCTCT  
GTGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGA  
ACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATG  
TGTCCCCCTATTCTGTGGGCTTTTCATACTTGCTACTGGGGCCCTGGCCCCGCAGCCTTCCTATGAGGGATGTT  
ACTGGGCTGTGGTCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCCTCGGGTGACCCTTCCCACACACCA  
GCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAGCC  
TGACTGGCTTCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTGCGTTCTTCGTGGTCCCAGGC  
CCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCAAGCTCTGGATTGGGCAGCAGATGTG  
CCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGC  
CTCCCTTACCCTGGGACTGTGGTTCCAAGGATGAGAGCAGGGGTGGAGCCATGGCCTTCTGGGAACCTATGGA  
GAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCACCATCA  
CACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTGAGCACAGGGCTGAGGATGGGGCTCCTATCCAC  
CCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAACTTGAATGGGACCCTGAGAGAGCCAGGGGTCCCC  
TGAGGGCCCCCTAGGGGCTTTCTGTCTGCCCCAGGGTGTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGT  
CAGGGCTGCCTTCATGGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGGCCGAGAAAAGGGTACAGCCTCTAGGT  
GGGGTTCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTG  
TTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG  
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAA

**FIGURE 59**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189  
><subunit 1 of 1, 412 aa, 1 stop  
><MW: 46658, pI: 6.65, NX(S/T): 4  
MGLHLRPYRVGLLPDGLLFLLLLLLMLLADPALPAGRHPVVLVPGDLGNQLEAKLDKPTVVH  
YLCSKKTESYFTIWLNLLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGV DVRVPGFGKTFSL  
EFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQ  
LYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRI  
PVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPPTINYTLRDYRKFFQDIGFEDGWLM  
RQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQ  
AWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLG

**Important features:****Signal peptide:**

amino acids 1-28

**Potential lipid substrate binding site:**

amino acids 147-164

**N-glycosylation sites.**

amino acids 99-102, 273-276, 289-292 and 398-401

**Lipases, serine proteins**

amino acids 189-201

**Beta-transducin family Trp-Asp repeat**

amino acids 353-365

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**FIGURE 60**

CGGACGCGTGGGCGGACGCGTGGGGCGGCGGCAGCGGCGGCGACGGCGACATGGAGAGCGGG  
GCCTACGGCGCGGCCAAGGCGGGCGGCTCCTTCGACCTGCGGCGCTTCCTGACGCAGCCGCA  
GGTGGTGGCGCGCGCCGTGTGCTTGGTCTTCGCCTTGATCGTGTTCTCCTGCATCTATGGTG  
AGGGCTACAGCAATGCCCACGAGTCTAAGCAGATGTACTGCGTGTTCAACCGCAACGAGGAT  
GCCTGCCGCTATGGCAGTGCCATCGGGGTGCTGGCCTTCCTGGCCTCGGCCTTCTTCTTGGT  
GGTCGACGCGTATTTCCCCCAGATCAGCAACGCCACTGACCGCAAGTACCTGGTCATTGGTG  
ACCTGCTCTTCTCAGCTCTCTGGACCTTCCTGTGGTTTGTGGTTTCTGCTTCCTCACCAAC  
CAGTGGGCAGTCACCAACCCGAAGGACGTGCTGGTGGGGGCCGACTCTGTGAGGGCAGCCAT  
CACCTTCAGCTTCTTTTCCATCTTCTCCTGGGGTGTGCTGGCCTCCCTGGCCTACCAGCGCT  
ACAAGGCTGGCGTGGACGACTTCATCCAGAATTACGTTGACCCCACTCCGGACCCCAACACT  
GCCTACGCCTCCTACCCAGGTGCATCTGTGGACAACTACCAACAGCCACCCTTCACCCAGAA  
CGCGGAGACCACCGAGGGGCTACCAGCCGCCCCCTGTGTACTTGAGTGGCGGTTAGCGTGGGAA  
GGGGGACAGAGAGGGCCCTCCCCTCTGCCCTGGACTTTCCCATCAGCCTCCTGGAAGTGCCA  
GCCCCTCTCTTTCACCTGTTCCATCCTGTGCAGCTGACACACAGCTAAGGAGCCTCATAGCC  
TGGCGGGGGCTGGCAGAGCCACACCCCAAGTGCCTGTGCCAGAGGGCTTCAGTCAGCCGCT  
CACTCCTCCAGGGCACTTTTAGGAAAGGGTTTTTAGCTAGTGTTTTTCTCGCTTTTAATGA  
CCTCAGCCCCGCCTGCAGTGGCTAGAAGCCAGCAGGTGCCCATGTGCTACTGACAAGTGCCT  
CAGCTTCCCCCGGCCCCGGGTCAGGCCGTGGGAGCCGCTATTATCTGCGTTCTCTGCCAAAG  
ACTCGTGGGGGCCATCACACCTGCCCTGTGCAGCGGAGCCGGACCAGGCTCTTGTGTCCTCA  
CTCAGGTTTGCTTCCCCTGTGCCCACTGCTGTATGATCTGGGGGCCACCACCCTGTGCCGGT  
GGCCTCTGGGCTGCCTCCCGTGGTGTGAGGGCGGGGCTGGTGCTCATGGCACTTCCTCCTTG  
CTCCCACCCCTGGCAGCAGGGAAGGGCTTTGCCTGACAACACCCAGCTTTATGTAAATATTC  
TGCAGTTGTTACTTAGGAAGCCTGGGGAGGGCAGGGGTGCCCCATGGCTCCCAGACTCTGTC  
TGTGCCGAGTGTATTATAAAATCGTGGGGGAGATGCCCGGCCTGGGATGCTGTTTGGAGACG  
GAATAAATGTTTTCTCATTCAAAG

**FIGURE 61**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48304

<subunit 1 of 1, 224 aa, 1 stop

<MW: 24810, pI: 4.75, NX(S/T): 1

MESGAYGAAKAGGSFDLRRFLTQPQVVARAVCLVFALIVFSCIYGEYSNAHESKQMYCVFN  
RNEDACRYGSAIGVLAFLASAFFLVVDAYFPQISNATDRKYLVIQDILLFSALWTFLWFGFC  
FLTNQWAVTNPKDVLVGADSVRAAITFSFFSIFSWGVLASLAYQRYKAGVDDFIQNYVDPTP  
DPNTAYASYPGASVDNYQQPPFTQNAETTEGYQPPPVY

**Important features:****Type II Transmembrane domain:**

amino acids 1-45

**Other transmembrane domains:**

amino acids 74-90, 108-126 and 145-161

**N-glycosylation site.**

amino acids 97-100

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**FIGURE 62**

GAGCCACCTACCCTGCTCCGAGGCCAGGCCTGCAGGGCCTCATCGGCCAGAGGGTGATCAGTGAGCAGAAGGATG  
CCCGTGGCCGAGGCCCCCCAGGTGGCTGGCGGGCAGGGGGACGGAGGTGATGGCGAGGAAGCGGAGCCAGAGGGG  
ATGTTCAAGGCCTGTGAGGACTCCAAGAGAAAAGCCCCGGGGCTACCTCCGCCTGGTGCCCTGTTTGTGCTGCTG  
GCCCTGCTCGTGCTGGCTTCGGCGGGGGTGCTACTCTGGTATTTCTAGGGGTACAAGGCGGAGGTGATGGTCAGC  
CAGGTGTACTCAGGCAGTCTGCGTGTACTCAATCGCCACTTCTCCAGGATCTTACCCGCCGGGAATCTAGTGCC  
TTCCGCAGTGAAACCGCCAAAGCCCCAGAAGATGCTCAAGGAGCTCATCACCAGCACCCGCCTGGGAACTTACTAC  
AACTCCAGCTCCGTCTATTCTTTGGGGAGGGACCCCTCACCTGCTTCTTCTGGTTTCATTCTCCAAATCCCCGAG  
CACCGCCGGCTGATGCTGAGCCCCGAGGTGGTGCAGGCACTGCTGGTGGAGGAGCTGCTGTCCACAGTCAACAGC  
TCGGCTGCCGTCCCCCTACAGGGCCGAGTACGAAGTGGACCCCGAGGGCCTAGTGATCCTGGAAGCCAGTGTGAAA  
GACATAGCTGCATTGAATTCCACGCTGGGTTGTTACCGCTACAGCTACGTGGGCCAGGGCCAGGTCTCCGGCTG  
AAGGGGCCTGACCACCTGGCCTCCAGCTGCCTGTGGCACCTGCAGGGCCCCAAGGACCTCATGCTCAAACCTCCGG  
CTGGAGTGGACGCTGGCAGAGTGCCGGGACCGACTGGCCATGTATGACGTGGCCGGGCCCCCTGGAGAAGAGGCTC  
ATCACCTCGGTGTACGGCTGCAGCCGCCAGGAGCCCGTGGTGGAGGTTCTGGCGTCGGGGGCCATCATGGCGGTC  
GTCTGGAAGAAGGGCCTGCACAGCTACTACGACCCCTTCGTGCTCTCGGTGCAGCCGGTGGTCTTCCAGGCCTGT  
GAAGTGAACCTGACGCTGGACAACAGGCTCGACTCCCAGGGCGTCTCAGCACCCCGTACTTCCCCAGCTACTAC  
TCGCCCCAAACCCACTGCTCCTGGCACCTCACGGTGCCCTCTCTGGACTACGGCTTGGCCCTCTGGTTTGATGCC  
TATGCACTGAGGAGGCAGAAGTATGATTTGCCGTGCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGT  
GGCTTGCGCATCCTGCAGCCCTACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACC  
TCCCAGATCTCCCTCACCGGGCCCCGTGTGCGGGTGCCTATGGCTTGTAACAACAGTCCGACCCCTGCCCTGGA  
GAGTTCCTCTGTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGACTGCCCCAACGGCCTGGAT  
GAGAGAACTGCGTTTGCAGAGCCACATTCAGTGCAAAGAGGACAGCACATGCATCTCACTGCCCAAGGTCTGT  
GATGGGCAGCCTGATTGTCTCAACGGCAGCGATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTACCC  
TTCCAGTGTGAGGACCGGAGCTGCGTGAAGAAGCCCCAACCCGAGTGTGATGGGCGGGCCCGACTGCAGGGACGGC  
TCGGATGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGTCTCCGAG  
GGTGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTCCGGGGTGCACACATCTGTGGGGGGGCCCTCATCGCTGACCGC  
TGGGTGATAACAGCTGCCCCACTGCTTCCAGGAGGACAGCATGGCCTCCACGGTGTGTGGACCGTGTTCCTGGGC  
AAGGTGTGGCAGAACTCGCGCTGGCCTGGAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCAC  
GAAGAGGACAGCCATGACTACGACGTGGCGCTGCTGCAGCTCGACACCCGGTGGTGCCTCGGCCGCGCTGCGC  
CCCGTCTGCCTGCCCGCGCGCTCCCACTTCTTCGAGCCCGCCCTGCACTGCTGGATTACGGGCTGGGGCGCCTTG  
CGCGAGGGCGGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTGATCCACAGGACCTGTGCAGCGAG  
GCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGCCGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGT  
GACTCAGGTGGTCCGCTGGTGTGCAAGGCACTCAGTGGCCGCTGGTTCTGGCGGGGCTGGTCAGCTGGGGCCTG  
GGCTGTGGCCGGCCTAACTACTTCCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGTG  
ACCTGAGGAAGTGGCCCCCTGCAAAGCAGGGCCCCACCTCCTGGACTCAGAGAGCCCAGGGCAACTGCCAAGCAGG  
GGGACAAGTATTCTGGCGGGGGGTGGGGGAGAGAGCAGGCCCTGTGGTGGCAGGAGGTGGCATCTTGTCTCGTCC  
CTGATGTCTGCTCCAGTGTGAGGAGGATGGAGAAGTGCCAGCAGCTGGGGGTCAAGACGTCCCTGAGGACC  
CAGGCCCACACCCAGCCCTTCTGCCTCCCAATTCTCTCTCCTCCGTCCCTTCTCCACTGCTGCCTAATGCAAG  
GCAGTGGCTCAGCAGCAAGAATGCTGGTTCTACATCCCGAGGAGTGTCTGAGGTGCGCCCCACTCTGTACAGAGG  
CTGTTTGGGCAGCCTTGCCTCCAGAGAGCAGATTCCAGCTTCGGAAGCCCTGGTCTAACTTGGGATCTGGGAAT  
GGAAGGTGCTCCCATCGGAGGGGACCCTCAGAGCCCTGGAGACTGCCAGGTGGGCCTGCTGCCACTGTAAGCCAA  
AAGGTGGGAAGTCTGACTCCAGGGTCTTGCCCCACCCCTGCCTGCCACCTGGGCCCTCACAGCCCAGACCCT  
CACTGGGAGGTGAGCTCAGCTGCCCTTTGGAATAAAGCTGCCTGATCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 63**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49152  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 88846, pI: 6.41, NX(S/T): 7  
MPVAEAPQVAGGQGDGGDGEEAEPEGMFKACEDSKRKARGYLRLVPLFVLLALLVLASAGVL  
LWYFLGYKAEVMVSQVYSGSLRVLNRHFSQDLTRRESSAFRSETAKAQKMLKELITSTRLGT  
YYNSSSVYSFGEGPLTCFFWFILQIPEHRRMLLSPEVVQALLVEELLSTVNSSAAVPYRAEY  
EVDPEGLVILEASVKDIAALNSTLGCYRYSYVGQGQVLRLKGPDLASSCLWHLQGPDKDML  
KLRLEWTLAECDRLAMYDVAGPLEKRLITSVYGCSRQEPVVEVLASGAIMAVVWKKGLHSY  
YDPFVLSVQPVVFQACEVNLTLDNRLDSQGVLSPTYFPSYSPQTHCSWHLTVPSLDYGLAL  
WFDAYALRRQKYDLPTQGGWTIQNRRLCGLRILQPYAERIPVVATAGITINFTSQISLTGP  
GVRVHYGLYNQSDPCPGEFLCSVNGLCVPACDGVKDCPNGLDERNCVCRATFQCKEDSTCIS  
LPKVCDGQPDCLNGSDEEQCQEGVPCGTFTFQCEDRSCVKKPNPQCDGRPDCRDGSDEEHCD  
CGLQGPSSRIVGGAVSSEGEWPWQASLQVRGRHICGGALIADRWVITAAHCFQEDSMAS TVL  
WTVFLGKVWQNSRWPGEVSFKVSRLLLHPYHEEDSHDYDVALLQLDHPVVRSAAVRPVCLPA  
RSHFFEPGLHCWITGWGALREGGPISNALQKVDVQLIPQDLCSEAYRYQVTPRMLCAGYRKG  
KKDACQGDSSGGLVCKALSGRWFLAGLVSWGLGCGRPNYFGVYTRITGVISWIQQVVT

**Important features:****Type II transmembrane domain:**

amino acids 46-67

**Serine proteases, trypsin family, histidine active site.**

amino acids 604-609

**N-glycosylation sites.**amino acids 127-130, 175-178, 207-210, 329-332, 424-427, 444-447  
and 509-512**Kringle domains.**

amino acids 746-758 and 592-609

**Homologous region to Kallikrein Light Chain:**

amino acids 568-779

**Homologous region to Low-density lipoprotein receptor:**

amino acids 451-567

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**FIGURE 64**

GCACCCAGGGCCAGTGGACGATCCAGAACAGGAGGCTGTGTGGCTTGCGCATCCTGCAGCCC  
TACGCCGAGAGGATCCCCGTGGTGGCCACGGCCGGGATCACCATCAACTTCACCTCCCAGAT  
CTCCCTCACCGGGCCCCGGTGTGCGGGTGCACTATGGCTTGTACAACCAGTCGGACCCCTGCC  
CTGGAGAGTTCCTCTGTTCTGTGAATGGACTCTGTGTCCCTGCCTGTGATGGGGTCAAGGAC  
TGCCCCAACGGCCTGGATGAGAGAACTGCGTTTGCAGAGCCACATTCCAGTGCAAAGAGGA  
CAGCACATGCATCTCACTGCCCCAAGGTCTGTGATGGGCAGCCTGATTGTCTCAACGGCAGCG  
ATGAAGAGCAGTGCCAGGAAGGGGTGCCATGTGGGACATTCACCTTCCAGTGTGAGGACCGG  
AGCTGCGTGAAGAAGCCCAACCCGCAGTGTGATGGGCGGCCCCGACTGCAGGGACGGCTCGGA  
TGAGGAGCACTGTGACTGTGGCCTCCAGGGCCCCCTCCAGCCGCATTGTTGGTGGAGCTGTGT  
CCTCCGAGGGTGAGTGGCCATGGCAGGCCAGCCTCCAGGTTTCGGGGTCGACACATCTGTGGG  
GGGGCCCTCATCGCTGACCGCTGGGTGATAACAGCTGCCCACTGCTTCCAGGAGGACAGCAT  
GGCCTCCACGGTGCTGTGGACCGTGTTCTTGGGCAAGGTGTGGCAGAACTCGCGCTGGCCTG  
GAGAGGTGTCCTTCAAGGTGAGCCGCCTGCTCCTGCACCCGTACCACGAAGAGGACAGCCAT  
GACTACGACGTGGCGCTGCTGCAGCTCGACCACCCGGTGGTGCCTCGGCCGCCGTGCGCCC  
CGTCTGCCTGCCCCGCGCTCCCACTTCTTCGAGCCCGGCCTGCACTGCTGGATTACGGGCT  
GGGGCGCCTTGCGCGAGGGCGGCCCCATCAGCAACGCTCTGCAGAAAGTGGATGTGCAGTTG  
ATCCCACAGGACCTGTGCAGCGAGGCCTATCGCTACCAGGTGACGCCACGCATGCTGTGTGC  
CGGCTACCGCAAGGGCAAGAAGGATGCCTGTCAGGGTGA CTGAGGTGGTCCGCTGGTGTGCA  
AGGCACTCAGTGGCCGCTGGTTCCTGGCGGGGCTGGTCAGCTGGGGCCTGGGCTGTGGCCGG  
CCTAACTACTTCGGCGTCTACACCCGCATCACAGGTGTGATCAGCTGGATCCAGCAAGTGGT  
GACCTGAGGAACTGCCCCCCTGCAAAGCAGGGGCCACCTCCTGGACTCAGAGAGCCCAGGGC  
AACTGCCAAGCAGGGGGACAAGTAT

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**FIGURE 65**

GGACGAGGGCAGATCTCGTTCTGGGGCAAGCCGTTGACACTCGCTCCCTGCCACCGCCCGGG  
CTCCGTGCCGCCAAGTTTTTCATTTTCCACCTTCTCTGCCTCCAGTCCCCCAGCCCCTGGCCG  
AGAGAAGGGTCTTACCGGCCGGGATTGCTGGAAACACCAAGAGGTGGTTTTTGTTTTTTAAA  
ACTTCTGTTTTCTTGGGAGGGGGTGTGGCGGGGCAGGATGAGCAACTCCGTTCCCTCTGCTCTG  
TTTCTGGAGCCTCTGCTATTGCTTTGCTGCGGGGAGCCCCGTACCTTTTGGTCCAGAGGGAC  
GGCTGGAAGATAAGCTCCACAAACCCAAAGCTACACAGACTGAGGTCAAACCATCTGTGAGG  
TTTAACCTCCGCACCTCCAAGGACCCAGAGCATGAAGGATGCTACCTCTCCGTCGGCCACAG  
CCAGCCCTTAGAAGACTGCAGTTTCAACATGACAGCTAAAACCTTTTTTCATCATTCACGGAT  
GGACGATGAGCGGTATCTTTGAAAACCTGGCTGCACAACTCGTGTGAGCCCTGCACACAAGA  
GAGAAAGACGCCAATGTAGTTGTGGTTGACTGGCTCCCCCTGGCCCACCAGCTTTACACGGA  
TGCGGTCAATAATACCAGGGTGGTGGGACACAGCATTGCCAGGATGCTCGACTGGCTGCAGG  
AGAAGGACGATTTTTCTCTCGGGAATGTCCACTTGATCGGCTACAGCCTCGGAGCGCACGTG  
GCCGGGTATGCAGGCAACTTCGTGAAAGGAACGGTGGGCCGAATCACAGGTTTGGATCCTGC  
CGGGCCCATGTTTGAAGGGGGCCGACATCCACAAGAGGCTCTCTCCGGACGATGCAGATTTTG  
TGGATGTCCTCCACACCTACACGCGTTCCTTCGGCTTGAGCATTGGTATTCAGATGCCTGTG  
GGCCACATTGACATCTACCCCAATGGGGGTGACTTCCAGCCAGGCTGTGGACTCAACGATGT  
CTTGGGATCAATTGCATATGGAACAATCACAGAGGTGGTAAAATGTGAGCATGAGCGAGCCG  
TCCACCTCTTTGTTGACTCTCTGGTGAATCAGGACAAGCCGAGTTTTGCCTTCCAGTGCCT  
GACTCCAATCGCTTCAAAAAGGGGATCTGTCTGAGCTGCCGCAAGAACCGTTGTAATAGCAT  
TGGCTACAATGCCAAGAAAATGAGGAACAAGAGGAACAGCAAAATGTACCTAAAAACCCGGG  
CAGGCATGCCTTTCAGAGGTAACCTTCAGTCCCTGGAGTGTCCCTGAGGAAGGCCCTTAATA  
CCTCCTTCTTAATACCATGCTGCAGAGCAGGGCACATCCTAGCCCAGGAGAAGTGGCCAGCA  
CAATCCAATCAAATCGTTGCAAATCAGATTACACTGTGCATGTCCTAGGAAAGGGAATCTTT  
ACAAAATAAACAGTGTGGACCCCTAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49646

><subunit 1 of 1, 354 aa, 1 stop

><MW: 39362, pI: 8.35, NX(S/T): 2

MSNSVPLLCFWSLCYCFAAGSPVPFGPEGRLEDKLHKPKATQTEVKPSVRFNLRRTSKDPEHE  
GCYLSVGHSQPLEDCSFNMTAKTFFIIHGWTMSGIFENWLHKLVSAHHTREKDANVVVVDWL  
PLAHQLYTDVNNTRVVGHSIARMLDWLQEKDDFSLGNVHLIGYSLGAHVAGYAGNFVKGTV  
GRITGLDPAGPMFEGADIAHKRLSPDDADFVDVLHTYTRSEGLSIGIQMPVGHIDIYPNGGDF  
QPGCGLNDVLGSIAYGTITEVVKCEHERAVHLEFVDSLVDKPSFAFQCTDSNRFKKGICLS  
CRKNRCNSIGYNAKKMRNKRNSKMYLKTRAGMPFRGNLQSLECP

**Important features:****Signal peptide:**

amino acids 1-16

**Lipases, serine active site.**

amino acids 163-172

**N-glycosylation sites.**

amino acids 80-83 and 136-139

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**FIGURE 67**

CGGACGCGTGGGCGGACGCGTGGGCCTGGGCAAGGGCCGGGGCGCCGGGGCCGAGCCACCTCTTCCCCTCCCCCGC  
TTCCCTGTGCGGCTCCGCTGGCTGGACGCGCTGGAGGAGTGGAGCAGCACCCGGCCGGCCCTGGGGGCTGACAGT  
CGGCAAAGTTTGGCCCGAAGAGGAAGTGGTCTCAAACCCCGGCAGGTGGCGACCAGGCCAGACCAGGGGCGCTCG  
CTGCCTGCGGGCGGGCTGTAGGCGAGGGCGCGCCCCAGTGCCGAGACCCGGGGCTTCAGGAGCCGGCCCCGGGAG  
AGAAGAGTGCGGCGGGCGGACGGAGAAAACAACCTCCAAAGTTGGCGAAAGGCACCGCCCCCTACTCCCGGGCTGCCG  
CCGCCTCCCCGCCCCCAGCCCTGGCATCCAGAGTACGGGTGAGGCCCGGGCCATGGAGCCCCCTGGGGAGGCGG  
CACCAGGGAGCCTGGGCGCCCCGGGGCTCCGCCGCGACCCCATCGGGTAGACCACAGAAGCTCCGGGACCCTTCCG  
GCACCTCTGGACAGCCCAGGATGCTGTTGGCCACCCTCCTCCTCCTCCTCCTTGGAGGCGCTCTGGCCCATCCAG  
ACCGGATTATTTTCCAAATCATGCTTGTGAGGACCCCCAGCAGTGCTCTTAGAAGTGCAGGGCACCTTACAGA  
GGCCCCCTGGTCCGGGACAGCCGCACCTCCCCCTGCCAACTGCACCTGGCTCATCTGGGCAGCAAGGAACAGACTG  
TCACCATCAGGTTCCAGAAGCTACACCTGGCCTGTGGCTCAGAGCGCTTAACCCTACGCTCCCCTCTCCAGCCAC  
TGATCTCCCTGTGTGAGGCACCTCCCAGCCCTCTGCAGCTGCCCGGGGGCAACGTCAACATCACTTACAGCTATG  
CTGGGGCCAGAGCACCCATGGGCCAGGGCTTCCTGCTCTCCTACAGCCAAGATTGGCTGATGTGCCTGCAGGAAG  
AGTTTCAGTGCCTGAACCACCGCTGTGTATCTGCTGTCCAGCGCTGTGATGGGGTTGATGCCTGTGGCGATGGCT  
CTGATGAAGCAGGTTGCAGCTCAGACCCCTTCCCTGGCCTGACCCCAAGACCCGTCCCCTCCCTGCCTTGCAATG  
TCACCTTGGAGGACTTCTATGGGGTCTTCTCCTCCTCCTGGATATACACACCTAGCCTCAGTCTCCACCCCCAGT  
CCTGCCATTGGCTGCTGGACCCCCATGATGGCCGGCGGGCTGGCCGTGCGCTTCACAGCCCTGGACTTGGGCTTTG  
GAGATGCAGTGCATGTGTATGACGGCCCTGGGCCCCCTGAGAGCTCCCGACTACTGCGTAGTCTCACCCACTTCA  
GCAATGGCAAGGCTGTCACTGTGGAGACACTGTCTGGCCAGGCTGTTGTGTCTTACCACACAGTTGCTTGGAGCA  
ATGGTTCGTGGCTTCAATGCCACCTACCATGTGCGGGGCTATTGCTTGCCTTGGGACAGACCCCTGTGGCTTAGGCT  
CTGGCCTGGGAGCTGGCGAAGGCCTAGGTGAGCGCTGCTACAGTGAGGCACAGCGCTGTGACGGCTCATGGGACT  
GTGCTGACGGCACAGATGAGGAGGACTGCCCAGGCTGCCACCTGGACACTTCCCCTGTGGGGCTGCTGGCACCT  
CTGGTGCCACAGCCTGCTACCTGCCTGCTGACCGCTGCAACTACCAGACTTTCTGTGCTGATGGAGCAGATGAGA  
GACGCTGTGCGCATTGCCAGCCTGGCAATTTCCGATGCCGGGACGAGAAGTGCGTGTATGAGACGTGGGTGTGCG  
ATGGGCAGCCAGACTGTGCGGACGGCAGTGATGAGTGGGACTGCTCCTATGTTCTGCCCCGCAAGGTCATTACAG  
CTGCAGTCATTGGCAGCCTAGTGTGCGGCCTGCTCCTGGTCACTCGCCCTGGGCTGCACCTGCAAGCTCTATGCCA  
TTGCGACCCAGGAGTACAGCATCTTTGCCCCCCTCTCCCGGATGGAGGCTGAGATTGTGCAGCAGCAGGCACCCC  
CTTCCTACGGGCAGCTCATTGCCAGGGTGCCATCCCACCTGTAGAAGACTTTCTACAGAGAATCCTAATGATA  
ACTCAGTGCTGGGCAACCTGCGTCTCTGCTACAGATCTTACGCCAGGATATGACTCCAGGAGGTGGCCAGGTG  
CCCGCCGTGCTCAGCGGGGCGCTTGATGCGACGCTGGTACGCCGTCTCCGCCGTGGGGCTGCTCCCTCGAA  
CCAACACCCCGGCTCGGGCCTCTGAGGCCAGATCCCAGGTACACCTTCTGCTGCTCCCCTTGAGGCCCTAGATG  
GTGGCACAGGTCCAGCCCCTGAGGGCGGGGCGAGTGGGTGGGCAAGATGGGGAGCAGGCACCCCCACTGCCCATCA  
AGGCTCCCCTCCCCTCTGCTAGCACGTCTCCAGCCCCCACTACTGTCCCTGAAGCCCCAGGGCCACTGCCCTCAC  
TGCCCCCTAGAGCCATCACTATTGTCTGGAGTGGTGCAGGCCCTGCGAGGCCGCTGTTGCCCAGCCTGGGGCCCC  
CAGGACCAACCCGGAGCCCCCCTGGACCCACACAGCAGTCCTGGCCCTGGAAGATGAGGACGATGTGCTACTGG  
TGCCACTGGCTGAGCCGGGGGTGTGGGTAGCTGAGGCAGAGGATGAGCCACTGCTTACCTGAGGGGACCTGGGGG  
CTCTACTGAGGCCTCTCCCCTGGGGGCTCTACTCATAGTGGCACAACCTTTTAGAGGTGGGTGAGCCTCCCCTCC  
ACCACTTCCTTCCCTGTCCCTGGATTTTCAGGGACTTGGTGGGCCTCCCGTTGACCCTATGTAGCTGCTATAAAGT  
TAAGTGTCCCTCAGGCAGGGAGAGGGCTCACAGAGTCTCCTCTGTACGTGGCCATGGCCAGACACCCCACTCCCT  
TCACCACCACCTGCTCCCCACGCCACCACCATTTGGGTGGCTGTTTTTAAAAAGTAAAGTTCTTAGAGGATCATA  
GGTCTGGACACTCCATCCTTGCCAAACCTCTACCCAAAAGTGGCCTTAAGCACCGGAATGCCAATTAAGTACAGAG  
CCCTCCAGCCCCCAAGGGGAGGATTTGGGCAGAACCTGAGGTTTTGCCATCCACAATCCCTCCTACAGGGCCTGG  
CTCACAAAAGAGTGCAACAAATGCTTCTATTCCATAGCTACGGCATTGCTCAGTAAGTTGAGGTCAAAAATAAA  
GGAATCATACATCTC

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**FIGURE 68**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49631

<subunit 1 of 1, 713 aa, 1 stop

<MW: 76193, pI: 5.42, NX(S/T): 4

MLLATLLLLLLGGALAHDPDRIIFPNHACEDPPAVLLEVQGTQLQRPLVRDSRTSPANCTWLIL  
GSKEQTVTIRFQKLHLACGSERLTLRSPLQPLISLCEAPPSPLQLPGGNVTITYSYAGARAP  
MGQGFLLSYSQDWLMCLQEEFQCLNHRCSVSAVQRCDGVDACGDGSDEAGCSSDPFPGLTPRP  
VPSLPCNVTLEDFYGVFSSPGYTHLASVSHPOQSCHWLLDPHDGRRRLAVRFTALDLGFGDAVH  
VYDGPGPPESSRLLRSLTHFSNGKAVTVETLSGQAVVSYHTVAWSNGRGFNATYHVRGYCLP  
WDRPCGLGSGLGAGEGLGERCYSEAQRCDGSWDCADGTDEEDCPGCPPGHFPCGAAGTSGAT  
ACYLPADRCNYQTFCADGADERRCRHCQPGNFRRCRDEKCVYETWVCDGQPD CADGSDEWDCS  
YVLPRKVITA AVIGSLVCGLLLVIALGCTCKLYAIRTQEYSIFAPLSRMEAEIVQQQAPPSY  
GQLIAQGAIPPVEDFPTENPNDNSVLGNLRSLLQILRQDMTPGGGPGARRRQGRRLMRRLVR  
RLRRWGLLPRTNTPARASEARSQVTPSAAPLEALDGGTGPA REGGAVGGQDGEQAPPLPIKA  
PLPSASTSPAPTTVPEAPGPLPSLPLEPSLLSGVVQALRGRLPSLGPPGPTRSPPGPHTAV  
LALEDEDDVLLVPLAEPGVWVAEAEDEPLL

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 442-462

**LDL-receptor class A (LDLRA) domain proteins**

amino acids 411-431, 152-171, 331-350 and 374-393

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**FIGURE 69**

CGAGCTGGGCGAGAAGTAGGGGAGGGCGGTGCTCCGCCGCGGTGGCGGTGCTATCGCTTCG  
CAGAACCTACTCAGGCAGCCAGCTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCA  
GACGCGATGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGG  
CCACGTGAAGATGCTGCGGCTGGCACTAACTGTGACATCTATGACCTTTTTTATCATCGCAC  
AAGCCCCTGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATA  
CTTTTATATGTA CT CAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATAT  
TATCAACTCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAG  
AAACCACAACATTGACAGTTGGTGGAGGGGTGTTTGCACTTGTGACAGCAGTATGCTGTCTT  
GCCGACGGGGCCCTTATTTACCGGAAGCTTCTGTTCAATCCCAGCGGTCCTTACCAGAAAAA  
GCCTGTGCATGAAAAAAAGAAGTTTTGTAATTTTATATTACTTTTTAGTTTGATACTAAGT  
ATTAAACATATTTCTGTATTCTTCCAAAAA

701237



**FIGURE 70**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49645  
><subunit 1 of 1, 152 aa, 1 stop  
><MW: 17170, pI: 9.62, NX(S/T): 1  
MDNVQPKIKHRPFCFSVKGHVKMLRLALTVTSMTEFFIIAQAPEPYIVITGFEVTVILFFILL  
YVLRDLRLMKWLFWPLLDIINSLVTTVFMLIVSVLALIPETTTTLTVGGGVFALVTAVCCCLAD  
GALIYRKLLFNPSGPYQKKPVHEKKEVL

**Important features:****Potential type II transmembrane domain:**

amino acids 26-42

**Other potential transmembrane domain:**

amino acids 44-65, 81-101 and 109-129

**Leucine zipper pattern**

amino acids 78-99 and 85-106

**N-myristoylation site.**

amino acids 110-115

**Ribonucleotide reductase large subunit protein**

amino acids 116-127

77 1237

**FIGURE 71**

GGGCGAGAAGTAGGGGAGGGCGTGTTCCGCCGCGGTGGCGGTTGCTATCGTTTTGCAGAACC  
TACTCAGGCAGCCAGNTGAGAAGAGTTGAGGGAAAGTGCTGCTGCTGGGTCTGCAGACGCGA  
TGGATAACGTGCAGCCGAAAATAAAACATCGCCCCTTCTGCTTCAGTGTGAAAGGCCACGTG  
AAGATGCTGCGGCTGGCACTAACTGNGACATCTATGACCTTTTTTATNATCGCACAAGCCCC  
TGAACCATATATTGTTATCACTGGATTTGAAGTCACCGTTATCTTATTTTTCATACTTTTAT  
ATGTACTCAGACTTGATCGATTAATGAAGTGGTTATTTTGGCCTTTGCTTGATATTATCAAC  
TCACTGGTAACAACAGTATTCATGCTCATCGTATCTGTGTTGGCACTGATACCAGAAACCAC  
AACATTGACAGTTGGTGGAGGGGTGTTTGCACCTTGTGACAGCAGTATGCTGTNTTGCCGAC

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**FIGURE 72**

CAGCCCCGCGCGCCGGCCGAGTCGCTGAGCCGCGGCTGCCGGACGGGACGGGACCGGCTAGG  
CTGGGCGCGCCCCCGGGCCCCGCGTGGGCATGGGCGCACTGGCCCCGGGCGCTGCTGCTGC  
CTCTGCTGGCCCAGTGGCTCCTGCGCGCCGCCCCGGAGCTGGCCCCCGCGCCCTTCACGCTG  
CCCCCTCCGGGTGGCCGCGGCCACGAACCGCGTAGTTGCGCCCACCCCGGGACCCGGGACCCC  
TGCCGAGCGCCACGCCGACGGCTTGGCGCTCGCCCTGGAGCCTGCCCTGGCGTCCCCCGCGG  
GCGCCGCCAACTTCTTGGCCATGGTAGACAACCTGCAGGGGGGACTCTGGCCGCGGCTACTAC  
CTGGAGATGCTGATCGGGACCCCCCGCAGAAGCTACAGATTCTCGTTGACACTGGAAGCAG  
TAACTTTGCCGTGGCAGGAACCCCGCACTCCTACATAGACACGTACTTTGACACAGAGAGGT  
CTAGCACATACCGCTCCAAGGGCTTTGACGTCACAGTGAAGTACACACAAGGAAGCTGGACG  
GGCTTCGTTGGGGAAGACCTCGTCACCATCCCCAAAGGCTTCAATACTTCTTTTCTTGTCAA  
CATTGCCACTATTTTTGAATCAGAGAATTTCTTTTTGCCTGGGATTAAATGGAATGGAATAC  
TTGGCCTAGCTTATGCCACACTTGCCAAGCCATCAAGTTCTCTGGAGACCTTCTTCGACTCC  
CTGGTGACACAAGCAAACATCCCCAACGTTTTCTCCATGCAGATGTGTGGAGCCGGCTTGCC  
CGTTGCTGGATCTGGGACCAACGGAGGTAGTCTTGTCTTGGGTGGAATTGAACCAAGTTTGT  
ATAAAGGAGACATCTGGTATACCCCTATTAAGGAAGAGTGGTACTACCAGATAGAAATTCTG  
AAATTGGAAATTGGAGGCCAAAGCCTTAATCTGGACTGCAGAGAGTATAACGCAGACAAGGC  
CATCGTGGACAGTGGCACCACGCTGCTGCGCCTGCCCCAGAAGGTGTTTGATGCGGTGGTGG  
AAGCTGTGGCCCGCGCATCTCTGATTCCAGAATTCTCTGATGGTTTCTGGACTGGGTCCCAG  
CTGGCGTGCTGGACGAATTCGGAAACACCTTGGTCTTACTTCCCTAAAATCTCCATCTACCT  
GAGAGACGAGAACTCCAGCAGGTCATTCCGTATCACAATCCTGCCTCAGCTTTACATTCAGC  
CCATGATGGGGGCGCGCCTGAATTATGAATGTTACCGATTCTGGCATTTCCTCCATCCACAAAT  
GCGCTGGTGATCGGTGCCACGGTGATGGAGGGCTTCTACGTCATCTTCGACAGAGCCCAGAA  
GAGGGTGGGCTTCGCAGCGAGCCCCTGTGCAGAAATTGCAGGTGCTGCAGTGTCTGAAATTT  
CCGGGCCTTTCTCAACAGAGGATGTAGCCAGCAACTGTGTCCCCGCTCAGTCTTTGAGCGAG  
CCCATTTTGTGGATTGTGTCCTATGCGCTCATGAGCGTCTGTGGAGCCATCCTCCTTGTCTT  
AATCGTCCTGCTGCTGCTGCCGTTCCGGTGTGAGCGTCGCCCCCGTGACCCTGAGGTGCTCA  
ATGATGAGTCCTCTCTGGTCAGACATCGCTGGAAATTGAATAGCCAGGCCTGACCTCAAGCAA  
CCATGAACTCAGCTATTAAGAAAATCACATTTCCAGGGCAGCAGCCGGGATCGATGGTGGCG  
CTTTCTCCTGTGCCACCCGTCTTCAATCTCTGTTCTGCTCCCAGATGCCTTCTAGATTAC  
TGTCTTTTGATTCTTGATTTTCAAGCTTTCAAATCCTCCCTACTTCCAAGAAAAATAATTAA  
AAAAAAACTTCATTCTAA

**FIGURE 73**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45493  
><subunit 1 of 1, 518 aa, 1 stop  
><MW: 56180, pI: 5.08, NX(S/T): 2  
MGALARALLPLLAQWLLRAAPELAPAPFTLPLRVAAATNRVVAPTGP GTPAERHADGLAL  
ALEPALASPAGAAANFLAMVDNLQGD SGRGYYLEMLIGTPPQKLQILVDTGSSNFAVAGTPHS  
YIDTYFDTERSSTYRSKGFDTV KYTQGSWTGFVGEDLVTIPKGFNTSFLVNIATIFESENF  
FLPGIKWNGILGLAYATLAKPSSSLETFFDSLVTQANIPNVFSMQMCGAGLPVAGSGTNGGS  
LVLGGIEPSLYKGDIWYTPIKEEWYYQIEILKLEIGGQSLNLD CREYNADKAIVD SGTTLLR  
LPQKVFD AVVEAVARASLIPEFSDGFWTGSQLACWTNSETPWSYFPKIS IYLRDENS SR SFR  
ITILPQLYIQPMMGAGLNYECYRFGISPSTNALVIGATVMEGFYVIFDRAQKRVGFAASPCA  
EIAGAAVSEISGPFSTEDVASNCVPAQSLSEPILWIVSYALMSVCGAILLV LIVLLLLLPFRC  
QRRPRDPEVVNDESSLVRHRWK

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 466-494

**N-glycosylation sites.**

amino acids 170-173 and 366-369

**Leucine zipper pattern.**

amino acids 10-31 and 197-118

**Eukaryotic and viral aspartyl proteases**

amino acids 109-118, 252-261 and 298-310

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**FIGURE 74**

CGCCTCCGCCTTCGGAGGCTGACGCGCCCGGGCGCCGTTCCAGGCCTGTGCAGGGCGGATCG  
GCAGCCGCCTGGCGGCGATCCAGGGCGGTGCGGGGCCTGGGCGGGAGCCGGGAGGCGCGGCC  
GGCATGGAGGCGCTGCTGCTGGGCGCGGGGTTGCTGCTGGGCGCTTACGTGCTTGTCTACTA  
CAACCTGGTGAAGGCCCCGCCGTGCGGCGGCATGGGCAACCTGCGGGGCGCGCACGGCCGTGG  
TCACGGGCGCCAACAGCGGCATCGGAAAGATGACGGCGCTGGAGCTGGCGCGCCGGGGAGCG  
CGCGTGGTGGCTGGCCTGCCGCAGCCAGGAGCGCGGGGAGGCGGCTGCCTTCGACCTCCGCCA  
GGAGAGTGGGAACAATGAGGTCATCTTCATGGCCTTGGACTTGGCCAGTCTGGCCTCGGTGC  
GGGCCTTTGCCACTGCCTTTCTGAGCTCTGAGCCACGGTTGGACATCCTCATCCACAATGCC  
GGTATCAGTTCCTGTGGCCGGACCCGTGAGGCGTTTAACCTGCTGCTTCGGGTGAACCATAT  
CGGTCCCTTTCTGCTGACACATCTGCTGCTGCCTTGCCTGAAGGCATGTGCCCCCTAGCCGCG  
TGGTGGTGGTAGCCTCAGCTGCCCACTGTCGGGGACGTCTTGACTTCAAACGCCTGGACCGC  
CCAGTGGTGGGCTGGCGGCAGGAGCTGCGGGCATATGCTGACACTAAGCTGGCTAATGTACT  
GTTTGCCCGGGAGCTCGCCAACCAGCTTGAGGCCACTGGCGTCACCTGCTATGCAGCCCACC  
CAGGGCCTGTGAACTCGGAGCTGTTCTGCGCCATGTTCTGGATGGCTGCGCCCCACTTTTG  
CGCCCATTGGCTTGGCTGGTGGTCCGGGACCAAGAGGGGGTGCCCAGACACCCCTGTATTG  
TGCTCTACAAGAGGGCATCGAGCCCCTCAGTGGGAGATATTTTGCCAACTGCCATGTGGAAG  
AGGTGCCTCCAGCTGCCCCGAGACGACCGGGCAGCCCATCGGCTATGGGAGGCCAGCAAGAGG  
CTGGCAGGGCTTGGGCCTGGGGAGGATGCTGAACCCGATGAAGACCCCCAGTCTGAGGACTC  
AGAGGCCCCATCTTCTCTAAGCACCCCCCACCTGAGGAGCCCACAGTTTCTCAACCTTACC  
CCAGCCCCTCAGAGCTCACCAGATTTGTCTAAGATGACGCACCGAATTCAGGCTAAAGTTGAG  
CCTGAGATCCAGCTCTCCTAACCCTCAGGCCAGGATGCTTGCCATGGCACTTCATGGTCCTT  
GAAAACCTCGGATGTGTGTGAGGCCATGCCCTGGACACTGACGGGTTTGTGATCTTGACCTC  
CGTGGTTACTTTCTGGGGCCCCAAGCTGTGCCCTGGACATCTCTTTTCTGGTTGAAGGAAT  
AATGGGTGATTATTTCTTCCTGAGAGTGACAGTAACCCCAGATGGAGAGATAGGGGTATGCT  
AGACACTGTGCTTCTCGGAAATTTGGATGTAGTATTTTCAGGCCCCACCCTTATTGATTCTG  
ATCAGCTCTGGAGCAGAGGCAGGGAGTTTGCAATGTGATGCACTGCCAACATTGAGAATTAG  
TGAACCTGATCCCTTTGCAACCGTCTAGCTAGGTAGTTAAATTACCCCCATGTTAATGAAGCG  
GAATTAGGCTCCCGAGCTAAGGGACTCGCCTAGGGTCTCACAGTGAGTAGGAGGAGGGCCTG  
GGATCTGAACCCAAGGGTCTGAGGCCAGGGCCGACTGCCGTAAGATGGGTGCTGAGAAGTGA  
GTCAGGGCAGGGCAGCTGGTATCGAGGTGCCCCATGGGAGTAAGGGGACGCCTTCCGGGCGG  
ATGCAGGGCTGGGGTCATCTGTATCTGAAGCCCCTCGGAATAAAGCGCGTTGACCGCCAAA  
AAAAAAAAAAAAAAAAAAAA



**FIGURE 75**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48227

<subunit 1 of 1, 377 aa, 1 stop

<MW: 40849, pI: 7.98, NX(S/T): 0

MEALLLGAGLLLGAYVLVYYNLVKAPPCGGMGNLRGRTAVVTGANS  
GIGKMTALELARRGAR  
VVLACRSQERGEAAAFDLRQESGNNEVIFMALDLASLASVRAFATAFLS  
SEPRLDILIHNAG  
ISSCGRTREAFNLLLRVNHIGPFLLTHLLLPCLKACAPSRVVVASAAHCR  
GRLDLDFKRLDRP  
VVGWRQELRAYADTKLANVLFARELANQLEATGVTCYAAHPGPVNSELFL  
RHVPGWLRPLLR  
PLAWLVLRAPRGGAQTPLYCALQEGIEPLSGRYFANCHVEEVPPAARD  
DRAAHLWEASKRL  
AGLGPGEDAEPDEDPQSEDSEAPSSLSTPHPEEPTVSQPYPSPOSSPD  
LSKMTHRIQAKVEP  
EIQLS

**Important features:****Signal peptide:**

amino acids 1-16

**Glycosaminoglycan attachment site.**

amino acids 46-49

**Short-chain alcohol dehydrogenase family**

amino acids 37-49 and 114-124

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**FIGURE 76**

GGAGGAGACAGCCTCCTGGGGGGCAGGGGTTCCCTGCCTCTGCTGCTCCTGCTCATCATGGGAGGCATGGCTCAG  
GACTCCCCGCCCCAGATCCTAGTCCACCCCCAGGACCAGCTGTTCCAGGGCCCTGGCCCTGCCAGGATGAGCTGC  
CAAGCCTCAGGCCAGCCACCTCCCACCATCCGCTGGTTGCTGAATGGGCAGCCCCCTGAGCATGGTGCCCCAGAC  
CCACACCACCTCCTGCCTGATGGGACCCTTCTGCTGCTACAGCCCCCTGCCCGGGGACATGCCACGATGGCCAG  
GCCCTGTCCACAGACCTGGGTGTCTACACATGTGAGGCCAGCAACCGGCTTGGCACGGCAGTCAGCAGAGGGCGCT  
CGGCTGTCTGTGGCTGTCCTCCGGGAGGATTTCCAGATCCAGCCTCGGGACATGGTGGCTGTGGTGGGTGAGCAG  
TTTACTCTGGAATGTGGGCGCCCTGGGGCCACCCAGAGCCCACAGTCTCATGGTGGAAAGATGGGAAACCCCTG  
GCCCTCCAGCCCGGAAGGCACACAGTGTCCGGGGGGTCCCTGCTGATGGCAAGAGCAGAGAAGAGTGACGAAGGG  
ACCTACATGTGTGTGGCCACCAACAGCGCAGGACATAGGGAGAGCCGCGCAGCCCGGGTTTCCATCCAGGAGCCC  
CAGGACTACACGGAGCCTGTGGAGCTTCTGGCTGTGCGAATTGAGCTGGAAAATGTGACACTGCTGAACCCGGAT  
CCTGCAGAGGGCCCCAAGCCTAGACCGGCGGTGTGGCTCAGCTGGAAGGTGAGTGGCCCTGCTGCGCCTGCCCAA  
TCTTACACGGCCTTGTTCAGGACCCAGACTGCCCGGGGAGGCCAGGGAGCTCCGTGGGCAGAGGAGCTGCTGGCC  
GGCTGGCAGAGCGCAGAGCTTGGAGGCCTCCACTGGGGCCAAGACTACGAGTTCAAAGTGAGACCATCCTCTGGC  
CGGGCTCGAGGGCCCTGACAGCAACGTGCTGCTCCTGAGGCTGCCGGAAGAGTGCCAGTGCCCCACCTCAGGAA  
GTGACTCTAAAGCCTGGCAATGGCACTGTCTTTGTGAGCTGGGTCCCACCACCTGCTGAAAACCACAATGGCATC  
ATCCGTGGCTACCAGGTCTGGAGCCTGGGCAACACATCACTGCCACCAGCCAACTGGACTGTAGTTGGTGAGCAG  
ACCCAGCTGGAAATCGCCACCCATATGCCAGGCTCCTACTGCGTGCAAGTGGCTGCAGTCACTGGTGCTGGAGCT  
GGGGAGCCCACTAGACCTGTCTGCCTCCTTTTAGAGCAGGCCATGGAGCGAGCCACCCAGAAGCCAGTGAGCAT  
GGTCCCTGGACCCTGGAGCAGCTGAGGGCTACCTTGAAGCGGCCTGAGGTGATTGCCACCTGCGGTGTTGCACTC  
TGGCTGCTGCTTCTGGGCACCGCCGCTGTGTATCCACCGCCGGCGCCGAGCTAGGGTGCACCTGGGCCCAGGTCTG  
TACAGATATACCAGTGAGGATGCCATCCTAAAACACAGGATGGATCACAGTGACTCCAGTGGTTGGCAGACACT  
TGGCGTTCCACCTCTGGCTCTCGGGACCTGAGCAGCAGCAGCAGCCTCAGCAGTGGCTGGGGCGGATGCCCGG  
GACCCACTAGACTGTGCTGCTCCTTGTCTCCTGGGACTCCCGAAGCCCCGGCGTGCCCTGCTTCCAGACACC  
AGCACTTTTTATGGCTCCCTCATCGCTGAGCTGCCCTCCAGTACCCAGCCAGGCCAAGTCCCCAGGTCCCAGCT  
GTCAGGCGCCTCCCACCCAGCTGGCCCAGCTCTCCAGCCCCCTGTTCCAGCTCAGACAGCCTCTGCAGCCGAGG  
GGACTCTCTTCTCCCCGCTTGTCTCTGGCCCCCTGCAGAGGCTTGGAAAGGCCAAAAGAAGCAGGAGCTGCAGCAT  
GCCAACAGTTCCCCACTGCTCCGGGGCAGCCACTCCTTGGAGCTCCGGGCGCTGTGAGTTAGGAAATAGAGGTTCC  
AAGAACCTTTCCCAAAGCCCAGGAGCTGTGCCCAAGCTCTGGTTGCCTGGCGGGCCCTGGGACCGAAACTCCTC  
AGCTCCTCAAATGAGCTGGTTACTCGTCATCTCCCTCCAGCACCCCTCTTTCTCATGAAACTCCCCCAACTCAG  
AGTCAACAGACCCAGCCTCCGGTGGCACCACAGGCTCCCTCCTCCATCCTGCTGCCAGCAGCCCCCATCCCCATC  
CTTAGCCCCCTGCAGTCCCCCTAGCCCCCAGGCCTCTTCCCTCTCTGGCCCCAGCCCAGCTTCCAGTGCCTGTCC  
AGCTCCTCACTGTATCCCTGGGGGAGGATCAAGACAGCGTGCTGACCCCTGAGGAGGTAGCCCTGTGCTTGGAA  
CTCAGTGAGGGTGAGGAGACTCCAGGAACAGCGTCTCTCCCATGCCAAGGGCTCCTTACCCCCCACCACCTAT  
GGGTACATCAGCGTCCCAACAGCCTCAGAGTTACCGGACATGGGCAGGACTGGAGGAGGGGTGGGGCCCAAGGGG  
GGAGTCTTGCTGTGCCACCTCGGCCCTGCCTACCCCCACCCCCAGCGAGGGGCTCCTTAGCCAATGGTTGGGGC  
TCAGCCTCTGAGGACAATGCCGCCAGCGCCAGAGCCAGCCTTGTGAGCTCCTCCGATGGCTCCTTCCCTGCTGAT  
GCTCACTTTGCCCGGGCCCTGGCAGTGGCTGTGGATAGCTTTGGTTTCGGTCTAGAGCCCAGGGAGGCAGACTGC  
GTCTTCATAGATGCCTCATCACCTCCCTCCCCACGGGATGAGATCTTCTGACCCCCAACCTCTCCCTGCCCCTG  
TGGGAGTGGAGGCCAGACTGGTTGGAAGACATGGAGGTCAGCCACACCCAGCGGCTGGGAAGGGGGATGCCTCCC  
TGGCCCCCTGACTCTCAGATCTCTTCCCAGAGAAGTCAGCTCCACTGTCGTATGCCCAAGGCTGGTGCTTCTCCT  
GTAGATTACTCCTGAACCGTGTCCCTGAGACTTCCCAGACGGGAATCAGAACCCTTCTCCTGTCCACCCACAAG  
ACCTGGGCTGTGGTGTGTGGGTCTTGGCCTGTGTTTCTCTGCAGCTGGGGTCCACCTTCCCAAGCCTCCAGAGAG  
TTCTCCCTCCACGATTGTGAAAACAAATGAAAACAAAATTAGAGCAAAGCTGACCTGGAGCCCTCAGGGAGCAAA  
ACATCATCTCCACCTGACTCCTAGCCACTGCTTTCTCCTCTGTGCCATCCACTCCCACCACCAGGTTGTTTTGGC  
CTGAGGAGCAGCCCTGCCTGCTGCTCTTCCCCCACCATTTGGATCACAGGAAGTGGAGGAGCCAGAGGTGCCTTT  
GTGGAGGACAGCAGTGGCTGCTGGGAGAGGGCTGTGGAGGAAGGAGCTTCTCGGAGCCCCCTCTCAGCCTTACCT  
GGGCCCCCTCCTCTAGAGAAGAGCTCAACTCTCTCCCAACCTCACCATGGAAAGAAAATAATTATGAATGCCACTG  
AGGCACCTGAGGCCCTACCTCATGCCAAACAAAGGGTTCAAGGCTGGGTCTAGCGAGGATGCTGAAGGAAGGGAGG  
TATGAGACCGTAGGTCAAAGCACCATCCTCGTACTGTTGTCACTATGAGCTTAAGAAATTTGATACCATAAAAT  
GGTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 77**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA41404

<subunit 1 of 1, 985 aa, 1 stop

<MW: 105336, pI: 6.55, NX(S/T): 7

MGGMAQDSPPQILVHPQDQLFQGPGRPARMSCQASGQPPPTIRWLLNGQPLSMVPPDPHHLLP  
DGTLLLLQPPARGHAHDGQALSTDLGVYTCEASNRLGTAVSRGARLSVAVLREDFQIQPRDM  
VAVVGEQFTLECGPPWGHPEPTVSWWKDGKPLALQPGRHTVSGGSLLMARAEEKSDEGTVMCV  
ATNSAGHRESRAARVSIQEPQDYTEPVELLAVRIQLENTLLNPDPAEGPKPRPAVWLSWKV  
SGPAAPAQSYTALFRTQTAPGGQGAPWAEELLAGWQSAELGGLHWGQDYEFKVRPSSGRARG  
PDSNVLLLRLPEKVPSAPPQEVTLKPGNGTVFVSWVPPPAENHNGIIRGYQVWSLGNTSLPP  
ANWTVVGEQTQLEIATHMPGSYCVQVAAVTGAGAGEPSRPVCLLLEQAMERATQEPSEHGWP  
TLEQLRATLKRPEVIATCGVALWLLLLGTAVCIHRRRRRARVHLGPGLYRYTSEDAILKHRMD  
HSDSQWLADTWRSTSGSRDLSSSSSLSSRLGADARDPLDCRRSLLSWDSRSPGVPLLPDTST  
FYGSLIAELPSSTPARPSPQVPAVRRLPPQLAQLSSPCSSSDSLCSRRGLSSPRLSLAPAEA  
WKAKKKQELQHANSPLLRGSHSLELRACELGNRGSKNLSQSPGAVPQALVAWRALGPKLLS  
SSNELVTRHLPPAPLFPHETPPTQSQQTQPPVAPQAPSSILLPAAPIPILSPCSPSPQASS  
LSGPSPASSRLSSSSSLSSLGEDQDSVLTPEEVALCLELSEGEETPRNSVSPMPRAPSPPTTY  
GYISVPTASEFTDMGRTGGGVGPKGGVLLCPRPCLTPTPSEGLANGWGSASEDNAASARA  
SLVSSSDGSFLADAHFARALAVAVDSFGFGLPREADCVFIDASSPPSPRDEIFLTPNLSLP  
LWEWRPDWLEDMEVSHTQRLGRGMPPWPPDSQISSQRSQLHCRMPKAGASPV DYS

**Important features:****Transmembrane domain:**

amino acids 448-467

**N-glycosylation sites:**

amino acids 224-227, 338-341, 367-370, 374-377, 658-661 and 926-929

**N-myristoylation sites.**

amino acids 47-52, 80-85, 88-93, 99-104, 105-110, 181-186, 272-277, 290-295, 355-360, 403-408, 462-467, 561-566, 652-657, 849-854 and 876-881

**Phosphotyrosine interaction domain proteins**

amino acids 740-753

781 237

**FIGURE 78**

CTCCACGGTGTCCAGCGCCCAGAAATGCGGCTTCTGGTCCTGCTATGGGGTTGCCTGCTGCT  
CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCTGAAGGGGACACTGTGT  
CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGGT  
GGGATCCTCTTCTCTCGCTGCTCTGGCACCATCTATGCAGAAGAAGAAGGCCAGGAGACAAT  
GAAGGGCAGGGTGTCCATCCGTGACAGCCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA  
ACCTCACCCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTTCGAAAAACGGGGCCCCGATGAG  
TCTTTACTGATCTCTCTGTTCGTCTTTCCAGGACCCTGCTGTCCTCCCTCCCCTTCTCCCAC  
CTTCCAGCCTCTGGCTACAACACGCCTGCAGCCCAAGGCAAAAGCTCAGCAAACCCAGCCCC  
CAGGATTGACTTCTCCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG  
GCTGAGGGCCCCTCCATTGCCAGGGACTTCCCAGTACGGGACAGAAAGGACTTCTCAGTACAC  
AGGAACCTCTCCTCACCCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCCCCATGCAGC  
TGGACTCCACCTCAGCAGAGGACACCAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCCAGG  
GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTGGTGCTGCTGAGCCTTCTGTCAGC  
CGCAGGCCTGATCGCCTTCTGCAGCCACCTGCTCCTGTGGAGAAAGGAAGCTCAACAGGCCA  
CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCACGCTTGACTGCGGAGGAAAAGGAAGCC  
CCTTCCCAGGGCCCCTGAGGGGGACGTGATCTCGATGCCTCCCCTCCACACATCTGAGGAGGA  
GCTGGGCTTCTCGAAGTTTGTCTCAGCGTAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT  
GAAGCAGTATGGCTGGCTGGATCAGCACCGATTCCCGAAAGCTTTCCACCTCAGCCTCAGAG  
TCCAGCTGCCCGGACTCCAGGGCTCTCCCCACCCTCCCCAGGCTCTCCTCTTGCAATGTTCCA  
GCCTGACCTAGAAGCGTTTGTCTAGCCCTGGAGCCCAGAGCGGTGGCCTTGCTCTTCCGGCTG  
GAGACTGGGACATCCCTGATAGGTTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA  
GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACTCCTGGGC  
CTCATGCCCAGTGTCTGGACCCTGCCTTCTCCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC  
TGGCGTCTCAGACTTAGTCCCACGGTCTCCTGCATCAGCTGGTGATGAAGAGGAGCATGCT  
GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACCACCTGCATCCAGCCCTTCAGGAAGCCT  
GTGAAAAACGTGATTCTGGCCCCACCAAGACCCACCAAAACCATCTCTGGGCTTGGTGCAG  
GACTCTGAATTCTAACAATGCCCAGTGAATGTCGCACTTGAGTTTGAGGGCCAGTGGGCTG  
ATGAACGCTCACACCCCTTCAGCTTAGAGTCTGCATTTGGGCTGTGACGTCTCCACCTGCCC  
CAATAGATCTGCTCTGTCTGCGACACCAGATCCACGTGGGGACTCCCCTGAGGCCTGCTAAG  
TCCAGGCCTTGGTCAGGTCAGGTGCACATTGCAGGATAAGCCCAGGACCGGCACAGAAGTGG  
TTGCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCCTTTGGAAAAAATGATGAAGA  
AAACCTTGGCTCCTTCTTGTCTGGAAAGGGTTACTTGCCCTATGGGTTCTGGTGGCTAGAGA  
GAAAAGTAGAAAACCAGAGTGCACGTAGGTGTCTAACACAGAGGAGAGTAGGAACAGGGCGG  
ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTTCGGGGGTGGTGGTAAAGTA  
GCACAACTACTATTTTTTTTTTCTTTTTTCCATTATTATTGTTTTTTAAGACAGAATCTCGTGCT  
GCTGCCCAGGCTGGAGTGCAGTGGCACGATCTGCAAACTCCGCCTCCTGGGTTCAAGTGATT  
CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACACCTGGCTAATT  
TTTGTACTTTTAGTAGAGATGGGGTTTACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGAC  
CTCAAATGAGCCTCCTGCTTCAGTCTCCCAAATTGCCGGGATTACAGGCATGAGCCACTGTG  
TCTGGCCCTATTTCTTTTAAAAAGTGAAATTAAGAGTTGTTTCAGTATGCAAACTTGGAAAG  
ATGGAGGAGAAAAAGAAAAGGAAGAAAAAATGTCACCCATAGTCTCACCAGAGACTATCAT  
TATTTGTTTTTGTGTACTTCTTCCACTCTTTTCTTCTTACATAATTTGCCGGTGTCTT  
TTTACAGAGCAATTATCTTGTATATACAACTTTGTATCCTGCCTTTTCCACCTTATCGTTCC  
ATCACTTTATTCCAGCACTTCTCTGTGTTTTACAGACCTTTTTTATAAATAAAATGTTTCATCA  
GCTGCATAAAAAAAAAAAAAA

791237

**FIGURE 79**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPTEEISGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS  
GTIYAEEEGQETMKGRVSIIRDSRQELSLIVTLWNLTLDAGEYWCGVEKRGPDSELLISLFV  
FPGPCCPPSPSPPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG  
TSQYGHERTSQYTGTSPHPATSPAGSSRPPMQLDSTSAEDTSPALSSGSSKPRVSIPMVRI  
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAEKEAPSQAPEGD  
VISMPPLHTSEEELGFSKFVSA

**Important features:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 248-269

**N-glycosylation site.**

amino acids 96-99

**Fibrinogen beta and gamma chains C-terminal domain.**

amino acids 104-113

**Ig like V-type domain:**

amino acids 13-128

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**FIGURE 80**

TTGTGACTAAAAGCTGGCCTAGCAGGCCAGGGAGTGCAGCTGCAGGCGTGGGGGTGGCAGGA  
GCCGCAGAGCCAGAGCAGACAGCCGAGAAACAGGTGGACAGTGTGAAAGAACCAGTGGTCTC  
GCTCTGTTGCCCAGGCTAGAGTGTACTGGCGTGATCATAGCTCACTGCAGCCTCAGACTCCT  
GGACTTGAGAAATCCTCCTGCCTTAGCCTCCTGCATATCTGGGACTCCAGGGGTGCACTCAA  
GCCCTGTTTCTTCTCCTTCTGTGAGTGGACCACGGAGGCTGGTGAGCTGCCTGTCATCCCAA  
AGCTCAGCTCTGAGCCAGAGTGGTGGTGGCTCCACCTCTGCCGCCGGCATAGAAGCCAGGAG  
CAGGGCTCTCAGAAGGCGGTGGTGCCAGCTGGGATCATGTTGTTGGCCCTGGTCTGTCTGC  
TCAGCTGCCTGCTACCCTCCAGTGAGGCCAAGCTCTACGGTCGTTGTGAACTGGCCAGAGTG  
CTACATGACTTCGGGCTGGACGGATAACGGGGATACAGCCTGGCTGACTGGGTCTGCCTTGC  
TTATTTACAAGCGGTTTCAACGCAGCTGCTTTGGACTACGAGGCTGATGGGAGCACCAACA  
ACGGGATCTTCCAGATCAACAGCCGGAGGTGGTGACGAACCTCACCCCGAACGTCCCCAAC  
GTGTGCCGGATGTACTGCTCAGATTTGTTGAATCCTAATCTCAAGGATACCGTTATCTGTGC  
CATGAAGATAACCCAAGAGCCTCAGGGTCTGGGTACTGGGAGGCCTGGAGGCATCACTGCC  
AGGGAAAAGACCTCACTGAATGGGTGGATGGCTGTGACTTCTTAGGATGGACGGAACCATGCA  
CAGCAGGCTGGGAAATGTGGTTTGGTTCCTGACCTAGGCTTGGGAAGACAAGCCAGCGAATA  
AAGGATGGTTGAACGTGAAA

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**FIGURE 81**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52187

<subunit 1 of 1, 146 aa, 1 stop

<MW: 16430, pI: 5.05, NX(S/T): 1

MLLALVCLLSCLLPSSSEAKLYGRCELARVLHDFGLDGYRGYSLADWVCLAYFTSGFNAAALD  
YEADGSTNNGIFQINSRRWCSNLTPNVPNVCRMYSDDLNPVLKDTVICAMKITQEPQGLGY  
WEAWRHHCQGKDLTEWVDGCDF

**Important features:****Signal peptide:**

amino acids 1-18

**N-myristoylation site.**

amino acids 67-72

**Homologous region to Alpha-lactalbumin / lysozyme C proteins.**

amino acids 34-58 (catalytic domain), 111-132 and 66-107

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**FIGURE 82**

AGCCGCTGCCCCGGGCGGGCGCCCGCGGCGGCACCAATGAGTCCCCGCTCGTGCCTGCGTTC  
GCTGCGCCTCCTCGTCTTCGCCGTCTTCTCAGCCGCCGCGAGCAACTGGCTGTACCTGGCCA  
AGCTGTCGTCGGTGGGGAGCATCTCAGAGGAGGAGACGTGCGAGAACTCAAGGGCCTGATC  
CAGAGGCAGGTGCAGATGTGCAAGCGGAACCTGGAAGTCATGGACTCGGTGCGCCGCGGTGC  
CCAGCTGGCCATTGAGGAGTGCCAGTACCAGTTCCGGAACCGGCGCTGGAAGTGTCCACAC  
TCGACTCCTTGCCCCGTCTTCGGCAAGGTGGTGACGCAAGGGACTCGGGAGGCGGCCTTCGTG  
TACGCCATCTCTTCGGCAGGTGTGGCCTTTGCAGTGACGCGGGCGTGCAGCAGTGGGGAGCT  
GGAGAAGTGCGGCTGTGACAGGACAGTGATGGGGTCAGCCCACAGGGCTTCCAGTGGTCAG  
GATGCTCTGACAACATCGCCTACGGTGTGGCCTTCTCACAGTCGTTTGTGGATGTGCGGGAG  
AGAAGCAAGGGGGGCTCGTCCAGCAGAGCCCTCATGAACCTCCACAACAATGAGGCCGGCAG  
GAAGGCCATCCTGACACACATGCGGGTGGAATGCAAGTGCCACGGGGTGTGAGGCTCCTGTG  
AGGTAAAGACGTGCTGGCGAGCCGTGCCGCCCTTCCGCCAGGTGGGTGACGCACTGAAGGAG  
AAGTTTGATGGTGCCACTGAGGTGGAGCCACGCCGCGTGGGCTCCTCCAGGGCACTGGTACC  
ACGCAACGCACAGTTCAAGCCGCACACAGATGAGGACCTGGTGTACTTGGAGCCTAGCCCCG  
ACTTCTGTGAGCAGGACATGCGCAGCGGCGTGCTGGGCACGAGGGGGCCGCACATGCAACAAG  
ACGTCCAAGGCCATCGACGGCTGTGAGCTGCTGTGCTGTGGCCGCGGCTTCCACACGGCGCA  
GGTGGAGCTGGCTGAACGCTGCAGCTGCAAATTCCACTGGTGCTGCTTCGTCAAGTGCCGGC  
AGTGCCAGCGGCTCGTGGAGTTGCACACGTGCCGATGACCGCCTGCCTAGCCCTGCGCCGGC  
AACCACCTAGTGGCCCAGGGAAGGCCGATAATTTAAACAGTCTCCCACCACCTACCCCAAGA  
GATACTGGTTGTATTTTTTGTCTGGTTTGGTTTTTGGGTCCTCATGTTATTTATTGCCGAA  
ACCAGGCAGGCAACCCCAAGGGCACCAACCAGGGCCTCCCCAAAGCCTGGGCCTTTGTGGCT  
GCCACTGACCAAAGGGACCTTGCTCGTGCCGCTGGCTGCCCCGCATGTGGCTGCCACTGACCA  
CTCAGTTGTTATCTGTGTCCGTTTTTCTACTTGCAGACCTAAGGTGGAGTAACAAGGAGTAT  
TACCACCACATGGCTACTGACCGTGTCATCGGGGAAGAGGGGGCCTTATGGCAGGGAAAATA  
GGTACCGACTTGATGGAAGTCACACCCTCTGGAAAAAAGAACTCTTAAGTCTCCAGCACACA  
TACACATGGACTCCTGGCAGCTTGAGCCTAGAAGCCATGTCTCTCAAATGCCCTGAGAAAGG  
GAACAAGCAGATAACCAGGTCAAGGGCACCAAGGTTTCAATTCAGCCCTTACATGGACAGCTAGA  
GGTTCGATATCTGTGGGTCCTTCCAGGCAAGAAGAGGGAGATGAGAGCAAGAGACGACTGAA  
GTCCCACCCTAGAACCCAGCCTGCCCCAGCCTGCCCCCTGGGAAGAGGAACTTAACCACTCC  
CCAGACCCACCTAGGCAGGCATATAGGCTGCCATCCTGGACCAGGGATCCCGGCTGTGCCTT  
TGCAGTCATGCCCGAGTCACCTTTCACAGCGCTGTTCTCCATGAAACTGAAAAACACACAC  
ACCTGCGAGA  
GAGAGGGAGGAAAGGGCTGTGCCTTTGCAGTCATGCCCGAGTCACCTTTCACAGCACTGTTCTC

**FIGURE 83**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48328

<subunit 1 of 1, 351 aa, 1 stop

<MW: 39052, pI: 8.97, NX(S/T): 2

MSPRSCLRSLRLLVFAVFSAAASNWLYLAKLSSVGSISEEETCEKLGKGLIQRQVQMCKRNLE  
VMDSVRRGAQLAIEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSAGVAFV  
TRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYGVAFSQSFVDVRERSKGASSSRALM  
NLHNNEAGRKAILTHMRVECKCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRR  
VGSSRALVPRNAQFKPHTDEDLVYLEPSPDFCEQDMRSGVLGTRGRTCNKTSKAIDGCELLC  
CGRGFHTAQVELAERCSCKFHWCCFVKCRQCQRLVELHTCR

**Important features:****Signal peptide:**

amino acids 1-22

**N-glycosylation sites.**

amino acids 88-91 and 297-300

**Wnt-1 family signature.**

amino acids 206-215

**Homologous region to Wnt-1 family proteins**

amino acids 183-235, 305-350, 97-138, 53-92 and 150 -174

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**FIGURE 84**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGGGTGCCTGCAT  
CGCCATGGACACCACCAGGTACAGCAAGTGGGGCGGCAGCTCCGAGGAGGTCCCCGGAGGGC  
CCTGGGGACGCTGGGTGCACTGGAGCAGGAGACCCCTCTTCTTGGCCCTGGCTGTCCTGGTC  
ACCACAGTCCTTTGGGCTGTGATTCTGAGTATCCTATTGTCCAAGGCCTCCACGGAGCGCGC  
GGCGCTGCTTGACGGCCACGACCTGCTGAGGACAAACGCCTCGAAGCAGACGGCGGGCGCTGG  
GTGCCCTGAAGGAGGAGGTGCGAGACTGCCACAGCTGCTGCTCGGGGACGCAGGCGCAGCTG  
CAGACCACGCGCGCGGAGCTTGGGGAGGCGCAGGCGAAGCTGATGGAGCAGGAGAGCGCCCT  
GCGGGAACTGCGTGAGCGCGTGACCCAGGGCTTGGCTGAAGCCGGCAGGGGGCCGTGAGGACG  
TCCGCACTGAGCTGTTCCGGGCGCTGGAGGCCGTGAGGCTCCAGAACAACCTCCTGCGAGCCG  
TGCCCCACGTCGTGGCTGTCCTTCGAGGGCTCCTGCTACTTTTTCTCTGTGCCAAAGACGAC  
GTGGGCGGCGGCGCAGGATCACTGCGCAGATGCCAGCGCGCACCTGGTGATCGTTGGGGGCC  
TGGATGAGCAGGGCTTCCTCACTCGGAACACGCGTGGCCGTGGTTACTGGCTGGGCCTGAGG  
GCTGTGCGCCATCTGGGCAAGGTTTCAGGGCTACCAGTGGGTGGACGGAGTCTCTCTCAGCTT  
CAGCCACTGGAACCAGGGAGAGCCCAATGACGCTTGGGGGCGCGAGAACTGTGTCATGATGC  
TGCACACGGGGCTGTGGAACGACGCACCGTGTGACAGCGAGAAGGACGGCTGGATCTGTGAG  
AAAAGGCACAACCTGCTTGACCCCGCCAGTGCCCTGGAGCCGCGCCCATTCAGCATGTCGTA  
TCCTGGGGGCTGCTCACCTCCCTGGCTCCTGGAGCTGATTGCCAAAGAGTTTTTTTCTTCCT  
CATCCACCGCTGCTGAGTCTCAGAAACACTTGGCCCAACATAGCCCTGTCCAGCCCAGTGCC  
TGGGCTCTGGGACCTCCATGCCGACCTCATCCTAACTCCACTCACGCAGACCCAACCTAACC  
TCCACTAGCTCCAAAATCCCTGCTCCTGCGTCCCCGTGATATGCCTCCACTTCTCTCCCTAA  
CCAAGGTTAGGTGACTGAGGACTGGAGCTGTTTGGTTTTCTCGCATTTTCCACCAAACCTGGA  
AGCTGTTTTTGCAGCCTGAGGAAGCATCAATAAATATTTGAGAAATGAAAAA

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**FIGURE 85**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56352

<subunit 1 of 1, 293 aa, 1 stop

<MW: 32562, pI: 6.53, NX(S/T): 2

MDTTRYSKWGGSSSEVPGGPWGRWVHWSRRPLFLALAVLVTTVLWAVILSILLSKASTERAA  
LLDGHDLLRTNASKQTAALGALKEEVGDCHSCCSGTQAQLQTTRAELGEAQAKLMEQESALR  
ELRERVTOGLAEAGRGREDVRTELFRALAVRLQNNSCPCPTSWLSFEGSCYFFSVPKTTW  
AAAQDHCADASAHLVIVGGLDEQGFLTRNTRGRGYWLGLRAVRHLGKVQGYQWVDGVSLSFS  
HWNQGEPNDAWGRENVCVMMMLHTGLWNDAPCDSEKDGWICEKRHNC

**Important features:****Type II transmembrane domain:**

amino acids 31-54

**N-glycosylation sites.**

amino acids 73-76 and 159-162

**Leucine zipper pattern.**

amino acids 102-123

**N-myristoylation sites.**

amino acids 18-23, 133-138 and 242-247

**C-type lectin domain signature.**

amino acids 264-287

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**FIGURE 86**

GCCAGGGGAAGAGGGTGATCCGACCCGGGGAAGGTCGCTGGGCAGGGCGAGTTGGGAAAGCG  
GCAGCCCCCGCCGCCCCCGCAGCCCCCTTCTCCTCCTTTCTCCCACGTCCTATCTGCCTCTCG  
CTGGAGGCCAGGCCGTGCAGCATCGAAGACAGGAGGAACTGGAGCCTCATTTGGCCGGCCCGG  
GGCGCCGGCCTCGGGCTTAAATAGGAGCTCCGGGCTCTGGCTGGGACCCGACCGCTGCCGGC  
CGCGCTCCCGCTGCTCCTGCCGGGTGATGGAAAACCCCAGCCCGGCCGCCCTGGGCAAG  
GCCCTCTGCGCTCTCCTCCTGGCCACTCTCGGCGCCGCCGGCCAGCCTCTTGGGGGAGAGTC  
CATCTGTTCCGCCAGAGCCCCGGCCAAATACAGCATCACCTTCACGGGCAAGTGGAGCCAGA  
CGGCCTTCCCCAAGCAGTACCCCCTGTTCCGCCCCCCTGCGCAGTGGTCTTCGCTGCTGGGG  
GCCGCGCATAGCTCCGACTACAGCATGTGGAGGAAGAACCAGTACGTCAGTAACGGGGCTGCG  
CGACTTTGCGGAGCGCGGCGAGGCCCTGGGCGCTGATGAAGGAGATCGAGGCGGCGGGGGAGG  
CGCTGCAGAGCGTGCACGAGGTGTTTTCGGCGCCCGCCGTCCCCAGCGGCACCGGGCAGACG  
TCGGCGGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGTCTCGTTTGTGGTGCGCATCGTGCC  
CAGCCCCGACTGGTTCGTGGGCGTGGACAGCCTGGACCTGTGCGACGGGGACCGTTGGCGGG  
AACAGGCGGCGCTGGACCTGTACCCCTACGACGCCGGGACGGACAGCGGCTTCACCTTCTCC  
TCCCCCAACTTCGCCACCATCCCGCAGGACACGGTGACCGAGATAACGTCCTCCTCTCCAG  
CCACCCGGCCAACTCCTTCTACTACCCGCGGGCTGAAGGCCCTGCCTCCCATCGCCAGGGTGA  
CACTGCTGCGGCTGCGACAGAGCCCCAGGGCCTTCATCCCTCCCGCCCCAGTCCTGCCCAGC  
AGGGACAATGAGATTGTAGACAGCGCCTCAGTTCCAGAAACGCCGCTGGACTGCGAGGTCTC  
CCTGTGGTCGTCCTGGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGGACCAAGAGCAGGA  
CTCGCTACGTCCGGGTCCAGCCCGCCAACAACGGGAGCCCCCTGCCCCGAGCTCGAAGAAGAG  
GCTGAGTGCGTCCCTGATAACTGCGTCTTAAGACCAGAGCCCCGCAGCCCCCTGGGGCCCCCGG  
GAGCCATGGGGTGTCGGGGGCTCCTGTGCAGGCTCATGCTGCAGGCGGCCGAGGGCACAGGG  
GGTTTCGCGCTGCTCCTGACCGCGGTGAGGCCGCGCCGACCATCTCTGCACTGAAGGGCCCT  
CTGGTGGCCGGCACGGGCATTGGGAAACAGCCTCCTCCTTTCCCAACCTTGCTTCTTAGGGG  
CCCCCGTGTCCCGTCTGCTCTCAGCCTCCTCCTCCTGCAGGATAAAGTCATCCCCAAGGCTC  
CAGCTACTCTAAATTATGTCTCCTTATAAGTTATTGCTGCTCCAGGAGATTGTCCTTCATCG  
TCCAGGGGCCTGGCTCCCACGTGGTTGCAGATACCTCAGACCTGGTGCTCTAGGCTGTGCTG  
AGCCCACTCTCCCGAGGGCGCATCCAAGCGGGGGCCACTTGAGAAGTGAATAAATGGGGCGG  
TTTCGGAAGCGTCAGTGTTTCCATGTTATGGATCTCTCTGCGTTTGAATAAAGACTATCTCT  
GTTGCTCACAAA

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**FIGURE 87**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53971

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35844, pI: 5.45, NX(S/T): 2

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPL  
FRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVF  
SAPAVPSGTGQTSAELEVQRRHSLVSFVVRIVPSPDWFVGVDSLDCDGDWRREQAALDLYP  
YDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLLRLRQSP  
RAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGR LGTKSRTRYVRVQPA  
NNGSPCPELEEEAECVPDNCV

**Important features:**

**Signal peptide:**

amino acids 1-26

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**FIGURE 88**

GGCGGCGTCCGTGAGGGGCTCCTTTGGGCAGGGGTAGTGTTTGGTGTCCCTGTCTTGCGTGA  
TATTGACAACTGAAGCTTTCCTGCACCACTGGACTTAAGGAAGAGTGTACTCGTAGGCGGA  
CAGCTTTAGTGGCCGGCCGGCCGCTCTCATCCCCGTAAGGAGCAGAGTCCTTTGTACTGAC  
CAAGATGAGCAACATCTACATCCAGGAGCCTCCCACGAATGGGAAGGTTTTATTGAAAATA  
CAGCTGGAGATATTGACATAGAGTTGTGGTCCAAAGAAGCTCCTAAAGCTTGCAGAAATTTT  
ATCCAACCTTTGTTTGGGAAGCTTATTATGACAATACCATTTTTTCATAGAGTTGTGCCTGGTTT  
CATAGTCCAAGGCGGAGATCCTACTGGCACAGGGAGTGGTGGAGAGTCTATCTATGGAGCGC  
CATTCAAAGATGAATTTTCATTCACGGTTGCGTTTTTAATCGGAGAGGACTGGTTGCCATGGCA  
AATGCTGGTTCTCATGATAATGGCAGCCAGTTTTTCTTCACACTGGGTGAGCAGATGAACT  
TAACAATAAGCATACCATCTTTGGAAAGGTTACAGGGGATACAGTATATAACATGTTGCGAC  
TGTCAGAAGTAGACATTGATGATGACGAAAGACCACATAATCCACACAAAATAAAAAGCTGT  
GAGGTTTTGTTTAATCCTTTTGATGACATCATTCCAAGGGAAATTAAAAGGCTGAAAAAGA  
GAAACCAGAGGAGGAAGTAAAGAAATTGAAACCCAAAGGCACAAAAAATTTTAGTTTACTTT  
CATTTGGAGAGGAAGCTGAGGAAGAAGAGGAGGAAGTAAATCGAGTTAGTCAGAGCATGAAG  
GGCAAAAGCAAAAGTAGTCATGACTTGCTTAAGGATGATCCACATCTCAGTTCTGTTCCAGT  
TGTAAGAAAGTGAAAAAGGTGATGCACCAGATTTAGTTGATGATGGAGAAGATGAAAGTGCAG  
AGCATGATGAATATATTGATGGTGATGAAAAGAACCTGATGAGAGAAAGAATTGCCAAAAAA  
TTAAAAAAGGACACAAGTGCGAATGTTAAATCAGCTGGAGAAGGAGAAGTGGAGAAGAAATC  
AGTCAGCCGCAGTGAAGAGCTCAGAAAAGAAGCAAGACAATTAAAACGGGAACCTCTTAGCAG  
CAAAACAAAAAAAAGTAGAAAATGCAGCAAAACAAGCAGAAAAAAGAAGTGAAGAGGAAGAA  
GCCCCCTCCAGATGGTGCTGTTGCCGAATACAGAAGAGAAAAGCAAAAGTATGAAGCTTTGAG  
GAAGCAACAGTCAAAGAAGGGAACCTTCCCGGGAAGATCAGACCCTTGCACTGCTGAACCAGT  
TTAAATCTAACTCACTCAAGCAATTGCTGAAACACCTGAAAATGACATTCCTGAAACAGAA  
GTAGAAGATGATGAAGGATGGATGTCACATGTACTTCAGTTTGAGGATAAAAGCAGAAAAGT  
GAAAGATGCAAGCATGCAAGACTCAGATACATTTGAAATCTATGATCCTCGGAATCCAGTGA  
ATAAAAGAAGGAGGGAAGAAAGCAAAAAGCTGATGAGAGAGAAAAAAGAAAGAAGATTAAAAT  
GAGAATAATGATAACCAGAACTTGCTGGAAATGTGCCTACAATGGCCTTGTAACAGCCATTG  
TTCCCAACAGCATCACTTAGGGGTGTGAAAAGAAGTATTTTTGAACCTGTTGTCTGGTTTTG  
AAAAACAATTATCTTGTGTTTGCAAATTGTGGAATGATGTAAGCAAATGCTTTTGGTTACTGG  
TACATGTGTTTTTTCCTAGCTGACCTTTTATATTGCTAAATCTGAAATAAAATAACTTTCCT  
TCCACAAAAA

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**FIGURE 89**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50919  
><subunit 1 of 1, 472 aa, 1 stop  
><MW: 53847, pI: 5.75, NX(S/T): 2  
MSNIYIQEPPTNGKVLLKTTAGDIDIELWSKEAPKACRNFIQLCLEAYYDNTIFHRVVPGFI  
VQGGDPTGTGSGGESIYGAPFKDEFHSRLRFNRRGLVAMANAGSHDNGSQFFFTLGRADELN  
NKHTIFGKVTGDTVYNMLRLSEVDIDDDERPHNPHKIKSCEVLFPFDDIIPREIKRLKKEK  
PEEEVKKLKPKGTKNFSLLSFGEAEAEAEAEAEVNRVSQSMKGKSKSSHDLKDDPHLSSVPVV  
ESEKGDAPDLVDDGEDESAEHDEYIDGDEKNLMRERIAKKLKKDTSANVKSAGEGEVEKKSV  
SRSEELRKEARQLKRELLAAKQKKVENAAKQAEKRSEEEEAPPDGAVAEYRREKQKYEALRK  
QQSKKGTSREDQTLALLNQFKSKLTQAI AETPENDIPETEVEDDEGWMSHVLQFEDKSRKVK  
DASMQDSDTFEIYDPRNPVNKRREESKKLMREKKERR

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 109-112 and 201-204

**Cyclophilin-type peptidyl-prolyl cis-trans isomerase signature.**

amino acids 49-66

**Homologous region to Cyclophilin-type peptidyl-prolyl cis-trans isomerase**

amino acids 96-140, 49-89 and 22-51

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**FIGURE 90**

CGCCGCCGTTGGGGCTGGAAGTTCCCGCCAGGTCCGTGCCGGGCGAGAGAGATGCTGCCCGG  
CCCGCCTCGGCTTTGAGGCGAGAGAAGTGTCCCAGACCCATTTCGCCTTGCTGACGGCGTCG  
AGCCCTGGCCAGACATGTCCACAGGGTTCTCCTTCGGGTCCGGGACTCTGGGCTCCACCACC  
GTGGCCGCCGGCGGGACCAGCACAGGCGGCGTTTTCTCCTTCGGAACGGGAACGTCTAGCAA  
CCCTTCTGTGGGGCTCAATTTTGGAAATCTTGGAAGTACTTCAACTCCAGCAACTACATCTG  
CTCCTTCAAGTGGTTTTTGGAAACCGGGCTCTTTGGATCTAAACCTGCCACTGGGTTCACTCTA  
GGAGGAACAAATACAGGTGCCTTGACACCAAGAGGGCTCAAGTGGTCACCAAAATATGGAAC  
CCTGCAAGGAAAACAGATGCATGTGGGGAAGACACCCATCCAAGTCTTTTATAGGAGTCCCCT  
TCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCCGGAGCCCTGGAAA  
GGAATCAGAGATGCTACCACCTACCCGCCTGGATGGAGTCTCGCTCTGTGCCAGGCTGGAG  
TGCAGTGGCACGATCTCGGCTCACTGCAACCTCCGCCTCCCGGGTTCAAGCGAGTCTCCTGC  
CTCAGCCTCTGAGTGTCTGGGGCTACAGGTGCCTGCAGGAGTCCTGGGGCCAGCTGGCCTCG  
ATGTACGTCAGCACGCGGGAACGGTACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACCT  
GAACGTGTACGCGCCGGCGCGCGCGCCCGGGGATCCCCAGCTGCCAGTGATGGTCTGGTTCC  
CGGGAGGCGCCTTCATCGTGGGCGCTGCTTCTTCGTACGAGGGCTCTGACTTGGCCGCCCGC  
GAGAAAGTGGTGTGTTTCTGCAGCACAGGCTCGGCATCTTCGGCTTCCTGAGCACGGA  
CGACAGCCACGCGCGCGGGAACCTGGGGGCTGCTGGACCAGATGGCGGCTCTGCGCTGGGTGC  
AGGAGAACATCGCAGCCTTCGGGGGAGACCCAGGAAATGTGACCCTGTTCCGGCCAGTCGGCG  
GGGGCCATGAGCATCTCAGGACTGATGATGTCAACCCCTAGCCTCGGGTCTCTTCCATCGGGC  
CATTTCCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAAGTGG  
CCAAGAAGGTTGCCCACCTGGCTGGATGCAACCACAACAGCACACAGATCCTGGTAAACTGC  
CTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCAACAAGATGAGATTCTTCCAAC  
GAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGG  
TGATCCCAGATGACCCTTTGGTGCTCCTGACCCAGGGGAAGGTTTCATCTGTGCCCTACCTT  
CTAGGTGTCAACAACCTGGAATTCAATTGGCTCTTGCCCTTATAATATCACCAAGGAGCAGGT  
ACCACTTGTGGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAA  
ACCGTATGATGGACATAGTTCAAGATGCCACTTTCGTGTATGCCACACTGCAGACTGCTCAC  
TACCACCGAGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTACAACAAGGATGAA  
AAGTACCTGCAGCTGGATTTTACCACAAGAGTGGGCATTGAAGCTCAAGGAGAAGAAGATGGC  
TTTTTGGATGAGTCTGTACCAGTCTCAAAGACCTGAGAAGCAGAGGCAATTCTAAGGGTGGC  
TATGCAGGAAGGAGCCAAAGAGGGGTTTGCCCCCACCATCCAGGCCCTGGGGAGACTAGCCA  
TGGACATACCTGGGGACAAGAGTTCTACCCACCCAGTTTAGAAGTGCAGGAGCTCCCTGCT  
GCCTCCAGGCCAAAGCTAGAGCTTTTGCCCTGTTGTGTGGGACCTGCACTGCCCTTTCCAGCC  
TGACATCCCATGATGCCCCCTCTACTTCACTGTTGACATCCAGTTAGGCCAGGCCCTGTCAAC  
ACCACACTGTGCTCAGCTCTCCAGCCTCAGGACAACCTCTTTTTTTCCCTTCTTCAAATCCT  
CCCACCCTTCAATGTCTCCTTGTGACTCCTTCTTATGGGAGGTGACCCAGACTGCCACTGC  
CCCTGTCACTGCACCCAGCTTGGCATTTACCATCCATCCTGCTCAACCTTGTTCTGTCTGT  
TCACATTGGCCTGGAGGCCTAGGGCAGGTTGTGACATGGAGCAAACCTTTTGGTAGTTTGGGA  
TCTTCTCTCCACCCACACTTATCTCCCCAGGGCCACTCCAAAGTCTATACACAGGGGTGG  
TCTCTTCAATAAAGAAGTGTTGATTAGAAAAA

**FIGURE 91**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44179

<subunit 1 of 1, 545 aa, 1 stop

<MW: 58934, pI: 9.45, NX(S/T): 4

MSTGFSFGSGTLGSTTVAAGGTSTGGVFSFGTGTSSNPSVGLNFGNLGSTSTPATTAPSSG  
FGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQMHVGKTPIQVFLGVPFSRPP  
LGILRFAPPEPPEPWKGIRDATTYPGWSLALSPGWSAVARSRLTATSASRVQASLLPQPLS  
VWGYRCLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVIYAPARAPGDPQLPVMVWFPGGAF  
IVGAASSYEGSDLAAREKVVLVFLQHRIGIFGFLSTDDSHARGNWGLLDQMAALRWVQENIA  
AFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKKVA  
HLAGCNHNSTQILVNCLRALSGTKVMRVSNNKMRFLQLNFQRPDEEIIWSMSPVVDGVVIPDD  
PLVLLTQGVSSVPYLLGVNNLEFNWLLPYNITKEQVPLVVEEYLDNVNEHDWKMLRNRMMD  
IVQDATFVYATLQTAHYHRETPMMGICPAGHATTRMKSTCSWILPQEWA

**Important features:****Signal peptide:**

amino acids 1-29

**Carboxylesterases type-B serine active site.**

amino acids 312-327

**Carboxylesterases type-B signature 2.**

amino acids 218-228

**N-glycosylation sites.**

amino acids 318-321, 380-383 and 465-468

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**FIGURE 92**

[illegible]

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**FIGURE 93**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA54002  
><subunit 1 of 1, 544 aa, 1 stop  
><MW: 60268, pI: 9.53, NX(S/T): 3  
MLLPLLLSSLLGGSQAMDGRFWIRVQESVMVPEGLCISVPCSF SYPRQDWTGSTPAYGYWFK  
AVTETTKGAPVATNHQSREVEMSTRGRFQLTGDPKAGNCSLVIRDAQMQDESQYFFRVERGS  
YVTYNFMNDGFFLKVTVLSFTPRPQDHNTDLTCHVDFSRKGVSAQRTVRLRVAYAPRDLVIS  
ISRDNTPALEPQPQGNVPYLEAQKGQFLRLLCAADSQPPATLSWVLQNRVLSSSHPWGPRPL  
GLELPGVKAGDSGRYTCRAENRLGSQQRALDLSVQYPPENLRVMVSQANRTVLENLGNGTSL  
PVLEGQSLCLVCVTHSSPPARLSWTQRGQVLSPSQPSDPGVLELPRVQVEHEGEFTCHARHP  
LGSQHVSLSLSVHYKKGLISTAFSNGAFLGIGITALLEFLCLALIIMKILPKRRTQTETPRPR  
FSRHSTILDYINVVPTAGPLAQKRNOQKATPNSPRTPPPPGAPSPESKKNQKKQYQLPSFPEP  
KSSTQAPESQESQEELHYATLNFPGVRPRPEARMPKGTQADYAEVKFQ

**Important features:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 399-418

**N-glycosylation site.**

amino acids 100-103, 297-300 and 306-309

**Immunoglobulins and major histocompatibility complex proteins  
signature.**

amino acids 365-371

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**FIGURE 94**

TGAAGAGTAATAGTTGGAATCAAAAGAGTCAACGCAATGAACTGTTATTTACTGCTGCGTTT  
TATGTTGGGAATTCCTCTCCTATGGCCTTGTCTTGGAGCAACAGAAAACCTCTCAAACAAAGA  
AAGTCAAGCAGCCAGTGCGATCTCATTGAGAGTGAAGCGTGGCTGGGTGTGGAACCAATTT  
TTTGTACCAGAGGAAATGAATACGACTAGTCATCACATCGGCCAGCTAAGATCTGATTTAGA  
CAATGGAAACAATTCTTTCCAGTACAAGCTTTTGGGAGCTGGAGCTGGAAGTACTTTTATCA  
TTGATGAAAGAACAGGTGACATATATGCCATACAGAAGCTTGATAGAGAGGAGCGATCCCTC  
TACATCTTAAGAGCCCAGGTAATAGACATCGCTACTGGAAGGGCTGTGGAACCTGAGTCTGA  
GTTTGTTCATCAAAGTTTCGGATATCAATGACAATGAACCAAAATTCCTAGATGAACCTTATG  
AGGCCATTGTACCAGAGATGTCTCCAGAAGGAACATTAGTTATCCAGGTGACAGCAAGTGAT  
GCTGACGATCCCTCAAGTGGTAATAATGCTCGTCTCCTCTACAGCTTACTTCAAGGCCAGCC  
ATATTTTTCTGTTGAACCAACAACAGGAGTCATAAGAATATCTTCTAAAATGGATAGAGAAC  
TGCAAGATGAGTATTGGGTAAATCATTCAGCCAAGGACATGATTGGTCAGCCAGGAGCGTTG  
TCTGGAACAACAAGTGTATTAATTAACCTTTCAGATGTAAATGACAATAAGCCTATATTTAA  
AGAAAGTTTATACCGCTTGACTGTCTCTGAATCTGCACCCACTGGGACTTCTATAGGAACAA  
TCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTACAGCATTGAAGAGGAT  
GATTCGCAAACATTTGACATTATTACTAATCATGAACTCAAGAAGGAATAGTTATATTTAA  
AAAGAAAGTGGATTTTGGAGCACCAGAACCACTACGGTATTAGAGCAAAAGTTAAAAACCATC  
ATGTTCTTGAGCAGCTCATGAAGTACCACACTGAGGCTTCCACCACTTTCATTAAGATCCAG  
GTGGAAGATGTTGATGAGCCTCCTCTTTTCTCCTTCCATATTATGTATTTGAAGTTTTTGA  
AGAAACCCACAGGGATCATTTGTAGGCGTGGTGTCTGCCACAGACCCAGACAATAGGAAAT  
CTCCTATCAGGTATTCTATTACTAGGAGCAAAGTGTTCAATATCAATGATAATGGTACAATC  
ACTACAAGTAACTCACTGGATCGTGAAATCAGTGCTTGGTACAACCTAAGTATTACAGCCAC  
AGAAAAATACAATATAGAACAGATCTCTTCGATCCCACTGTATGTGCAAGTTCTTAACATCA  
ATGATCATGCTCCTGAGTTCTCTCAATACTATGAGACTTATGTTTGTGAAAATGCAGGCTCT  
GGTCAGGTAATTCAGACTATCAGTGCAAGTGGATAGAGATGAATCCATAGAAGAGCACCATTT  
TTACTTTAATCTATCTGTAGAAGACACTAACAATTCAAGTTTTACAATCATAGATAATCAAG  
ATAACACAGCTGTCATTTTGGACTAATAGAAGTGGTTTTAACCTTCAAGAAGAACCTGTCTTC  
TACATCTCCATCTTAATTGCCGACAATGGAATCCCGTCACTTACAAGTACAAACACCCTTAC  
CATCCATGTCTGTGACTGTGGTGACAGTGGGAGCACACAGACCTGCCAGTACCAGGAGCTTG  
TGCTTTCCATGGGATTCAAGACAGAAGTTATCATTGCTATTCTCATTTGCATTATGATCATA  
TTTGGGTTTATTTTTTTTGGACTTTGGGTTTAAAACAACGGAGAAAACAGATTCTATTTCTGA  
GAAAAGTGAAGATTTTCAGAGAGAATATATTTCCAATATGATGATGAAGGGGGTGGAGAAGAAG  
ATACAGAGGCCTTTGATATAGCAGAGCTGAGGAGTAGTACCATAATGCGGGAACGCAAGACT  
CGGAAAACCACAAGCGCTGAGATCAGGAGCCTATACAGGCAGTCTTTGCAAGTTGGCCCCGA  
CAGTGCCATATTCAAGGAAATTCATTCTGGAAAAGCTCGAAGAAGCTAATACTGATCCGTGTG  
CCCCTCCTTTTGAATCCCTCCAGACCTACGCTTTTGGAGGGAACAGGGTCATTAGCTGGATCC  
CTGAGCTCCTTAGAATCAGCAGTCTCTGATCAGGATGAAAGCTATGATTACCTTAATGAGTT  
GGGACCTCGCTTTAAAAGATTAGCATGCATGTTTGGTTCTGCAGTGCAGTCAAATAATTAGG  
GCTTTTTTACCATCAAATTTTTTAAAAGTGCTAATGTGTATTTCGAACCCAATGGTAGTCTTAA  
AGAGTTTTGTGCCCTGGCTCTATGGCGGGGAAAGCCCTAGTCTATGGAGTTTTCTGATTTCC  
CTGGAGTAAATACTCCATGGTTATTTTTAAGCTACCTACATGCTGTTCATTGAACAGAGATGTG  
GGGAGAAATGTAAACAATCAGCTCACAGGCATCAATACAACCAGATTTGAAGTAAATAATG  
TAGGAAGATATTAAAAGTAGATGAGAGGACACAAGATGTAGTCGATCCTTATGCGATTATAT  
CATTATTTACTTAGGAAAGAGTAAAAATACCAAACGAGAAAATTTAAAGGAGCAAAAATTTG  
CAAGTCAAATAGAAATGTACAAATCGAGATAACATTTACATTTCTATCATATTGACATGAAA  
ATTGAAAATGTATAGTCAGAGAAATTTTCATGAATTATCCATGAAGTATTGTTTCCTTTAT  
TTAA

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**FIGURE 95**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53906  
><subunit 1 of 1, 772 aa, 1 stop  
><MW: 87002, pI: 4.64, NX(S/T): 8  
MNCYLLLRFMLGIPLLWPCLGATENSQTKKVKQPVRSHLRVKGWVWNQFFVPEEMNTTSHH  
IGQLRSDLDNGNNSFQYKLLGAGAGSTFIIDERTGDIYAIQKLDREERSLYILRAQVIDIAT  
GRAVEPESEFVIKVS DINDNEPKFLDEPYEAIVPEMSPEGTLVIQVTASDADDPSSGNNARL  
LYSLLQGQPYFSVEPTTG VIRISSKMDRELQDEYWVIIQAKDMIGQPGALSGTTSVLIKLS D  
VNDNKPIFKESLYRLTVSESAPTGT SIGTIMAYDNDIGENAEMDYSIEEDDSQTFDIITNHE  
TQEGIVILKKKVD FEHQNHYGIRAKVKNHHVPEQLMKYHTEASTTFIKIQVEDVDEPPLFLL  
PYYVFEVFEETPQGSFVGVSATDPDNRKSPIRYSITRSKVFNINDNGTITTSNSLDREISA  
WYNLSITATEKYNIEQISSIPLYVQVLNINDHAPEFSQYYETYVCENAGSGQVIQTISAVDR  
DESIEEHHFYFNLSVEDTNNSSFTIIDNQDNTAVILTNRTGFNLQEEPVFYISILIADNGIP  
SLTSTNTLTIHVCD CGDSGSTQTCQYQELVLSMGFKTEVIIAILICIMIIFGFIFLTLGLKQ  
RRKQILFPEKSEDFRENIFQYDDEGGGEEDTEAFDIAELRSSTIMRERKTRKTTSAEIRSLY  
RQSLQVGPDSAI FRKFILEKLEEANTDPCAPPFDSLQTYAFEGTGSLAGSLSSLES AVSDQD  
ESYDYLNELGPRFKRLACMFGSAVQSNN

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domain:**

amino acids 597-617

**N-glycosylation sites.**amino acids 57-60, 74-77, 419-423, 437-440, 508-511, 515-518,  
516-519 and 534-537**Cadherins extracellular repeated domain signature.**

amino acids 136-146 and 244-254

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**FIGURE 96**

ATTTCAAGGCCAGCCATATTTTNTGTTGAACCAACAACAGGAGTCATAAGAATATTTNTA  
AAATGGATAGAGAACTGCAAGATGAGTATTGGGTAATCATTCAAGCCAAGGACATGATTGGT  
CAGCCAGGAGCGTTGTNTGGAACAACAAGTGTATTAATTAACTTTCAGATGTTAATGACAA  
TAAGCCTATATTTAAAGAAAGTTTATACCGCTTGACTGTNTNTGAATCTGCACCCACTGGGA  
NTTNTATAGGAACAATCATGGCATATGATAATGACATAGGAGAGAATGCAGAAATGGATTAC  
AGCATTGAAGAGGATGATTCGCAAACATTTGACATTATT

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**FIGURE 97**

GCAACCTCAGCTTCTAGTATCCAGACTCCAGCGCCGCCCCGGGCGCGGACCCCAACCCCGAC  
CCAGAGCTTCTCCAGCGGCGGCGCAGCGAGCAGGGCTCCCCGCCTTAACCTCCTCCGCGGGG  
CCCAGCCACCTTCGGGAGTCCGGGTTGCCACCTGCAAACCTCTCCGCCTTCTGCACCTGCCA  
CCCCTGAGCCAGCGCGGGGCCCCCGAGCGAGTCATGGCCAACGCGGGGCTGCAGCTGTTGGGC  
TTCATTCTCGCCTTCCTGGGATGGATCGGCGCCATCGTCAGCACTGCCCTGCCCCAGTGGAG  
GATTTACTCCTATGCCGGCGACAACATCGTGACCGCCCAGGCCATGTACGAGGGGCTGTGGA  
TGTCTGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAAT  
CTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTGGCATCCTCCTGGGAGTGAT  
AGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGC  
AGAAGATGAGGATGGCTGTCATTGGGGGTGCGATATTTCTTCTTGCAAGTCTGGCTATTTTA  
GTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCCAGT  
CAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCC  
TTCTGGGAGGTGCCCTACTTTGCTGTTCTGTCCCCGAAAAACAACCTCTTACCCAACACCA  
AGGCCCTATCCAAAACCTGCACCTTCCAGCGGGAAAGACTACGTGTGACACAGAGGCAAAAG  
GAGAAAATCATGTTGAAACAAACCGAAAATGGACATTGAGATACTATCATTAACATTAGGAC  
CTTAGAATTTTGGGTATTGTAATCTGAAGTATGGTATTACAAAACAAACAAACAAACAAAA  
ACCCATGTGTTAAAATACTCAGTGCTAAACATGGCTTAATCTTATTTTATCTTCTTCTCCTCA  
ATATAGGAGGGAAGATTTTCCATTTGTATTACTGCTTCCCATTGAGTAATCATACTCAAAT  
GGGGGAAGGGGTGCTCCTTAAATATATATAGATATGTATATATACATGTTTTTCTATTAAAA  
ATAGACAGTAAAATACTATTCTCATTATGTTGATACTAGCATACTTAAAATATCTCTAAAAT  
AGGTAAATGTATTTAATTCCATATTGATGAAGATGTTTATTGGTATATTTTCTTTTTCGTCC  
TTATATACATATGTAACAGTCAAATATCATTTACTCTTCTTCATTAGCTTTGGGTGCCTTTG  
CCACAAGACCTAGCCTAATTTACCAAGGATGAATTCTTTCAATTCTTCATGCGTGCCCTTTT  
CATATACTTATTTTATTTTACCATAATCTTATAGCACTTGCATCGTTATTAAGCCCTTAT  
TTGTTTTGTGTTTCATTGGTCTCTATCTCCTGAATCTAACACATTTTCATAGCCTACATTTTA  
GTTTCTAAAGCCAAGAAGAATTTATTACAAATCAGAACTTTGGAGGCAAATCTTTCTGCATG  
ACCAAAGTGATAAATTCCTGTTGACCTTCCCACACAATCCCTGTACTCTGACCCATAGCACT  
CTTGTTTGCTTTGAAAATATTTGTCCAATTGAGTAGCTGCATGCTGTTCCCCCAGGTGTTGT  
AACACAACCTTTATTGATTGAATTTTAAAGCTACTTATTCATAGTTTTATATCCCCCTAACT  
ACCTTTTTTGTTCCCCATTCCCTTAATTGTATTGTTTTCCCAAGTGTAATTATCATGCGTTTTA  
TATCTTCCTAATAAGGTGTGGTCTGTTTGTCTGAACAAAGTGCTAGACTTTCTGGAGTGATA  
ATCTGGTGACAAATATTCTCTCTGTAGCTGTAAGCAAGTCACTTAATCTTTCTACCTCTTTT  
TTCTATCTGCCAAATTGAGATAATGATACTTAACCAGTTAGAAGAGGTAGTGTGAATATTAA  
TTAGTTTATATTACTCTTATTCTTTGAACATGAACATATGCCTATGTAGTGTCTTTATTTGCT  
CAGCTGGCTGAGACACTGAAGAAGTCACTGAACAAAACCTACACACGTACCTTCATGTGATT  
CACTGCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACACACATACCTTCAT  
GTGGTTCAGTGCCCTTCCTCTCTCTACCAGTCTATTTCCACTGAACAAAACCTACGCACATAC  
CTTCATGTGGCTCAGTGCCCTTCCTCTCTCTACCAGTCTATTTCCATTCTTTCAGCTGTGTCT  
GACATGTTTGTGCTCTGTTCCATTTTAAACAACCTGCTCTTACTTTTCCAGTCTGTACAGAATG  
CTATTTCACTTGAGCAAGATGATGTAATGGAAAGGGTGTGGCACTGGTGTCTGGAGACCTG  
GATTTGAGTCTTGGTGCTATCAATCACCGTCTGTGTTTGAGCAAGGCATTTGGCTGCTGTAA  
GCTTATTGCTTCATCTGTAAGCGGTGGTTTGTAAATTCCTGATCTTCCCACCTCACAGTGATG  
TTGTGGGGATCCAGTGAGATAGAATACATGTAAGTGTGGTTTTGTAAATTTAAAAGTGCTAT  
ACTAAGGGAAAGAATTGAGGAATTAACCTGCATACGTTTTGGTGTGCTTTTCAAATGTTTGA  
AAATAAAAAAATGTTAAG

**FIGURE 98**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52185

><subunit 1 of 1, 211 aa, 1 stop

><MW: 22744, pI: 8.51, NX(S/T): 1

MANAGLQLLGFILAF LGWIGAIVSTALPQWRIYSYAGDNIVTAQAMY EGLWMSCVSQSTGQI  
QCKVFDSLNLSS TLQATRALMVVGILLGVIAIFVATVGMKCMKCLEDDDEVQKMRMAVIGGA  
IFLLAGLAILVATAWYGNRIVQEFYDPMTFVNARYEFGQALETGWAAASLCLLGALLCCSC  
PRKTTSYPTPRPYPKPAPSSGKD YV

**Important features:****Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-102, 118-142 and 161-187

**N-glycosylation site.**

amino acids 72-75

**PMP-22 / EMP / MP20 family proteins**

amino acids 70-111

**ABC-2 type transport system integral membrane protein**

amino acids 119-133

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**FIGURE 99**

TTCTGGCCAAACCCGGGGCTNCAGCTGTTGGGCTTCATCTCGCCTTCCTGGGATGGATCGGC  
GCCATCNTCACACTGCCCTTCCCCAGTGGAGGATTTTACTCCCTATGCTGGCGACAACATCG  
TGACCGCCCAGCCCATGTACGAGGGGCTGTGGATGTCCNGCGTGTTCGCAGAGCACCGGGCAG  
ATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCCGTGC  
CTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGA  
AGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGC  
GCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAAN  
CNTTCAACANTTCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCA  
GGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCT  
GTTCCCTGTCCC

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**FIGURE 100**

ACCCTTGACCCAACGCGGGCCCCCGACCGNTTCATGGCCAAACGCGGGNCTCCAGCTGTTGG  
GCTTCATTCTCCCCTTCCTGGGATGGACCGGCGCCCATCNTCAGCACTGCCCTGCCCCAGTG  
GAGGATTTACTCCTATNCCGGCNACAACATCGTGACCGCCCAGGCCNTGTACGAGGGGCTGT  
GGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCCTTGCT  
GAATCTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGTGGTTGGCATCCTCCTGGGAG  
TGATAGCAATCTTNNTGGCCACCGTTGTNNNTGAAGTGTATGAAGTGCTTGGAAGACGATGA  
GGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTA  
TTTtagTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTATGACCCTATGACCGA

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**FIGURE 101**

GGGCCC GACCATTATCCAACCGGGNTCACTGTTGGCTCATCTCCCTCCTGGATGAANCGCGC  
CATCNTCAGACTCCCTGCCCCATGGAGATTTNNCCTATGCTGGCGACAACATCNTGACCCCC  
AGCCATGTACGAGGGGCTTTGAACGTCNGCGTGTGCGAGANCACCGGGCAGATCCAGTGCAA  
AGTCTTTGACTCCTTGCTGAATCTGNGCAGCACATTGCAGCAACCCNTGCCCTGATGGTGGT  
TGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGT  
GCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTT  
CTTGCAGGTCTGGCTATTTNNNGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAAT  
TCTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGC  
TGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCTCCTGCGA

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**FIGURE 102**

ATTCTCCCCTCCTGGATGGATCGCNCCACCGTCACATTGCCTTCCCCCANTGGAGGATTNAC  
TCCTATGCTGGCGACAACATCGTGACCCCCCAGGCCATTTACCGAGGGGGCTTTGGATGTCNT  
GCNTGTCGCAGAGCACCGGGCAGATCCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAG  
CAGCACATTGCAAGCAACCCGTGCCTTGATGGGGTTGGCATCCTCCTGGGAGTGATAGCAAC  
CTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTGAAGACGATGAGGTGCCAGAAG  
ATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTGTTGCAGGTCTGGCTATTTTAGTNGC  
CACAGCATGGTATGGCAATAGANTNNTTCNNGNNNTCTATGACCCTATGACCCCAGTCAATG  
CCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTG  
GGAGGTGCCCTACTTTGCTGTTTCCTGTCCC

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**FIGURE 103**

AGAGCACCGGCAGATCCCAGTNCAAAGTCTTTGACCCTTGCTGAATCTGAGCAGCACATTNC  
AAGCAACCCCTTGCCTTGAAGGTGGTTGNCATCCCCCCTGGGAGTGAATAGCAATCTTTGTG  
GCCACCGTTGGCATGAAGTNTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGACAGGTCTGGCTATTTTAGTNNCCACAGCAT  
GGTATGGCAATAGNATNNTTCGNGGNTTCTATGACCCTATGACCCCAGTCAATGCCAGGTAC  
GAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTGC  
CCTACTTTGCTGTTCTGTCCCGAA

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**FIGURE 104**

AGCAATGCCCTGCCCCCAGTGGAGGATTAATTCCTATGNTGGGGACAACATTGTGACNGCCC  
AGGCCATGTACGGGGGGCTGTGGATGTCCTGCGTGTCGCAGAGCACCGGGCAGATCCAGTGC  
AAAGTNTTTGACTCCTTGCTGAATTTGAGCAGCACATTGCAAGCAACCCGTGCCTTGATGGT  
GGTTGGCATCTTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTGGNAATGAAGTGTATGA  
AGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTT  
CTTNTTGCAGGTCTGGCTATTTTAGTTGCCACAGCATGGTATGGCAATAGAATNGTTCAAGA  
ATTTTATGACCCTATGACCCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTTTNTTCACTG  
GCTGGGCTGCTGCTTNTTCTGCCTTNTGGGAGGTGCCCTANTTTGCTGTTCTGCGAACC

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**FIGURE 105**

TCATAGGGGGGCGCGATATTTTTCTTGCAGGTNTGGTTATTTTAGTTGCCACAGCATGGTA  
TGGCAATAGAATCGTTCAAGAATTNTATGACCCTATGACCCAGTCAATGCCAGGTACGAAT  
TTGGTCAGGCTCTNTTCACTGGNTGGGCTGCTGCTTCTNTNNGCCTTNTGGGAGGTGCCCTA  
CTTTGCTGTTCTG

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**FIGURE 106**

TTCCTGGGATGGATCCGCCCCCATCNTCACATGCCCTGCCCCNTGGAGATTTACNCCTATGC  
TGGCGAACAACATCNTGACCGCCCAGGCCATGTACGAGGGGCTGTGGAATGTCCTGCGTGTC  
CCAGAGCACCGGGCAGATCCAGTGCAAAGTCTTTGACTCCTTGCTGAATCTGAGCAGCACAT  
TGCAAGCAACCNTGCCTTGATGGTGGTTGGCATCCTCCTGGGAGTGATAGCAATCTTTGTGG  
CCACCGTTGGCATGAAAGTGTATGAAGTGCTTGGAAGACGATGAGGTGCAGAAGATGAGGAT  
GGCTGTCATTGGGGGCGCGATATTTCTTCTTGCAGGTCTGGCTATTTTAGNNGCCACAGCAT  
GGTATGGCAATCAGACCCNNTCANAACTCTATGACCCTATGACCCCAGTCAATGCCAGGTA  
CGAATTTGGTCAGGCTCTCTTCACTGGCTGGGCTGCTGCTTCTCTCTGCCTTCTGGGAGGTG  
CCCTACTTTGCTGTTCCTGTCCCCGAAAAACAACCTCTTACCCACG

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**FIGURE 107**

CGGGGCTGCAGCTGTTGGGCTTCATCTCGCTTCCTGGGATGGAATCGGCGCCATCGTCAGCA  
CTGCCCTGCCCCATGGAGGATTTACTCNTATGCTGGCGACAACATCGTGACCNCCCAGGCCA  
TGTACGAGGGGCTGTGGATGTCNGCGTGTGCGCAGAGCACCGGGCAGATCCAGTGCAAAGTCT  
TTGACTCCTTGCTGAATCTGAGCAGCACATTGCAAGCAACCNCGCCTTGATGGTGGTTGGCA  
TCCTCCTGGGAGTGATAGCAATCTTTGTGGCCACCGTTGGCATGAAGTGTATGAAGTGCTTG  
GAAGACGATGAGGTGCAGAAGATGAGGATGGCTGTCATTGGGGGCGCGATATTTCTTCTTGC  
AGGTCTGGCTATTTNTAGTTGCCACAGCATGGTATGGCAATAGAATCGTTCAAGAATTCTAT  
GACCCTATGACCCAGTCAATGCCAGGTACGAATTTGGTCAGGCTCTCTTCACTGGCTGGGC  
TGCTGCTTCTCTCTGCCTTCTGGGAGGTGCCCTACTTTGCTGTTCCCTGCGAA

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**FIGURE 108**

GCGTGCCGTCAGCTCGCCGGGCACCGCGGCCCTCGCCCTCGCCCTCCGCCCCCTGCGCCTGCAC  
CGCGTAGACCGACCCCCCCCCCTCCAGCGCGCCACCCGGTAGAGGACCCCCGCCCCGTGCCCCG  
ACCGGTCCCCGCCTTTTTGTAAACTTAAAGCGGGCGCAGCATTAAAGCTTCCCGCCCCGGT  
GACCTCTCAGGGGTCTCCCCGCCAAAGGTGCTCCGCCGCTAAGGAACATGGCGAAGGTGGAG  
CAGGTCCTGAGCCTCGAGCCGCAGCACGAGCTCAAATTCGAGGTCCCTTCACCGATGTTGT  
CACCACCAACCTAAAGCTTGGCAACCCGACAGACCGAAATGTGTGTTTTAAGGTGAAGACTA  
CAGCACCACGTAGGTACTGTGTGAGGCCCAACAGCGGAATCATCGATGCAGGGGCCTCAATT  
AATGTATCTGTGATGTTACAGCCTTTCGATTATGATCCCAATGAGAAAAGTAAACACAAGTT  
TATGGTTCAGTCTATGTTTGCTCCAACCTGACACTTCAGATATGGAAGCAGTATGGAAGGAGG  
CAAAACCGGAAGACCTTATGGATTCAAACTTAGATGTGTGTTTGAATTGCCAGCAGAGAAT  
GATAAACACATGATGTAGAAATAAATAAAATTATATCCACAACCTGCATCAAAGACAGAAAC  
ACCAATAGTGTCTAAGTCTCTGAGTTCTTCTTTGGATGACACCGAAGTTAAGAAGGTTATGG  
AAGAATGTAAGAGGCTGCAAGGTGAAGTTCAGAGGCTACGGGAGGAGAACAAGCAGTTCAG  
GAAGAAGATGGACTGCGGATGAGGAAGACAGTGCAGAGCAACAGCCCCATTTACAGCATTAGC  
CCCAACTGGGAAGGAAGAAGGCCTTAGCACCCGGCTCTTGGCTCTGGTGGTTTTGTTCTTTA  
TCGTTGGTGTAATTATTGGGAAGATTGCCTTGTAGAGGTTAGCATGCACAGGATGGTAAATTG  
GATTGGTGGATCCACCATATCATGGGATTTAAATTTATCATAACCATGTGTAAAAAGAAATT  
AATGTATGATGACATCTCACAGGTCTTGCCTTTAAATTACCCCTCCCTGCACACACATACAC  
AGATACACACACACAAATATAATGTAACGATCTTTTAGAAAGTTAAAAATGTATAGTAACTG  
ATTGAGGGGGAAAAAGAATGATCTTTATTAATGACAAGGGAAACCATGAGTAATGCCACAAT  
GGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGCTGGATTACCTC  
TCTTAAATGACACCCTTCCTCGCTGTTGGTGCTGGCCCTTGGGGAGCTGGAGCCCAGCAT  
GCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCAGGCTG  
CTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGA  
AGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTGTGT  
TGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGACCAA  
GCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACCTGTTATTCAGAGATGTTTAATGCATA  
TTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGC  
TGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTGTGGGCTCCTCT  
GTCTCTGGAGAGTCTGGTCATGTGGAGGTGGGGTTTATTGGGATGCTGGAGAAGAGCTGCCA  
GGAAGTGTTTTTTCTGGGTGAGTAAATAACAACCTGTCATAGGGAGGGAAATTCTCAGTAGTG  
ACAGTCAACTCTAGGTTACCTTTTTTAAATGAAGAGTAGTCAGTCTTCTAGATTGTTCTTATA  
CCACCTCTCAACCATTAACCTCACACTTCCAGCGCCCAGGTCCAAGTCTGAGCCTGACCTCCCC  
TTGGGGACCTAGCCTGGAGTCAGGACAAATGGATCGGGCTGCAGAGGGTTAGAAGCGAGGGC  
ACCAGCAGTTGTGGGTGGGGAGCAAGGGAAGAGAGAACTCTTCAGCGAATCCTTCTAGTAC  
TAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATAAAAGACCAACCCAGTTCTGTTTGA  
CTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCCCCAAAATTAAGAAAA

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**FIGURE 109**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53977

<subunit 1 of 1, 243 aa, 1 stop

<MW: 27228, pI: 7.43, NX(S/T): 2

MAKVEQVLSLEPQHELKFERGPFSTDVVTNLKLGNPTRNVCFKVKTTAPRRYCVRPNSGIID  
AGASINVSVMLOPFDYDPNEKSKHKFMVQSMFAPTDTSMEAVWKEAKPEDLMDSKLRVFE  
LPAENDKPHDVEINKIISTTASKTETPIVSKSLSSSLDDTEVKKVMEECKRLQGEVQRLREE  
NKQFKEEDGLRMRKTVQSNPISALAPTGKEEGLSTRLLALVVLFFIVGVIIGKIAL

**Important features:****Transmembrane domain:**

amino acids 224-239

**N-glycosylation site.**

amino acids 68-71

**N-myristoylation site.**

amino acids 59-64, 64-69 and 235-240

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**FIGURE 110**

GTCAGTCTTCTAGATTGTCCTTATCCACCTTTCAACCANTACTCACATTTTCNAGCGCCCAG  
GTCCANGTCTGAGCCTGACTTCCCCTTGGGGACCTAGCCTGGAGTCAGGACAATGGNTCGGG  
CTGCAGAGGNTTAGAAGCGAGGGCACCAGCAGTTTTGGGTGGGGAGCAAGGGNNGAGAGAAA  
CTCTTCAGCGAATCCTTCTAGTACTAGTTGAGAGTTTGACTGTGAATTAATTTTATGCCATA  
AAAGACNAACCCAGTTCTGTTTGACTATGTAGCATCTTGAAAAGAAAAATTATAATAAGCC  
CCAAAATTAAGAATTCTTTTGTCAATTTTGTACATTTGCTCTATGGGGGGAATTATTATTTT  
ATCATTTTTATTATTTTGCCATTGGAAGGTAACTTTAAAATGAGC

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**FIGURE 111**

TATTGTAAAGGCCATTTTAAACCATTTGGTAGGCCTTGGTACATGATGCTGGATTACCTCCTT  
AAATGACACCNTTCCTCGCCTGTTGGTGCTGGCCNTTGGGGAGCTGGAGCCCCAGCATGCTG  
GGGAGTGCGGTCAGCTCCACACAGTAGTCCCCACGTGGCCCACTCCCGGCCCCAGGCTGCTTT  
CCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTGATGAACAGAGTCAGAAGCC  
CAAAGGAATTGCCACTGTGGCAGCATCAGACGTA CTGTCATAAGTGAGAGGCGTGTGTTGA  
CTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACCTTAAAGGGACCAAGCT  
AAATTGTATTGGTTCATGTAGTGAAGTCAAAC TGTATTTCAGAGATGTTTAATGCATATTTA  
ACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAATGCTGCG  
TGCTGCTGAACTCTGTTGGGTGAACTGGTATTGCTGCTGGAGGGCTG

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**FIGURE 112**

CCCTGGTGGTTTTGTTCTTTAATTCGTTGGTGTAATTNTTGGGAAGATTGCTTGTAGAGGTA  
GNATGCACCNGGCTGGTAAATTGGATTGGTGGATCCACCATATCCATGGGATTTAAATTTAT  
CATAACCATGTGTAAAAAGAAATTAATGTATGATGACATNTCACAGGTATTGCCTTTAAATT  
ACCCATCCCTGNANACACATACACAGATACACANANACAAATNTAATGTAACGATNTTTTAG  
AAAGTTAAAAATGTATAGTAAC

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FIGURE 113

GGTGGCCCATTCCTCGGCCAGGCTGCTTTCCGGTNTTCAGTTCTGTCCAAGCCATCAGCTCC  
TTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATNAGACGTAC  
TTGTNATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGT  
GCTTTGTTTCANTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAAGTGA  
TTATTCAGAGATGTTTAAATGCATATTTAANTTATTTAATGTATTTNATNTCATGTTTTCTTA  
TTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAANTNTGTTGGGTGAACTGGTATTGC  
TGCTGGAGGGCTGTGGGCTCCTCTGTCTTTGGAGAGTCTGGTCATGTGGAGGTGGG

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**FIGURE 114**

TGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGACTTGATGAACAGAGTC  
AGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACGTACTCGTCATAAGTGAGAGGCGTG  
TGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTCACTTAAAGGGAC  
CAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAACGTGTTATTCAGAGATGTTTAATGC  
ATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTCTTATTGTCACAAGAGTACAGTTAA  
TGCTGCGTGC

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**FIGURE 115**

AAACCTTTAAAAGTTGAGGGGAAAAGAATGATCCTTTATTAATGACAAGGGAAACCN TGNGT  
AATGCCACAATGGCATATTGTAAATGTCATTTTAAACATTGGTAGGCCTTGGTACATGATGC  
TGGATTACCTCTCTTAAAATGACACCCTTCCTCGCCTGTTGGTGCTGGCCCTTGGGGAGCTN  
GAGCCCAGCATGCTGGGGAGTGCGGTCTGCTCCACACAGTAGTCCCCANGTGGCCCANTCCC  
GGCCCAGGCTGCTTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGCTCCTTGGGANTGATGA  
ACAGAGTCAGAAGCCCCAAAGGAATTGCANTGTGGCAGCATCAGANGTANTNGTCATAAGTGA  
GAGGCGTGTGTTGANTGATTGACCCAGCGCTTTGGAAATAAATGGCAGTGCTTTGTTTCANTT  
AAAGGGNCCAAGNTAAATTTGTATTGGTTCATGTAGTGAAGTCAAANTGTTATTCAGAGATG  
TTAATGCATATTTAANTTATTTAATGTATTTTCATNTCATGTTTTCTTATTGTCACAAGGGT  
ACAGTTAATGCTGCGTGCTGCTGAANTCTGTTGGGTGAANTGGTATTGCTG

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**FIGURE 116**

GGCCCTTGGGGAGCTGGAGCCCAGCATGCTGGGGAGTGCGGTCAGCTCCACACAGTAGTCCC  
CACGTGGCCCACTCCCGGCCAGGCTGCTTCCGTGTCTTCAGTTCTGTCCAAGCCATCAGC  
TCCTTGGGACTGATGAACAGAGTCAGAAGCCCAAAGGAATTGCACTGTGGCAGCATCAGACG  
TACTCGTCATAAGTGAGAGGCGTGTGTTGACTGATTGACCCAGCGCTTTGGAAATAAATGGC  
AGTGCTTTGTTCACTTAAAGGGACCAAGCTAAATTTGTATTGGTTCATGTAGTGAAGTCAAA  
CTGTTATTCAGAGATGTTTAATGCATATTTAACTTATTTAATGTATTTTCATCTCATGTTTTT  
TTATTGTCACAAGAGTACAGTTAATGCTGCGTGCTGCTGAACTCTGTTGGGTGAACTGGTAT  
TGCTGCTGGAGGGCTGTGGGCTCCTCTGTCTCTGGAGAGTCTGGTCATGTGGAGGTGGG

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**FIGURE 117**

GCGAGCTCCGGGTGCTGTGGCCCCGGCCTTGGCGGGGCGGCCTCCGGCTCAGGCTGGCTGAGA  
GGCTCCCAGCTGCAGCGTCCCCGCCCCGCCTCCTCGGGAGCTCTGATCTCAGCTGACAGTGCC  
CTCGGGGACCAAACAAGCCTGGCAGGGTCTCACTTTGTTGCCCAGGCTGGAGTTCAGTGCCA  
TGATCATGGTTTACTGCAGCCTTGACCTCCTGGGTTCAGCGATCCTGCTGAGTAGCTGGGA  
CTACAGGACAAAATTAGAAGATCAAAATGGAAATATGCTGCTTTGGTTGATATTTTTCACC  
CCTGGGTGGACCCTCATTGATGGATCTGAAATGGAATGGGATTTTATGTGGCACTTGAGAAA  
GGTACCCCGGATTGTGAGTGAAAGGACTTTCCATCTCACCAGCCCCGCATTTGAGGCAGATG  
CTAAGATGATGGTAAATACAGTGTGTGGCATCGAATGCCAGAAAGAACTCCCAACTCCCAGC  
CTTTCTGAATTGGAGGATTATCTTTCCTATGAGACTGTCTTTGAGAATGGCACCCGAACCTT  
AACCAGGGTGAAAGTTCAAGATTTGGTTCTTGAGCCGACTCAAATATCACCACAAAGGGAG  
TATCTGTTAGGAGAAAGAGACAGGTGTATGGCACCGACAGCAGGTTTCAGCATCTTGGACAAA  
AGGTTCTTAACCAATTTCCCTTTCAGCACAGCTGTGAAGCTTTCCACGGGCTGTAGTGGCAT  
TCTCATTTCCCCTCAGCATGTTCTAACTGCTGCCCACTGTGTTTCATGATGGAAAGGACTATG  
TCAAAGGGAGTAAAAAGCTAAGGGTAGGGTTGTTGAAGATGAGGAATAAAAGTGGAGGCAAG  
AAACGTCGAGGTTCTAAGAGGAGCAGGAGAGAAGCTAGTGGTGGTGACCAAAGAGAGGGTAC  
CAGAGAGCATCTGCAGGAGAGAGCGAAGGGTGGGAGAAGAAGAAAAAATCTGGCCGGGGTC  
AGAGGATTGCCGAAGGGAGGCCTTCCTTTTCAAGTGGACCCGGGTCAAGAATACCCACATTCCG  
AAGGGCTGGGCACGAGGAGGCATGGGGGACGCTACCTTGGACTATGACTATGCTCTTCTGGA  
GCTGAAGCGTGCTCACAAAAGAAATACATGGAACCTTGAATCAGCCCAACGATCAAGAAAA  
TGCCTGGTGGAATGATCCACTTCTCAGGATTTGATAACGATAGGGCTGATCAGTTGGTCTAT  
CGGTTTTTGCAGTGTGTCCGACGAATCCAATGATCTCCTTTACCAATACTGCGATGCTGAGTC  
GGGCTCCACCGGTTCCGGGGTCTATCTGCGTCTGAAAGATCCAGACAAAAAGAATTGGAAGC  
GCAAAATCATTGCGGTCTACTCAGGGCACCAGTGGGTGGATGTCCACGGGGTTCAGAAGGAC  
TACAACGTTGCTGTTTCGCATCACTCCCCTAAAATACGCCCAGATTTGCCTCTGGATTACCGG  
GAACGATGCCAATTGTGCTTACGGCTAAACAGAGACCTGAAACAGGGCGGTGTATCATCTAAA  
TCACAGAGAAAACCAGCTCTGCTTACCGTAGTGAGATCACTTCATAGGTTATGCCTGGACTT  
GAACTCTGTCAATAGCATTTCAACATTTTTTCAAATCAGGAGATTTTCGTCCATTTAAAAAA  
TGTATAGGTGCAGATATTGAACTAGGTGGGCACCTTCAATGCCAAGTATATACTCTTCTTTA  
CATGGTGATGAGTTTCATTTGTAGAAAAATTTTGTGCTTCTTAAAAATTAGACACACTTT  
AAACCTTCAAACAGGTATTATAAATAACATGTGACTCCTTAATGGACTTATTCTCAGGGTCC  
TACTCTAAGAAGAATCTAATAGGATGCTGGTTGTGTATTAAATGTGAAATTGCATAGATAAA  
GGTAGATGGTAAAGCAATTAGTATCAGAATAGAGACAGAAAGTTACAACACAGTTTGTACTA  
CTCTGAGATGGATCCATTCAGCTCATGCCCTCAATGTTTATATTGTGTTATCTGTTGGGTCT  
GGGACATTTAGTTTAGTTTTTTTTGAAGAATTACAAATCAGAAGAAAAAGCAAGCATTATAAA  
CAAACTAATAACTGTTTTACTGCTTTAAGAAATAACAATTACAATGTGTATTATTTAAAAA  
TGGGAGAAATAGTTTGTCTATGAAATAAACCTAGTTTAGAAATAGGGAAGCTGAGACATTT  
TAAGATCTCAAGTTTTTATTTAACTAATACTCAAATATGGACTTTTCATGTATGCATAGGG  
AAGACACTTCACAAATTATGAATGATCATGTGTTGAAAGCCACATTATTTTATGCTATACAT  
TCTATGTATGAGGTGCTACATTTTTAGGACAAAGAATTCTGTAATCTTTTTCAAGAAAGAGT  
CTTTTTCTCCTTGACAAAATCCAGCTTTTGTATGAGGACTATAGGGTGAATTCTCTGATTAG  
TAATTTTAGATATGTCCTTTCCTAAAAATGAATAAAATTTATGAATATGA

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**FIGURE 118**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57253

<subunit 1 of 1, 413 aa, 1 stop

<MW: 47070, pI: 9.92, NX(S/T): 3

MENMLLWLIFFTPGWTLIDGSEMEWDFMWHLRKVPRIVSERTFHLTSPAFAEADAKMMVNTVC  
GIECQKELPTPSLSELEDYLSYETVFENGTRTLTRVKVQDLVLEPTQNITTKGVSVRRKRQV  
YGTDSRFSILDKRFLTNFPFSTAVKLSTGCSGILISPQHVLTAAHCVHDGKDYVKGSKKLRV  
GLLKMRNKSGGKKRRGSKRSRREASGGDQREGTREHLQERAKGRRRKSGRGQRIAEGRPS  
FQWTRVKNTHIPKGWARGGMGDATLDYDYALLELKRAHKKKYMELGISPTIKKMPGGMIHFS  
GFDNDRADQLVYRFCSVSDSNLLYQYCDAESGSTGSGVYLRKDPDKKNWKRKIIAVYSG  
HQWVDVHGVQKDYNVAVRITPLKYAQICLWIHGNDANCAYG

**Important features:****Signal peptide:**

amino acids 1-16

**N-glycosylation sites.**

amino acids 90-93, 110-113 and 193-196

**Glycosaminoglycan attachment site.**

amino acids 236-239

**Serine proteases, trypsin family, histidine active site.**

amino acids 165-170

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**FIGURE 119**

AATGTGAGAGGGGCTGATGGAAGCTGATAGGCAGGACTGGAGTGTTAGCACCAGTACTGGAT  
GTGACAGCAGGCAGAGGAGCACTTAGCAGCTTATTCAGTGTCCGATTCTGATTCCGGCAAGG  
ATCCAAGCATGGGAATGCTGCCGTCGGGCAACTCCTGGCACACTGCTCCTCTTTCTGGCTTTC  
CTGCTCCTGAGTTCCAGGACCGCACGCTCCGAGGAGGACCGGGACGGCCTATGGGATGCCTG  
GGGCCCATGGAGTGAATGCTCACGCACCTGCGGGGGAGGGGCCTCCTACTCTCTGAGGCGCT  
GCCTGAGCAGCAAGAGCTGTGAAGGAAGAAATATCCGATACAGAACATGCAGTAATGTGGAC  
TGCCCACCAGAAGCAGGTGATTTCCGAGCTCAGCAATGCTCAGCTCATAATGATGTCAAGCA  
CCATGGCCAGTTTTATGAATGGCTTCCTGTGTCTAATGACCCTGACAACCCATGTTCACTCA  
AGTGCCAAGCCAAAGGAACAACCCTGGTTGTTGAACTAGCACCTAAGGTCTTAGATGGTACG  
CGTTGCTATACAGAATCTTTGGATATGTGCATCAGTGGTTTATGCCAAATTGTTGGCTGCGA  
TCACCAGCTGGGAAGCACCGTCAAGGAAGATAACTGTGGGGTCTGCAACGGAGATGGGTCCA  
CCTGCCGGCTGGTCCGAGGGCAGTATAAATCCCAGCTCTCCGCAACCAAATCGGATGATACT  
GTGGTTGCACTTCCCTATGGAAGTAGACATATTCGCCTTGTCTTAAAAGGTCCTGATCACTT  
ATATCTGGAAACCAAACCCTCCAGGGGACTAAAGGTGAAAACAGTCTCAGCTCCACAGGAA  
CTTTCCTTGTGGACAATTCTAGTGTGGACTTCCAGAAATTTCCAGACAAAGAGATACTGAGA  
ATGGCTGGACCACTCACAGCAGATTTCAATTGTCAAGATTCGTAACCTCGGGCTCCGCTGACAG  
TACAGTCCAGTTCATCTTCTATCAACCCATCATCCACCGATGGAGGGAGACGGATTTCTTTC  
CTTGCTCAGCAACCTGTGGAGGAGGTTATCAGCTGACATCGGCTGAGTGCTACGATCTGAGG  
AGCAACCGTGTGGTTGCTGACCAATACTGTCACTATTACCCAGAGAACATCAAACCCAAACC  
CAAGCTTCAGGAGTGCAACTTGGATCCTTGTCCAGCCAGTGACGGATACAAGCAGATCATGC  
CTTATGACCTCTACCATCCCCCTTCCTCGGTGGGAGGGCCACCCCATGGACCGCGTGCTCCTCC  
TCGTGTGGGGGGGGCATCCAGAGCCGGGCAGTTTCCTGTGTGGAGGAGGACATCCAGGGGCA  
TGTCACCTTCAGTGGAAGAGTGGAATGCATGTACACCCCTAAGATGCCCATCGCGCAGCCCT  
GCAACATTTTTGACTGCCCTAAATGGCTGGCACAGGAGTGGTCTCCGTGCACAGTGACATGT  
GGCCAGGGCCTCAGATACCGTGTGGTCCTCTGCATCGACCATCGAGGAATGCACACAGGAGG  
CTGTAGCCCAAAAACAAAGCCCCACATAAAAGAGGAATGCATCGTACCCACTCCCTGCTATA  
AACCCAAAGAGAACTTCCAGTCGAGGCCAAGTTGCCATGGTTCAAACAAGCTCAAGAGCTA  
GAAGAAGGAGCTGCTGTGTCAGAGGAGCCCTCGTAAGTTGTAAAAGCACAGACTGTTCTATA  
TTTGAAACTGTTTTGTTTAAAGAAAGCAGTGTCTCACTGGTTGTAGCTTTCATGGGTTCTGA  
ACTAAGTGTAATCATCTCACCAAAGCTTTTTGGCTCTCAAATTAAAGATTGATTAGTTTCAA  
AAAAAAAAA

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**FIGURE 120**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58847

<subunit 1 of 1, 525 aa, 1 stop

<MW: 58416, pI: 6.62, NX(S/T): 1

MECCRRATPGTLLLFLAFLLLSSRTARSEEDRDGLWDAWGPWSECSRTC GGGASYSLRRCLS  
SKSCEGRNIRYRTCSNVDCPPEAGDFRAQQCSAHNDVKHHGQFYEWLPVSNPDNPCSLKCQ  
AKGTTLVVELAPKVLDGTRCYTESLDMCISGLCQIVGCDHQLGSTVKEDNCGVCNGDGSTCR  
LVRGQYKSQLSATKSDDTVVALPYGSRHIRLV LKGPDHLYLETKTLQGTKGENSLSSSTGTFL  
VDNSSVDFQKFPDKEILRMAGPLTADFIVKIRNSGSADSTVQFIFYQPIIHRWRETDFFP  
ATCGGGYQLTSAECYDLRSNRVVADQYCHYYPENIKPKPKLQECNLDPCPASDGYKQIMPYD  
LYHPLPRWEATPWTACSSSSCGGGIQSRAVSCVEEDIQGHVTSVEEWKCMYTPKMPIAQPCNI  
FDCPKWLAQEWSPCTVTCGOGLRYRVVLCIDHRGMHTGGCSPKTKPHIKEECIVPTPCYKPK  
EKL PVEAKLPWFKQAQEELEEGA AVSEEPS

**Important features:****Signal peptide:**

amino acids 1-25

**N-glycosylation site.**

amino acids 251-254

**Thrombospondin 1**

amino acids 385-399

**von Willebrand factor type C domain proteins**

amino acids 385-399, 445-459 and 42-56

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**FIGURE 121**

CGGACGCGTGGGCGGCGGCTGCGGAACTCCCGTGGAGGGGCGGCTGGGCCCTCGGGCCTGAC  
AGATGGCGAGTGGCCACTGCGGCGGCAGTACTGGCCGCTCTGGGCGGGGCGCTGTGGCTGGCG  
GCCCCCGGTTTCGTGGGGCCCAGGGTCCAGCGGCTGCGCAGAGGGCGGGGACCCCGGCCTCAT  
GCACGGGAAGACTGTGCTGATCACCGGGGCGAACAGCGGCCTGGGCCGCGCCACGGCCGCCG  
AGCTACTGCGCCTGGGAGCGCGGGTGATCATGGGCTGCCGGGACCGCGCGCGCGCCGAGGAG  
GCGGCGGGTCAGCTCCGCCGCGAGCTCCGCCAGGCCGCGGAGTGCGGCCAGAGCCTGGCGT  
CAGCGGGGTGGGCGAGCTCATAGTCCGGGAGCTGGACCTCGCCTCGCTGCGCTCGGTGCGCG  
CCTTCTGCCAGGAAATGCTCCAGGAAGAGCCTAGGCTGGATGTCTTGATCAATAACGCAGGG  
ATCTTCCAGTGCCCTTACATGAAGACTGAAGATGGGTTTGAGATGCAGTTCGGAGTGAACCA  
TCTGGGGCACTTTCTACTCACCAATCTTCTCCTTGGACTCCTCAAAAGTTCAGCTCCCAGCA  
GGATTGTGGTAGTTTCTTCCAACTTTATAAATACGGAGACATCAATTTTGATGACTTGAAC  
AGTGAACAAAGCTATAATAAAAGCTTTTGTATAGCCGGAGCAAACCTGGCTAACATTCTTTT  
TACCAGGGAACTAGCCCGCCGCTTAGAAGGCACAAATGTCACCGTCAATGTGTTGCATCCTG  
GTATTGTACGGACAAATCTGGGGAGGCACATACACATTCCACTGTTGGTCAAACCACTCTTC  
AATTTGGTGTGATGGGCTTTTTTTCAAACCTCCAGTAGAAGGTGCCCAGACTTCCATTTATTT  
GGCCTCTTCACCTGAGGTAGAAGGAGTGTCAGGAAGATACTTTGGGGATTGTAAAGAGGAAG  
AACTGTTGCCCAAAGCTATGGATGAATCTGTTGCAAGAAAACCTCTGGGATATCAGTGAAGTG  
ATGGTTGGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTTTATAAACTGCATATCAG  
TTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACTTGAAGAAAAGAATTTTG  
ATATTGGAATAGCCTGCTAAGAGGTACATGTGGGTATTTTGGAGTTACTGAAAAATTATTTT  
TGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGTAAGTATAATGAATAATAA  
GTACAATGAAAAATAACAATTATATTGTAAAATTATAACTGGGCAAGCATGGATGACATATTA  
ATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTTTTCAAGTATCTTTGAGTT  
TCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTGTTGTGTGGAAATTATCTGC  
CTGGTGTGTGCACACAAGTCTTACTTGAATAAAATTTACTGGTAC

**FIGURE 122**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58747

<subunit 1 of 1, 336 aa, 1 stop

<MW: 36865, pI: 9.15, NX(S/T): 2

MAVATAAAVLAAALGGALWLAARRFVGPRVQRLRRGGDPGLMHGKTVLITGANSGLGRATAAE  
LLRLGARVIMGCRDRARAEAAAGQLRREL RQAAECGPEPGVSGVGELIVRELDLASLRSVRA  
FCQEMLQEEPRLDVLINNAGIFQCPYMKTEDGFEMQFGVNH LGHFLLTNLLLGLLKSSAPSR  
IVVSSKLYKYGDINFDDLNSEQSYNKSFCYSRSKLANILFTRELARRLEGTVNVTNVLHPG  
IVRTNLGRHIHIPLLVKPLFNLVSWAFFKTPVEGAQTSIYLASSPEVEGVSGRYFGDCKEEE  
LLPKAMDESVARKLWDISEVMVGLLK

**Important features:****Signal peptide:**

amino acids 1-21

**Short-chain alcohol dehydrogenase family protein**

amino acids 134-144, 44-56 and 239-248

**N-glycosylation site.**

amino acids 212-215 and 239-242

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**FIGURE 123**

GGGGATTGTAAAGAGGAAGNACTGTGCCCAAAGNTATGGATGAATCTGTTGCAAGAAAATTN  
TGGGATATCAGTGAAGTGATGGTTNGCCTGCTAAAATAGGAACAAGGAGTAAAAGAGCTGTT  
TATAAACTGCATATCAGTTATATCTGTGATCAGGAATGGTGTGGATTGAGAACTTGTTACT  
TGAAGAAAAAGAATTTTGATATTGGAATAGCCTGNTAAGAGGNACATGTGGGTATTTTGGAG  
TTACTGAAAAATTATTTTGGGATAAGAGAATTTTCAGCAAAGATGTTTTAAATATATATAGT  
AAGTATAATGAATAATAAGTACAATGAAAAATACAATTATATTGTAAAATTATAACTGGGCA  
AGCATGGATGACATATTAATATTTGTCAGAATTAAGTGACTCAAAGTGCTATCGAGAGGTTT  
TTCAAGTATCTTTGAGTTTCATGGCCAAAGTGTTAACTAGTTTTACTACAATGTTTGGTGTT  
TGTGTGGAAATTATCTGCCTGGCTT

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**FIGURE 124**

GAGAGGACGAGGTGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCC  
CTTTCCTAACCCAACCCAACCTAGCCCAGTCCCAGCCGCCAGCGCCTGTCCCTGTCACGGAC  
CCCAGCGTTACCATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCT  
GCTCCTGGTAACTTGGGTTTTTACTCCTGTAACAACCTGAAATAACAAGTCTTGCTACAGAGA  
ATATAGATGAAATTTTAAACAATGCTGATGTTGCTTTAGTAAATTTTTATGCTGACTGGTGT  
CGTTTCAGTCAGATGTTGCATCCAATTTTTTGAGGAAGCTTCCGATGTCATTAAGGAAGAATT  
TCCAAATGAAAATCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCC  
AGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAG  
AGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGCAACAAAAAAG  
TGACCCCATTCAGAAATTCGGGACTTAGCAGAAATCACCACCTCTTGATCGCAGCAAAAGAA  
ATATCATTGGATATTTTGAGCAAAAGGACTCGGACAACCTATAGAGTTTTTGAACGAGTAGCG  
AATATTTTGCATGATGACTGTGCCTTTCTTTCTGCATTTGGGGATGTTTCAAACCGGAAG  
ATATAGTGGCGACAACATAATCTACAAACCACCAGGGCATTCTGCTCCGGATATGGTGTACT  
TGGGAGCTATGACAAATTTTGATGTGACTTACAATTGGATTCAAGATAAATGTGTTCTCTT  
GTCCGAGAAATAACATTTGAAAATGGAGAGGAATTGACAGAAGAAGGACTGCCTTTTCTCAT  
ACTCTTTCACATGAAAGAAGATACAGAAAGTTTAGAAATATTCCAGAATGAAGTAGCTCGGC  
AATTAATAAGTGAAAAAGGTACAATAAACTTTTTACATGCCGATTGTGACAAATTTAGACAT  
CCTCTTCTGCACATACAGAAAACCTCCAGCAGATTGTCCTGTAATCGCTATTGACAGCTTTAG  
GCATATGTATGTGTTTGGAGACTTCAAAGATGTATTAATTCCTGGAAAACCTCAAGCAATTCG  
TATTTGACTTACATTCTGGAAAACCTGCACAGAGAATTCCATCATGGACCTGACCCAACTGAT  
ACAGCCCCAGGAGAGCAAGCCCAAGATGTAGCAAGCAGTCCACCTGAGAGCTCCTTCCAGAA  
ACTAGCACCCAGTGAATATAGGTATACTCTATTGAGGGATCGAGATGAGCTTTAAAACTTG  
AAAAACAGTTTGTAAGCCTTTCAACAGCAGCATCAACCTACGTGGTGGAAATAGTAAACCTA  
TATTTTCATAATTCTATGTGTATTTTTATTTTGAATAAACAGAAAGAAATTTAAAAA  
AAAAA

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**FIGURE 125**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57689

<subunit 1 of 1, 406 aa, 1 stop

<MW: 46927, pI: 5.21, NX(S/T): 0

MHPAVFLSLPDLRCSLLLLVTWVFTPVTTEITSLATENIDEILNNADVALVNFYADWCRFSQ  
MLHPIFEEASDVIKEEFPNENQVVVFARVDCDQHSDIAQRYRISKYPTLKLFRNGMMMKREYR  
GQRSVKALADYIRQQKSDPIQEIRDLAEITTLDRSKRNIIGYFEQKSDNYRVFERVANILH  
DDCAFLSAFGDVSKPERYSGDNIIYKPPGHSAPDMVYLGAMTNFDVTYNWIQDKCVPLVREI  
TFENGEELTEEGLPFLILFHMKEDTESLEIFQNEVARQLISEKGTINFLHADCDKFRHPLLH  
IQKTPADCPVIAIDSFRHMYVFGDFKDVLIPGKLKQFVFDLHSGKLHREFHHGPDPTDTAPG  
EQAQDVASSPPESSFQKLAPSEYRYTLLRDRDEL

**Important features:****Signal peptide:**

amino acids 1-29

**Endoplasmic reticulum targeting sequence.**

amino acids 403-406

**Tyrosine kinase phosphorylation site.**

amino acids 203-211

**Thioredoxin family proteins**

amino acids 50-66

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**FIGURE 126**

ATTAAGGAAGAATTTCCAAATGAAAATCAAGTAGTNTTTGCCAGAGTNGATTGTGATCAGCA  
CTCTGACATAGCCCAGAGATACAGGATAAGCAAATACCCAACCCTCAAATTGTTTCGTAATG  
GGATGATGATGAAGAGAGAATACAGGGGTCAGCGATCAGTGAAAGCATTGGCAGATTA

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**FIGURE 127**

AGAGGCCTCTCTGGAAGTTGTCCCGGGTGTTCGCCGCNGGAGCCCCGGGTCGAGAGGACNAGG  
TGCCGCTGCCTGGAGAATCCTCCGCTGCCGTCGGCTCCCGGAGCCCAGCCCTTTCCTAACCC  
AACCCAACCTAGCCCNGTCCCAGCCGCCAGCGCCTGTCCCTGTCNCGGANCCCAGCGTNACC  
ATGCATCCTGCCGTCTTCCTATCCTTACCCGACCTCAGATGCTCCCTTCTGCTCCTGGTAAC  
TTGGGTTTTTACTCCTGTAACAACTGAAATAACNNGTCTTGATACNNAGAATATAGATGAAA  
TTTTAAACNATGCTGATGTGGCTTTAGTCAATTTTTATGCTGACTGGTGTCTGTTTCAGTCAG  
ATGTGGCATCCAATTTTTTGAGGANGCTTCCGATGTCATTAAGGAAGAATTTCCAAATGAAAA  
TCAAGTAGTGTTTGCCAGAGTTGATTGTGATCAGCACTCTGACATAGCCCAGAGATACAGGA  
TAAGCAAATACCCAACCCTCAAATTGTTTCGTAATGGGATGATGATGAAGAGAGAATACAGG  
GGTCAGCGATCAGTGAAAGCATTGGCAGATTACATCAGGC

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**FIGURE 128**

GCCCACGCGTCCGATGGCGTTCACGTTGCGGGCCTTCTGCTACATGCTGGCGCTGCTGCTCA  
CTGCCGCGCTCATCTTCTTCGCCATTTGGCACATTATAGCATTTGATGAGCTGAAGACTGAT  
TACAAGAATCCTATAGACCAGTGTAATACCCTGAATCCCCTTGTA TACTCCCAGAGTACCTCAT  
CCACGCTTTCTTCTGTGTCATGTTTCTTTGTGCAGCAGAGTGGCTTACACTGGGTCTCAATA  
TGCCCCCTCTTGGCATATCATATTTGGAGGTATATGAGTAGACCAGTGATGAGTGGCCCAGGA  
CTCTATGACCCTACAACCATCATGAATGCAGATATTCTAGCATATTGTCAGAAGGAAGGATG  
GTGCAAATTAGCTTTTTTATCTTCTAGCATTTTTTTTACTACCTATATGGCATGATCTATGTTT  
TGGTGAGCTCTTAGAACAACACACAGAAGAATTGGTCCAGTTAAGTGCATGCAAAAAGCCAC  
CAAATGAAGGGATTCTATCCAGCAAGATCCTGTCCAAGAGTAGCCTGTGGAATCTGATCAGT  
TACTTTAAAAAATGACTCCTTATTTTTTAAATGTTTCCACATTTTTTGCTTGTGGAAAGACTG  
TTTTCATATGTTATACTCAGATAAAGATTTTAAATGGTATTACGTATAAATTAATATAAAAT  
GATTACCTCTGGTGTTGACAGGTTTGAACCTTGCACTTCTTAAGGAACAGCCATAATCCTCTG  
AATGATGCATTAATTA CTGACTGTCCTAGTACATTGGAAGCTTTTGTTTATAGGAACTTGTA  
GGGCTCATTTTGGTTTCATTGAAACAGTATCTAATTATAAATTAGCTGTAGATATCAGGTGC  
TTCTGATGAAGTGAAAATGTATATCTGACTAGTGGGAACTTCATGGGTTTCCTCATCTGTC  
ATGTCGATGATTATATATGGATACATTTACAAAAATAAAAAGCGGGAATTTTCCCTTCGCTT  
GAATATTATCCCTGTATATTGCATGAATGAGAGATTTCCCATATTTCCATCAGAGTAATAAA  
TATACTTGCTTTAATTCTTAAGCATAAGTAAACATGATATAAAAATATATGCTGAATTACTT  
GTGAAGAATGCATTTAAAGCTATTTTAAATGTGTTTTTATTTGTAAGACATTACTTATTAAG  
AAATTGGTTATTATGCTTACTGTTCTAATCTGGTGGTAAAGGTATTCTTAAGAATTTGCAGG  
TACTACAGATTTTCAAACTGAATGAGAGAAAATTGTATAACCATCCTGCTGTTCCCTTTAGT  
GCAATACAATAAACTCTGAAATTAAGACTC

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**FIGURE 129**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA23330

<subunit 1 of 1, 144 aa, 1 stop

<MW: 16699, pI: 5.60, NX(S/T): 0

MAFTFAAFCYMLALLLTAAALIFFAIWHIIAFDELKTDYKNPIDQCNTLNPLVLPEYLIHAFF  
CVMFLCAAEWLTGLNMPLLAYHIWRYMSRPVMSGPGLYDPTTIMNADILAYCQKEGWCKLA  
FYLLAFFYYLYGMIYVLVSS

**Important features:****Signal peptide:**

amino acids 1-20

**Type II transmembrane domain:**

amino acids 11-31

**Other transmembrane domain:**

amino acids 57-77 and 123-143

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**FIGURE 130**

ATTATAGCATTTGATGAGCTGAAGACTGATTACAAGATCCTATAGACCAGTGTAATACCCTG  
AATCCCCTTGTA CTCCCAGAGTACCTCATCCACGCTTTCTTCTGTGTCATGTTTCTTTGTGC  
AGCAGAGTGGCTTACACTGGGTCTCAATATGCCCCTCTTGGCATATCATATTTGGAGGTATA  
TGAGTAGACCAGTGATGAGTGGCCCAGGACTCTATGACCCTACAACCATCATGAATGCAGAT  
ATTCTAGCATATTGTCAGAAGGAAGGATGGTGCAAATTAGCTTTTTATCTTCTAGCATTTTT  
TTACTACCTATATGGCATGATCTATGTTTTGGTGAGCTCTTAGAACAACACACAGAAGAATT  
GGTCCAGTTAAGTGCATGCAAAAAGCCACCAAATGAAGGGATTCTATCCAGCAAGATCCTGT  
CCAAGAGTAGCCTGTGGAATCTGATCAGTTACTTTAAAAAATG

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**FIGURE 131**

CGGACGCGTGGGGGAAACCCTTCCGAGAAAACAGCAACAAGCTGAGCTGCTGTGACAGAGGG  
GAACAAGATGGCGGCGCCGAAGGGGAGCCTCTGGGTGAGGACCCAACTGGGGCTCCCGCCGC  
TGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCGCTTCGGCTGAAGCATTTGAC  
TCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTTGCACAC  
CTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTC  
AGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACA  
GAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCC  
ATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCCAAAAATGCACCTACTCTTTC  
CTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGCACAGAGCTTCATAACC  
TCTTCATGGACTTTTTATCTTCAAGCCGATGACGGAAAAATAGTTATATTCCAGTCTAAGCC  
AGAAATCCAGTACGCACCACATTTGGAGCAGGAGCCTACAAATTTGAGAGAATCATCTCTAA  
GCAAAATGTCCTATCTGCAAATGAGAAATTCACAAGCGCACAGGAATTTTCTTGAAGATGGA  
GAAAGTGATGGCTTTTTAAGATGCCTCTCTCTTAACTCTGGGTGGATTTTAACTACAACCTCT  
TGTCTCTCGGTGATGGTATTGCTTTGGATTTGTTGTGCAACTGTTGCTACAGCTGTGGAGC  
AGTATGTTCCCTCTGAGAAGCTGAGTATCTATGGTGACTTGGAGTTTATGAATGAACAAAAG  
CTAAACAGATATCCAGCTTCTTCTCTTGTGGTTGTTAGATCTAAAACTGAAGATCATGAAGA  
AGCAGGGCCTCTACCTACAAAAGTGAATCTTGCTCATTCTGAAATTTAAGCATTTTTCTTTT  
AAAAGACAAGTGTAATAGACATCTAAAATTCCACTCCTCATAGAGCTTTTAAAATGGTTTCA  
TTGGATATAGGCCTTAAGAAATCACTATAAAATGCAAATAAAGTTACTCAAATCTGTG

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**FIGURE 132**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA26847

<subunit 1 of 1, 323 aa, 1 stop

<MW: 36223, pI: 5.06, NX(S/T): 1

MAAPKGSLWVRTQLGLPPLLLLTMALAGGSGTASAEAFDSVLGDTASCHRAQCLTYPLHTYP  
KEEELYACQRCRLFSICQFVDDGIDLNRKLECESACTEAYSQSDEQYACHLGCQNQLPFA  
ELRQEQLMSLMPKMHLLFPLTLVRSFWSMMDSAQSFITSSWTFYQLQADDGKIVIFQSKPEI  
QYAPHLEQEPTNLRESSLSKMSYLQMRNSQAHRNFLEDGESDGLRCLSLNSGWILTTTLVL  
SVMVLLWICCATVATAVEQYVPSEKLSIYGDLEFMNEQKLNRYPASSLVVVRSKTEDHEEAG  
PLPTKVNLAHSEI

**Important features:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation site.**

amino acids 90-93

733 1237

FIGURE 133

TTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAGTTGACCTACCCCTGCACACCTACCC  
TAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTGCAGGCTGTTTTCAATTTGTCAGTTTG  
TGGATGATGGAATTGACTTAAATCGAACTAAATTGGAATGTGAATCTGCATGTACAGAAGCA  
TATCCCAATCTGATGAGCAATATGCTTGCCATCTTGGTTGCCAGAATCAGCTGCCATTCGC  
TGAAGTGAAGACAAGAACAACCTTATGTCCCTGATGCCAAAATGCACCTACTCTTTCCTCTAA  
CTCTGGTGAGGTCATTCTGGAGTGACATGATGGACTCCGC

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**FIGURE 134**

CACACTGGCCGGATCTTTTAGAGTCCTTTGACCTTGACCAAGGGTCNGGAAAACAGCAACAA  
GCTGAGCTGCTGTGACAGAGGGAACAAGATGGCGGCGCCGAAGGGAGCCTTTGGGTGAGGAC  
CCAACTGGGGCTCCCGCCGCTGCTGCTGCTGACCATGGCCTTGGCCGGAGGTTCTGGGGACCG  
CTTCGGCTGAAGCATTGACTCGGTCTTGGGTGATACGGCGTCTTGCCACCGGGCCTGTCAG  
TTGACCTACCCCTTGACACCTACCCTAAGGAAGAGGAGTTGTACGCATGTCAGAGAGGTTG  
CAGGCTGTTTTCAATTTGTCAGTTTGTGGATGATGGAATTGACTTAAATCGAACTAAATTGG  
AATGTGAATCTGCATGTACAGAAGCATATTCCCAATCTGATGAGCAATATGCTTGCCATCTT  
GGTTGCCAGAATCAGCTGCCATTCGCTGAACTGAGACAAGAACAACCTTATGTCCCTGATGCC  
AAAAATGCACCTACTCTTTCCTCTAACTCTGGTGAGGTCATTCTGGAGTGACATGATGGACT  
CCGC

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**FIGURE 135**

GCGAGGTGGCGATCGCTGAGAGGCAGGAGGGCCGAGGCGGGCCTGGGAGGCGGCCCCGGAGGT  
GGGGCGCCGCTGGGGCCGGCCCGCACGGGCTTCATCTGAGGGCGCACGGCCCCGCGACCGAGC  
GTGCGGACTGGCCTCCCAAGCGTGGGGCGACAAGCTGCCGGAGCTGCAATGGGGCCGCGGCTG  
GGGATTCTTGTTTGGCCTCCTGGGCGCCGTGTGGCTGCTCAGCTCGGGCCACGGAGAGGAGC  
AGCCCCCGGAGACAGCGGCACAGAGGTGCTTCTGCCAGGTTAGTGGTTACTTGGATGATTGT  
ACCTGTGATGTTGAAACCATTGATAGATTTAATAACTACAGGCTTTTCCCAAGACTACAAAA  
ACTTCTTGAAAGTGACTACTTTAGGTATTACAAGGTAAACCTGAAGAGGCCGTGTCCTTTCT  
GGAATGACATCAGCCAGTGTGGAAGAAGGGACTGTGCTGTCAAACCATGTCAATCTGATGAA  
GTTCTGATGGAATTAAATCTGCGAGCTACAAGTATTCTGAAGAAGCCAATAATCTCATTGA  
AGAATGTGAACAAGCTGAACGACTTGGAGCAGTGGATGAATCTCTGAGTGAGGAAACACAGA  
AGGCTGTTCTTCAGTGGACCAAGCATGATGATTCTTCAGATAACTTCTGTGAAGCTGATGAC  
ATTCAGTCCCCTGAAGCTGAATATGTAGATTTGCTTCTTAATCCTGAGCGCTACACTGGTTA  
CAAGGGACCAGATGCTTGGAAAATATGGAATGTCATCTACGAAGAAACTGTTTTAAGCCAC  
AGACAATTAAAAGACCTTTAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGAACT  
TTTTACAGTTGGCTAGAAGGTCTCTGTGTAGAAAAAGAGCATTCTACAGACTTATATCTGG  
CCTACATGCAAGCATTAAATGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAG  
AAAAGAAATGGGGACACAACATTACAGAATTTCAACAGCGATTTGATGGAATTTTGAAGTAA  
GGAGAAGGTCCAAGAAGGCTTAAGAAGTGTATTTTCTCTACTTAATAGAACTAAGGGCTTT  
ATCCAAAGTGTTACCATTTCTTCGAGCGCCAGATTTTCAACTCTTTACTGGAAATAAAATTC  
AGGATGAGGAAAACAAAATGTTACTTCTGGAAATACTTCATGAAATCAAGTCATTTCTTTG  
CATTTTGATGAGAATTCATTTTTTGCTGGGGATAAAAAAGACACAACTAAAGGAGGA  
CTTTCGACTGCATTTTAGAAATATTTCAAGAATTATGGATTGTGTTGGTTGTTTTAAATGTC  
GTCTGTGGGGAAAGCTTCAGACTCAGGGTTTGGGCACTGCTCTGAAGATCTTATTTTCTGAG  
AAATTGATAGCAAATATGCCAGAAAGTGGACCTAGTTATGAATTCCATCTAACCAGACAAGA  
AATAGTATCATTATTCAACGCATTTGGAAGAATTTCTACAAGTGTGAAAGAATTAGAAAAT  
TCAGGAACTTGTTACAGAATATTCATTAAAGAAAACAAGCTGATATGTGCCTGTTTCTGGAC  
AATGGAGGCGAAAGAGTGGAAATTTCAATTCAAAGGCATAATAGCAATGACAGTCTTAAGCCAA  
ACATTTTATATAAAGTTGCTTTTGTAAGGAGAATTATATTGTTTTAAGTAAACACATTTTT  
AAAAATTGTGTTAAGTCTATGTATAATACTACTGTGAGTAAAGTAATACTTTAATAATGTG  
GTACAAATTTTAAAGTTTAATATTGAATAAAAGGAGGATTATCAAATTAATAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 136**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53974  
<subunit 1 of 1, 468 aa, 1 stop  
<MW: 54393, pI: 5.63, NX(S/T): 2  
MGRGWGFLFGLLGAVWLLSSGHGEEQPPETAARCFQVSGYLDDCTCDVETIDRFNNYRLF  
PRLQKLLESDFRYKVNLRPCPFWNDISQCGRRDCAVKPCQSDEVDPDGIKSASYKYSEEA  
NNLIEECEQAERLGAVDESLSEETQKAVLQWTKHDDSSDNFCEADDIQSPEAEYVDLLLNPE  
RYTGYKGPDAWKIWNVIYEENCFKPQTIKRPLNPLASGQGTSEENTFYSWLEGLCVEKRAFY  
RLISGLHASINVHLSARYLLQETWLEKKWGHNITEFQQRFDGILTEGEGPRRLKNLYFLYLI  
ELRALSKVLPFFERPDLFTGNKIQDEENKMLLLEILHEIKSFPLHFDENSFFAGDKKEAH  
KLKEDFRLHFRNISRIMDCVGCFCRLWGKLQTOGLGTALKILFSEKLIANMPESGPSYEFH  
LTRQEIVSLFNAFGRISTSVKELENFRNLLQNIH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 280-283 and 384-387

**Amidation site.**

amino acids 94-97

**Glycosaminoglycan attachment site.**

amino acids 20-23 and 223-226

**Aminotransferases class-V pyridoxal-phosphate**

amino acids 216-222

**Interleukin-7 proteins**

amino acids 338-343

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**FIGURE 137**

GCTGGAAATATGGATGTCATCTACGAGAACTGTTTTAAGCCACAGACAATTAAAAGACCTT  
TAAATCCTTTGGCTTCTGGTCAAGGGACAAGTGAAGAGNACACTTTTACAGTTGGCTAGAA  
GGTCTCTGTGTAGAAAAAAGAGCATTCTACAGACTTATATCTGGCCTACATGCAAGCATTAA  
TGTGCATTTGAGTGCAAGATATCTTTTACAAGAGACCTGGTTAGAAAAGAAATGGGGACACA  
ACATTACAGAATTTNAACAGCGATTTGATGGAATTTTGACTGAAGGAGAAGGTCCAAGAAGG  
CTTAAGAACTTGTATTTTCTCTACTTAATAGAACTAAGGGCTTTATCCAAAGTGTTACCATT  
CTTNGAGCGCCCAGATTTTCAACTNTTTACTGGAAATAAAATTCAGGATGAGGNAAACAAAA  
TGTTACTTTTGGAATACTTCATGAAATCAAGTCATTCCTTTGCATTTTGATGAGAATTCA  
TTTTTTTGCTG

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**FIGURE 138**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTGGGAGGGGGCAGGATGGGAGGGAA  
AGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGACTTCTCATACTGGACAGAAAC  
CGATCAGGCATGGAACTCCCCTTCGTCACTCACCTGTTCTTGCCCCCTGGTGTTCTTGACAGG  
TCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCTATTCCCAGGGCCACCAGAAG  
CTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGACAGCGATGGATGCTGGTGGGC  
GCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTTTATCGCTGCCCTGTAGGGGG  
GGCCACAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTACCAACTGGGAAATTCATCTC  
ATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGTTAGAGACAGATGGTGATGGGGGATTC  
ATGGTGAGCTAAGAGAGGGTGGTGGCAGTGTCTCTGAAGGTCCATAAAAGAAAAAGAGAA  
GTGTGGTAAGGGAAAATGGTCTGTGTGGAGGGGTCAAGGAGTTAAAAACCCTAGAAAGCAAA  
AGGTAGGTAATGTCAGGGAGTAGTCTTCATGCCTCCTTCAACTGGGAGCATGTTCTGAGGGT  
GCCCTCCCAAGCCTGGGAGTAACTATTTCCCCCATCCCCAGGCCTGTGCCCTCTCTGGTCT  
CGTGCTTGTGGCAGCTCTGTCTTCAGTTCTGGGATATGTGCCCGTGTGGATGCTTCATTCCA  
GCCTCAGGGAAGCCTGGCACCCACTGCCCAACGTGAGCCAGAGGAAGGCTGAGTACTTGGTT  
CCCAGAAGGAGATACTGGGTGGGAAAAAGATGGGGCAAAGCGGTATGATGCCTGGCAAAGGG  
CCTGCATGGCTATCCTCATTGCTACCTAATGTGCTTGCAAAAGCTCCATGTTTCCTAACAGA  
TTCAGACTCCTGGCCAGGTGTGGTGGCCACACCTGTAATTCTAGCACTTTGGGAGGCCAAG  
GTGGGCAGATCACTTGAGGTCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACTCCAT  
CTCTACTAAAAAATAACAAAAATTAGCTGGGTGCGCTAGTGCATGCCTGTAATCTC  
ATCTACTCGGGAGGCTAAGACAGGAGACTCTCACTTCAACCCAGGAGGTGGAGGTTGCGGTG  
AGCCAAGATTGTGCCTCTGCACTCTAGCGTGGGTGACAGAGTAAGCGAGACTCCATCTCAA  
AATAATAATAATAATAATTCAGACTCCTTATCAGGAGTCCATGATCTGGCCTGGCACAGTAA  
CTCATGCCTGTAATCCCAACATTTTGGGAGGCCAACGCAGGAGGATTGCTTGAGGTCTGGAG  
GTTTGAGACCAGCCTGGGCAACATAGAAAGACCCCATCTCTAAATAAATGTTTAAAAAT

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**FIGURE 139**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57039  
><subunit 1 of 1, 124 aa, 1 stop  
><MW: 13352, pI: 5.99, NX(S/T): 1  
MELPFVTHLFLPLVFLTGLCSPFNLDEHHPRLEFPGPPEAEFGYSVLQHVGGGQRWMLVGAPW  
DGPSGDRRGDVYRCPVGGAHNAPCAKGHLGDYQLGNSSHPAVNMHLGMSLLETGDGGFMVS

**Important features:****Signal peptide:**

amino acids 1-22

**Cell attachment sequence.**

amino acids 70-73

**N-glycosylation site.**

amino acids 98-101

**Integrins alpha chain proteins**

amino acids 67-81

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**FIGURE 140**

CACAGTTCCCCACCATCACTCNTCCCATTCCTTCCAACCTTTATTTT TAGCTTGCCATTGGGA  
GGGGGCAGGATGGGAGGGAAAGTGAAGAAAACAGAAAAGGAGAGGGACAGAGGCCAGAGGAC  
TTCTCATACTGGACAGAAACCGATCAGGCATGGAAC TCCCCTTCGTCACCTCACCTGTTCTTG  
CCCCTGGTGTTCTTGACAGGTCTCTGCTCCCCCTTTAACCTGGATGAACATCACCCACGCCT  
ATTCCCAGGGCCACCAGAAGCTGAATTTGGATACAGTGTCTTACAACATGTTGGGGGTGGAC  
AGCGATGGATGCTGGTGGGCGCCCCCTGGGATGGGCCTTCAGGCGACCGGAGGGGGGACGTT  
TATCGCTGCCCTGTAGGGGGGGCCCAATGCCCCATGTGCCAAGGGCCACTTAGGTGACTA  
CCAAC TGGGAAATTCATCTCATCCTGCTGTGAATATGCACCTGGGGATGTCTCTGT TAGAGA  
CAGATGGTGATGG

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**FIGURE 141**

AAAGTTACATTTTCTCTGGAACCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG  
GGCAGAAAGGAGGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCCTGGGCGGGCTCTAGAACA  
ATTCAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT  
GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA  
**AATGC**CAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCTTTTCATGTGGTTTTTCT  
ACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC  
TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCAGTGATCGCGCCTGGAGA  
AACAGTGTACTATTCTGTGAATAACAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT  
GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTGATGTCACTGATGACATC  
ACGGCCACTGTGCCATACAACCTTCGTGTCAGGGCCACATTGGGCTCACAGACCTCAGCCTG  
GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA  
TCACCAAAGATGGCTTCCACCTGGTTATTGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC  
CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAAATGGTGAGGAGTGG  
GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCCAGA  
CATTTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA  
GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTGTGTTGGCTTCATGCTGATCCTTGT  
GGTCGTGCCACTGTTTCGTCTGGAAATGGGCGGGCTGCTCCAGTACTCCTGTTGCCCGTGG  
TGGTCCTCCCAGACACCTTGAAAATAACCAATTCACCCCAGAAGTTAATCAGCTGCAGAAGG  
GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCTCCTGAGGAACTCCTCAGGGCCTGGAT  
CTC**ATAG**GTTTTCGGGAAGGGCCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAAACC  
ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA  
GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC  
TGA CTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGGCTGCCACTTGCTGGCTGAGCAACC  
CTGGGAAAAGTGACTTCATCCCTTCGGTCCCTAAGTTTTCTCATCTGTAATGGGGGAATTACC  
TACACACCTGCTAAACACACACACACAGAGTCTCTCTCTATATATACACACGTACACATAAA  
TACACCCAGCACTTGCAAGGCTAGAGGGGAACTGGTGACACTCTACAGTCTGACTGATTCAG  
TGTTTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT  
GGCTTGGAGAGCCCACTTTCCCAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG  
TGTTGAGTTCACCTCAAGCCCAATGCCGGTGACAGAGGGGAATGGCTTAGCGAGCTCTACAGT  
AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC  
CATGAACTACTGTAAAGTGTTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT  
GTGCAATGCGACGAGAATGCAGAAGTCAGTAACATGTGCATGTTTGTGTGCTCCTTTTTTC  
TGTTGGTAAAGTACAGAATTCAGCAAATAAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA  
AAAAAAAAAA

742 1237

**FIGURE 142**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57033

<subunit 1 of 1, 311 aa, 1 stop

<MW: 35076, pI: 5.04, NX(S/T): 2

MQTFTMVLEEIWTSLFMWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAFGE  
TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITATVPYNLRVRATLGSQTSW  
SILKHPFNRNSTILTRPGMEITKDGFHLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG  
GIPVHLETMEPGAAYCVKAQTFVKAIGRYSQTECQVEVQGEAIPVLALFAFVGFMLILV  
VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

**Important features:****Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 230-255

**N-glycosylation site.**

amino acids 40-43 and 134-137

**Tissue factor proteins.**

amino acids 92-119

**Integrins alpha chain proteins**

amino acids 232-262

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**FIGURE 143**

TCCTGCTGATGCACATCTGGGTTTGGCAAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT  
CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA  
TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGG  
TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT  
TTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC  
CTGCCCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA  
GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGGAATACCAGGGGGAGTACGAGAGCCT  
GTACACGAGCCACATCTGGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG  
ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC  
TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAAACTCAACCATCCTTAC  
CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG  
GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGGCGAACCCTTGCGGGCGCAAGGG  
GTTNGCGAACCCTTGCGGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCC  
ACATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

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**FIGURE 144**

CCCACGCGTCCGCCACGCGTCCGAGGGACAAGAGAGAAGAGAGACTGAAACAGGGAGAAGA  
GGCAGGAGAGGAGGAGGTGGGGAGAGCACGAAGCTGGAGGCCGACACTGAGGGAGGGCGGGA  
GGAGGTGAAGAAGGAGAGAGGGGAGAAGAGGCAGGAGCTGGAAAGGAGAGAGGGAGGAGGAG  
GAGGAGATGCGGGATGGAGACCTGGAGTTAGGTGGCTTGGGAGAGCTTAATGAAAAGAGAAC  
GGAGAGGAGGTGTGGGTTAGGAACCAAGAGGTAGCCCTGTGGGCAGCAGAAGGCTGAGAGGA  
GTAGGAAGATCAGGAGCTAGAGGGAGACTGGAGGGTTCCGGGAAAAGAGCAGAGGAAAGAGG  
AAAGACACAGAGAGACGGGAGAGAGAAGAAGAGTGGGTTTGAAGGGCGGATCTCAGTCCCTG  
GCTGCTTTGGCATTGTTGGGGAAGTGGGACTCCCTGTGGGGAGGAGAGGAAAGCTGGAAGTCCT  
GGAGGGACAGGGTCCCAGAAGGAGGGGACAGAGGAGCTGAGAGAGGGGGGCAGGGCGTTGGG  
CAGGGGTCCCTCGGAGGCCTCCTGGGGATGGGGGGCTGCAGCTCGTCTGAGCGCCCTCGAGC  
GCTGGTACTCTGGGCTGCACTGGGGGCAGCAGCTCACATCGGACCAGCACCTGACCCCGAGG  
ACTGGTGGAGCTACAAGGATAATCTCCAGGGAACTTCGTGCCAGGGCCTCCTTTCTGGGGC  
CTGGTGAATGCAGCGTGGAGTCTGTGTGCTGTGGGGAAGCGGCAGAGCCCCGTGGATGTGGA  
GCTGAAGAGGGTTCTTTATGACCCCTTTCTGCCCCATTAAGGCTCAGCACTGGAGGAGAGA  
AGCTCCGGGGAACTTGTACAACACCGGCCGACATGTCTCCTTCCTGCCTGCACCCCGACCT  
GTGGTCAATGTGTCTGGAGGTCCCCTCCTTTACAGCCACCGACTCAGTGAAGTGCAGGCTGCT  
GTTTGGAGCTCGCGACGGAGCCGGCTCGGAACATCAGATCAACCACCAGGGCTTCTCTGCTG  
AGGTGCAGCTCATTCACCTCAACCAGGAACTCTACGGGAATTCAGCGCTGCCTCCCGCGGC  
CCCAATGGCCTGGCCATTCTCAGCCTCTTTGTCAACGTTGCCAGTACCTCTAACCATTCTC  
CAGTCGCCTCCTTAACCGCGACACCATCACTCGCATCTCCTACAAGAATGATGCCTACTTTC  
TTCAAGACCTGAGCCTGGAGCTCCTGTTCCCTGAATCCTTCGGCTTCATCACCTATCAGGGC  
TCTCTCAGCACCCCGCCCTGCTCCGAGACTGTCACCTGGATCCTCATTGACCGGGCCCTCAA  
TATCACCTCCCTTCAGATGCACTCCCTGAGACTCCTGAGCCAGAATCCTCCATCTCAGATCT  
TCCAGAGCCTCAGCGGTAACAGCCGGCCCCCTGCAGCCCTTGGCCCACAGGGCACTGAGGGGC  
AACAGGGACCCCCGGCACCCCGAGAGGCGCTGCCGAGGCCCACTACCGCCTGCATGTGGA  
TGGTGTCCCCCATGGTCGCTGAGACTCCCCTTCGAGGATTGCACCCGCCCCGTCTAAGCCTC  
CCCACAAGGCGAGGGGAGTTACCCCTAAAACAAAGCTATTAAAGGGACAGAATACTTA

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**FIGURE 145**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA34353

<subunit 1 of 1, 328 aa, 1 stop

<MW: 36238, pI: 9.90, NX(S/T): 3

MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLC  
AVGKRQSPVDVELKRVLYDPFLPPLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPL  
LYSHRLSELRLLEFGARDGAGSEHQINHQGFSAEVQLIHFNQELYGNFSAASRGPNGLAILSL  
FVNVASTSNPFLSRLNLRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE  
TVTWILIDRALNITSLQMHSRLRLSQNPFSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPER  
RCRGPNYRLHVDGVPHGR

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 177-199

**N-glycosylation site.**

amino acids 118-121, 170-173 and 260-263

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 222-270, 128-164 and 45-92

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**FIGURE 146**

GGCGCCTGGTTCTGCGCGTACTGGCTGTACGGAGCAGGAGCAAGAGGTGCGCGCCAGCCTCCGCCGCCGAGCCTC  
GTTCTGTGTCCTCGCTCCTGCAGCTACTGCTCAGAAACGCTGGGGCGCCACCCTGGCAGACTAACGAA  
GCAGCTCCCTTCCCACCCCAACTGCAGGTCTAATTTTGGACGCTTTGCTGCCATTTCTTCCAGGTTGAGGGAGC  
CGCAGAGGCGGAGGCTCGCGTATTCTGCACTCAGCACCCACGTCGCCCCCGGACGCTCGGTGCTCAGGCCCTTC  
GCGAGCGGGGCTCTCCGTCTGCGGTCCCTTGTGAAGGCTCTGGGCGGCTGCAGAGGCCGGCCGTCCGGTTTGGCT  
CACCTCTCCAGGAACTTCACACTGGAGAGCCAAAAGGAGTGAAGAGCCTGTCTTGGAGATTTTCTGGGGAA  
ATCCTGAGGTCATTTCATTATGAAGTGTACCGCGCGGGAGTGGCTCAGAGTAACCACAGTGCTGTTTCATGGCTAGA  
GCAATTCCAGCCATGGTGGTTCCCAATGCCACTTTATTGGAGAACTTTTGGAAAAATACATGGATGAGGATGGT  
GAGTGGTGGATAGCCAAACAACGAGGGAAAAGGGCCATCACAGACAATGACATGCAGAGTATTTTGGACCTTCAT  
AATAAATTACGAAGTCAGGTGTATCCAACAGCCTCTAATATGGAGTATATGACATGGGATGTAGAGCTGGAAAGA  
TCTGCAGAATCCTGGGCTGAAAGTTGCTTGTGGGAACATGGACCTGCAAGCTTGCTTCCATCAATTGGACAGAAT  
TTGGGAGCACACTGGGGAAGATATAGGCCCCCGACGTTTCATGTACAATCGTGGTATGATGAAGTGAAGACTTT  
AGCTACCCATATGAACATGAATGCAACCCATATTGTCCATTCAGGTGTTCTGGCCCTGTATGTACACATTATACA  
CAGTCTGTGGGCAACTAGTAACAGAATCGGTTGTGCCATTAATTTGTGTACATAACATGAACATCTGGGGGCAG  
ATATGGCCCAAAGCTGTCTACCTGGTGTGCAATTACTCCCCAAAGGGAACTGGTGGGGCCATGCCCTTACAAA  
CATGGGCGGCCCTGTTCTGCTTGCCACCTAGTTTTGGAGGGGGCTGTAGAGAAAATCTGTGCTACAAAGAAGGG  
TCAGACAGGTATTATCCCCCTCGAGAAGAGGAAACAAATGAAATAGAACGACAGCAGTCACAAGTCCATGACACC  
CATGTCCGGACAAGATCAGATGATAGTAGCAGAAATGAAGTCATAAGCGCACAGCAAATGTCCCAAATTTGTTCT  
TGTGAAGTAAGATTAAGAGATCAGTGCAAGGAACAACCTGCAATAGGTACGAATGTCCTGCTGGCTGTTTGGAT  
AGTAAAGCTAAAGTTATTGGCAGTGTACATTATGAAATGCAATCCAGCATCTGTAGAGCTGCAATTCATTATGGT  
ATAATAGACAATGATGGTGGCTGGGTAGATATCACTAGACAAGGAAGAAAGCATTATTTTCATCAAGTCCAATAGA  
AATGGTATTCAAACAATTGGCAAATATCAGTCTGCTAATTCCTTCACAGTCTCTAAAGTAACAGTTCAGGCTGTG  
ACTTGTGAAACAACCTGTGGAACAGCTCTGTCCATTTTCATAAGCCTGCTTCACATTGCCCAAGAGTATACTGTCT  
CGTAACTGTATGCAAGCAAATCCACATTATGCTCGTGTAAATGGAACCTCGAGTTTATTCTGATCTGTCCAGTATC  
TGCAGAGCAGCAGTACATGCTGGAGTGGTTCGAAATCACGGTGGTTATGTTGATGTAATGCCTGTGGACAAAAGA  
AAGACCTACATTGCTTCTTTTCAGAATGGAATCTTCTCAGAAAGTTTACAGAATCCTCCAGGAGGAAAGGCATTC  
AGAGTGTGTTGCTGTTGTGTAAGTGAATACTTGGAAAGAGGACCATAAAGACTATTCCAAATGCAATATTTCTGA  
ATTTTGTATAAACTGTAACATTACTGTACAGAGTACATCAACTATTTTCAGCCCAAAAGGTGCCAAATGCATA  
TAAATCTTGATAAACAAAGTCTATAAAATAAACATGGGACATTAGCTTTGGGAAAAGTAATGAAAATATAATGG  
TTTTAGAAATCCTGTGTAAATATTGCTATATTTTCTTAGCAGTTATTTCTACAGTTAATTACATAGTCATGATT  
GTTCTACGTTTCATATATTATATGGTGCTTTGTATATGCCACTAATAAAATGAATCTAAACATTGAATGTGAATG  
GCCCTCAGAAAATCATCTAGTGCATTTAAAAATAATCGACTCTAAACTGAAAGAAACCTTATCACATTTTCCCC  
AGTTCAATGCTATGCCATTACCAACTCCAAATAATCTCAAATAATTTTCCACTTAATAACTGTAAAGTTTTTTTC  
TGTTAATTTAGGCATATAGAATATTAAATTCCTGATATTGCACTTCTTATTTTATATAAAATAATCCTTTAATATC  
CAATGAATCTGTAAAATGTTTGATTCTTGGGAATGGCCTTAAAAATAAATGTAATAAAGTCAGAGTGGTGGT  
ATGAAAACATTCTAGTGATCATGTAGTAAATGTAGGGTTAAGCATGGACAGCCAGAGCTTCTATGTACTGTTA  
AAATTGAGGTCACATATTTTCTTTTGTATCCTGGCAAATACTCCTGCAGGCCAGGAAGTATAATAGCAAAAAGTT  
GAACAAAGATGAACTAATGTATTACATTACCATTGCCACTGATTTTTTTTTTAAATGGTAAATGACCTTGTATATAA  
ATATTGCCATATCATGGTACCTATAATGGTGATATATTTGTTTCTATGAAAAATGTATTGTGCTTTGATACTAAA  
AATCTGTAAAATGTTAGTTTTTGGTAATTTTTTTTTCTGCTGGTGGATTACATATTAAATTTTTTCTGCTGGTGG  
TAAACATTAAATTAATCATGTTTCAAAAAAAAAAAAAA

**FIGURE 147**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45417

<subunit 1 of 1, 500 aa, 1 stop

<MW: 56888, pI: 8.53, NX(S/T): 2

MKCTAREWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEEDGEWWIAKQRGKRAITDNDM  
QSILDLHNKLRSQVYPTASNMEYMTWDVELERSAESWAESCLWEHGPASLLPSIGQNLGAHW  
GRYRPPTFHVQSWYDEVKDFSYPYEHECNPYCFRCSGPVCTHYTQVWVWATSNRIGCAINLC  
HNMNIWGQIWPKAVYLVCNYSKGNWWGHAPYKHGRPCSACPPSFGGGCRENL CYKEGSDRY  
YPPREEETNEIERQQSQVHDTHVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTTCNR  
YECPAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITRQGRKH YFIKSNRNGI  
QTIGKYQSANSFTVSKVTVQAVTCETTVEQLCPFHKPASHCPRVYCPRNCMQANPHYARVIG  
TRVYSDLSSICRAAVHAGVVRNHGGYVDVMPVDKRKTYIASFQNGIFSESLQNPPGGKA FRV  
FAVV

**Important features:**

**Signal peptide:**

amino acids 1-20

**Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 protein**

amino acids 165-186, 196-218, 134-146, 96-108 and 58-77

**N-glycosylation site**

amino acids 28-31

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**FIGURE 148**

GCGGAGACAAGCGCAGAGCGCAGCGCACGGCCACAGACAGCCCTGGGCATCCACCGACGGCG  
CAGCCGGAGCCAGCAGAGCCGGAAGGCGCGCCCCGGGCAGAGAAAGCCGAGCAGAGCTGGGT  
GGCGTCTCCGGGCGCGCTCCGACGGGCCAGCGCCCTCCCCATGTCCCTGCTCCCACGCCG  
CGCCCTCCGGTCAGCATGAGGCTCCTGGCGGCCGCGCTGCTCCTGCTGCTGCTGGCGCTGT  
ACACCGCGCGTGTGGACGGGTCCAAATGCAAGTGCTCCCGGAAGGGACCCAAGATCCGCTAC  
AGCGACGTGAAGAAGCTGGAAATGAAGCCAAAGTACCCGCACTGCGAGGAGAAGATGGTTAT  
CATCACCACCAAGAGCGTGTCCAGGTACCGAGGTGAGGAGCACTGCCTGCACCCCAAGCTGC  
AGAGCACCAAGCGCTTCATCAAGTGGTACAACGCCTGGAACGAGAAGCGCAGGGTCTACGAA  
GAATAGGGTGAAAAACCTCAGAAGGGAAAACCTCCAAACCAGTTGGGAGACTTGTGCAAAGGA  
CTTTGCAGATTAAGCCTTTC  
TTTCTCACAGGCATAAGACACAAATTATATATTGTTATGAAGCACTTTTTACCAACGGTCAG  
TTTTTACATTTTATAGCTGCGTGCGAAAGGCTTCCAGATGGGAGACCCATCTCTCTTGTGCT  
CCAGACTTCATCACAGGCTGCTTTTTATCAAAAAGGGGAAAACCTCATGCCTTTCCTTTTTAA  
AAAATGCTTTTTTGTATTTGTCCATACGTCACTATACATCTGAGCTTTATAAGCGCCCGGGA  
GGAACAATGAGCTTGGTGGACACATTTTCATTGCAGTGTTGCTCCATTCCTAGCTTGGGAAGC  
TTCCGCTTAGAGGTCCTGGCGCCTCGGCACAGCTGCCACGGGCTCTCCTGGGCTTATGGCCG  
GTCACAGCCTCAGTGTGACTCCACAGTGGCCCCTGTAGCCGGGCAAGCAGGAGCAGGTCTCT  
CTGCATCTGTTCTCTGAGGAACTCAAGTTTGGTTGCCAGAAAATGTGCTTCATTCCCCCCT  
GGTTAATTTTACACACCCTAGGAAACATTTCCAAGATCCTGTGATGGCGAGACAAATGATC  
CTTAAAGAAGGTGTGGGGTCTTTCCCAACCTGAGGATTTCTGAAAGGTTACAGGTTCAATA  
TTTAATGCTTCAGAAGCATGTGAGGTTCCCAACACTGTCAGCAAAAACCTTAGGAGAAAAC  
TAAAAATATATGAATACATGCGCAATACACAGCTACAGACACACATTCTGTTGACAAGGGAA  
AACCTTCAAAGCATGTTTCTTTCCCTCACCACAACAGAACATGCAGTACTAAAGCAATATAT  
TTGTGATTCCCCATGTAATTCTTCAATGTTAAACAGTGCAGTCCTCTTTGAAAGCTAAGAT  
GACCATGCGCCCTTTCCTCTGTACATATACCCTTAAGAACGCCCCCTCCACACACTGCCCC  
CAGTATATGCCGCATTGTACTGCTGTGTTATATGCTATGTACATGTCAGAAACCATTAGCAT  
TGCATGCAGGTTTCATATTCTTTCTAAGATGGAAAGTAATAAAATATATTTGAAATGTAAAA  
AAAAAAAAAAAA

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**FIGURE 149**

MSLLPRRAPPVSMRLAAALLLLLLALYTARVDGSKCKCSRKGPKIRYSDVKKLEMKPKYPH  
CEEKMVIITTKSVSRYRGQEHCLHPKLQSTKRFIKWYNWNEKRRVYEE

**Signal sequence:**

amino acids 1-34

750/237

**FIGURE 150**

CCCCAGGGACTGCTATGGCTTCCTTTGTTGTTCACCCCGGTCTGCGTCAATGTTAAACTCCAATGTCCTCCTGTG  
GTTAACTGCTCTTGCCATCAAGTTCACCCTCATTGACAGCCAAGCACAGTATCCAGTTGTCAACACAAATTATGG  
CAAAATCCGGGGCCTAAGAACACCGTTACCCAATGAGATCTTGGGTCCAGTGGAGCAGTACTTAGGGGTCCCCTA  
TGCCTCACCCCCCACTGGAGAGAGGCGGTTTCAGCCCCCAGAACCCCCGTCCTCCTGGACTGGCATCCGAAATAC  
TACTCAGTTTGCTGCTGTGTGCCCCCAGCACCTGGATGAGAGATCCTTACTGCATGACATGCTGCCCATCTGGTT  
TACCGCCAATTTGGATACTTTGATGACCTATGTTCAAGATCAAAATGAAGACTGCCTTTACTTAAACATCTACGT  
GCCCACGGAAGATGGAGCCAACACAAAGAAAAACGCAGATGATATAACGAGTAATGACCGTGGTGAAGACGAAGA  
TATTCATGATCAGAACAGTAAGAAGCCCGTCATGGTCTATATCCATGGGGGATCTTACATGGAGGGCACCGGCAA  
CATGATTGACGGCAGCATTTTGGCAAGCTACGGAAACGTCATCGTGATCACCATTAACTACCGTCTGGGAATACT  
AGGGTTTTTAAAGTACCGGTGACCAGGCAGCAAAAGGCAACTATGGGCTCCTGGATCAGATTCAAGCACTGCGGTG  
GATTGAGGAGAATGTGGGAGCCTTTGGCGGGGACCCCAAGAGAGTGACCATCTTTGGCTCGGGGGCTGGGGCCTC  
CTGTGTCAGCCTGTTGACCCTGTCCCACTACTCAGAAGGTCTCTTCCAGAAGGCCATCATTAGAGCGGCACCGC  
CCTGTCCAGCTGGGCAGTGAACCTACCAGCCGGCCAAGTACACTCGGATATTGGCAGACAAGGTCGGCTGCAACAT  
GCTGGACACCACGGACATGGTAGAATGCCTGCGGAACAAGAACTACAAGGAGCTCATCCAGCAGACCATCACCCC  
GGCCACCTACCACATAGCCTTCGGGCGGGTGATCGACGGCGACGTCATCCCAGACGACCCCCAGATCCTGATGGA  
GCAAGGCGAGTTCCTCAACTACGACATCATGCTGGGCGTCAACCAAGGGGAAGGCCTGAAGTTCGTGGACGGCAT  
CGTGGATAACGAGGACGGTGTGACGCCCAACGACTTTGACTTCTCCGTGTCCAACCTTCGTGGACAACCTTTACGG  
CTACCCTGAAGGGAAAGACACTTTGCGGGGAGACTATCAAGTTCATGTACACAGACTGGGCCGATAAGGAAAACCC  
GGAGACGCGGCGGAAAACCTGGTGGCTCTCTTTACTGACCACCAGTGGGTGGCCCCCGCGTGGCCGCGACCT  
GCACGCGCAGTACGGCTCCCCACCTACTTCTATGCCTTCTATCATCACTGCCAAAGCGAAATGAAGCCAGCTG  
GGCAGATTCCGGCCCATGGTGATGAGGTCCCTTATGTCTTCGGCATCCCATGATCGGTCCCACCGAGCTCTTCAG  
TTGTAACCTTTTCCAAGAACGACGTCATGCTCAGCGCCGTGGTCATGACCTACTGGACGAACTTCGCCAAACTGG  
TGATCCAAATCAACCAGTTCCTCAGGATACCAAGTTCATTACACAAAACCCCAACCGCTTTGAAGAAGTGGCCTG  
GTCCAAGTATAATCCCAAAGACCAGCTCTATCTGCATATTGGCTTGAAACCCAGAGTGAGAGATCACTACCGGGC  
AACGAAAGTGGCTTTCTGGTTGGAACCTCGTTCCTCATTTGCACAACCTGAACGAGATATTCCAGTATGTTTCAAC  
AACCACAAAGGTTCTCCACCAGACATGACATCATTTCCCTATGGCACCCGGCGATCTCCCGCCAAGATATGGCC  
AACCACCAAACGCCCAGCAATCACTCCTGCCAACAATCCCAAACACTCTAAGGACCCTCACAAAACAGGGCCTGA  
GGACACAACCTGTCCTCATTGAAACCAAACGAGATTATTCCACCGAATTAAGTGTACCATTGCCGTGGGGCGTC  
GCTCCTCTTCCTCAACATCTTAGCTTTTGGCGCGCTGTACTACAAAAGGACAAGAGGGCGCCATGAGACTCACAG  
GCGCCCCAGTCCCCAGAGAAACACCACAAATGATATCGCTCACATCCAGAACGAAGAGATCATGTCTCTGCAGAT  
GAAGCAGCTGGAACACGATCACGAGTGTGAGTGCCTGCAGGCACACGACACACTGAGGCTCACCTGCCCGCCAGA  
CTACACCCTCACGCTGCGCCGGTCCGCCAGATGACATCCCACTTATGACGCCAAACACCATCACCATGATTCCAAA  
CACACTGACGGGGATGCAGCCTTTGCACACTTTTAACACCTTCAGTGGAGGACAAAACAGTACAAATTTACCCCA  
CGGACATTCCACCCTAGAGTATTAGCTTTGCCCTATTTCCCTTCCTATCCCTCTGCCCTACCCGCTCAGCAACAT  
AGAAGAGGGGAAGGAAAGAGAGAAGGAAAGAGAGAGAGAAAGAAAGTCTCCAGACCAGGAATGTTTTTGTCCCACT  
GACTTAAGACAAAAATGCAAAAAGGCAGTCATCCCATCCCGGCAGACCCTTATCGTTGGTGTTCCTCAGTATTAC  
AAGATCAACTTCTGACCCTGTGAAATGTGAGAAGTACACATTTCTGTAAATAACTGCTTTAAGATCTCTACCA  
CTCCAATCAATGTTTAGTGTGATAGGACATCACCATTTCAAGGCCCGGGTGTTCCTAACGTCATGGAAGCAGCT  
GACACTTCTGAAACTCAGCCAAGGACACTTGATATTTTTTAATTACAATGGAAGTTTAAACATTTCTTTCTGTGC  
CACACAATGGATGGCTCTCCTTAAGTGAAGAAAGAGTCAATGAGATTTTGCCCAGCACATGGAGCTGTAATCCAG  
AGAGAAGGAAACGTAGAAATTTATTATTAAGAATGGACTGTGCAGCGAAATCTGTACGGTCTGTGCAAAGAG  
GTGTTTTGCCAGCCTGAACCTATATTTAAGAGACTTTGT

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**FIGURE 151**

MLNSNVLLWLTALAIKFTLIDSQAQYPVVNTNYGKIRGLRTPLPNEILGPVEQYLGVVPYASP  
PTGERRFQPPPEPPSSWTGIRNTTQFAAVCPQHLDERSLLHDMPLIWFTANLDTLMTYVQDQN  
EDCLYLNIIYVPTEDGANTKKNADDITSNDRGEDEDIHDQNSKKPVMVYIHGGSYMEGTGNMI  
DGSILASYGNVIVITINYRLGILGFLSTGDQAAKGNYGLLDQIQALRWIEENVGAFGGDPKR  
VTIFGSGAGASCVSLLTSLSHYSEGLFQKAI IQSGTALSSWAVNYQPAKYTRILADKVGCMNL  
DTTDMVECLRNKNYKELIQQTITPATYHIAFGPVIDGDVIPDDPQILMEQGEFLNYDIMLGV  
NQGEGLKFVDGIVDNEDGVTPNDFDFSVSNFVDNLYGYPEGKDTLRETIKFMYPDWADKENP  
ETRRKTLVALFTDHQWVAPAVAADLHAQYGSPTYFYAFYHHCQSEMKP SWADSAHGDEVPIV  
FGIPMIGPTELFSCNFSKNDVMLS AVVM TYWTNFAKTGDPNQVPVQDTKFIHTKPNRFEEVA  
WSKYNPKDQLYLHIGLKPRVRDHYRATKVAFWLELVPHLHNLNEIFQYVSTTTKVPPPDMTS  
FPYGTRRSPAKIWPTTKRPAITPANNPKHSDPHKTGPEDTTVLIETKRDYSTE LSVTI AVG  
ASLLFLNILAFAALYYKKDKRRHETHRRPSPQRNTTNDIAHIQNEEIMSLQMKQLEHDHECE  
SLQAHDTLRLTCPPDYTLTLRRSPDDIPLMTPNTITMIPNTLTGMQPLHTFNTFSGGQNSTN  
LPHGHSTTRV

**Signal sequence:**

amino acids 1-24

**Transmembrane domains:**

amino acids 189-204, 675-692

752/237

**FIGURE 152**

GGGAAAGATGGCGGCGACTCTGGGACCCCTTGGGTCTGGCAGCAGTGGCGGCGATGTTTGT  
CGGCTCGGGATGGGTCCAGGATGTTACTCCTTCTTCTTTTGTGGGGTCTGGGCAGGGGCCA  
CAGCAAGTCGGGGCGGGTCAAACGTTTCGAGTACTTGAAACGGGAGCACTCGCTGTCAAGCC  
CTACCAGGGTGTGGGCACAGGCAGTTCCTCACTGTGGAATCTGATGGGCAATGCCATGGTGA  
TGACCCAGTATATCCGCCTTACCCAGATATGCAAAGTAAACAGGGTGCCTTGTGGAACCGG  
GTGCCATGTTTCCTGAGAGACTGGGAGTTGCAGGTGCACTTCAAAATCCATGGACAAGGAAA  
GAAGAATCTGCATGGGGATGGCTTGGCAATCTGGTACACAAAGGATCGGATGCAGCCAGGGC  
CTGTGTTTGGAAACATGGACAAATTTGTGGGGCTGGGAGTATTTGTAGACACCTACCCCAAT  
GAGGAGAAGCAGCAAGAGCGGGTATTTCCCTACATCTCAGCCATGGTGAACAACGGCTCCCT  
CAGCTATGATCATGAGCGGGATGGGCGGCCTACAGAGCTGGGAGGCTGCACAGCCATTGTCC  
GCAATCTTCATTACGACACCTTCTTGGTGATTCGCTACGTCAAGAGGCATTTGACGATAATG  
ATGGATATTGATGGCAAGCATGAGTGGAGGGACTGCATTGAAGTGCCCGGAGTCCGCCTGCC  
CCGCGGCTACTACTTCGGCACCTCCTCCATCACTGGGGATCTCTCAGATAATCATGATGTCA  
TTTCTTGAAGTTGTTTGAAGTGCAGTGGAGAGAACCCAGAAAGAGGAAAAGCTCCATCGA  
GATGTGTTCTTGCCCTCAGTGGACAATATGAAGCTGCCTGAGATGACAGCTCCACTGCCGCC  
CCTGAGTGGCCTGGCCCTCTTCTCATCGTCTTTTCTCCCTGGTGTTTTCTGTATTTGCCA  
TAGTCATTGGTATCATACTCTACAACAAATGGCAGGAACAGAGCCGAAAGCGCTTCTACTGA  
GCCCTCCTGCTGCCACCACCTTTTGTGACTGTCACCCATGAGGTATGGAAGGAGCAGGCACTG  
GCCTGAGCATGCAGCCTGGAGAGTGTTCTTGTCTCTAGCAGCTGGTTGGGGACTATATTCTG  
TCACTGGAGTTTTGAATGCAGGGACCCCGCATTCCCATGGTTGTGCATGGGGACATCTAACT  
CTGGTCTGGGAAGCCACCCACCCAGGGCAATGCTGCTGTGATGTGCCTTTCCCTGCAGTCC  
TTCCATGTGGGAGCAGAGGTGTGAAGAGAATTTACGTGGTTGTGATGCCAAAATCACAGAAC  
AGAATTTCATAGCCCAGGCTGCCGTGTTGTTTGAAGTCAAGAGGCCCTTCTACTTCAGTTTTG  
AATCCACAAAGAATTAATAAAGTGGTAACACCACAGGCTTTCTGACCATCCATTTCGTTGGGT  
TTGCATTTGACCCAACCCTCTGCCTACCTGAGGAGCTTTCTTTGGAAACCAGGATGGAACT  
TCTTCCCTGCCTTACCTTCCTTTCACTCCATTCAATTGTCCTCTCTGTGTGCAACCTGAGCTG  
GGAAAGGCATTTGGATGCCTCTCTGTTGGGGCCTGGGGCTGCAGAACACACCTGCGTTTCAC  
TGGCCTTCATTAGGTGGCCCTAGGGAGATGGCTTTCTGCTTTGGATCACTGTTCCCTAGCAT  
GGGTCTTGGGTCTATTGGCATGTCCATGGCCTTCCCAATCAAGTCTCTTCAGGCCCTCAGTG  
AAGTTTGGCTAAAGGTTGGTGTAATAATCAAGAGAAGCCTGGAAGACATCATGGATGCCATG  
GATTAGCTGTGCAACTGACCAGCTCCAGGTTTGATCAAACCAAAAGCAACATTTGTCATGTG  
GTCTGACCATGTGGAGATGTTTCTGGACTTGCTAGAGCCTGCTTAGCTGCATGTTTTGTAGT  
TACGATTTTGGGAATCCCACTTTGAGTGCTGAAAGTGTAAGGAAGCTTTCTTCTTACACCTT  
GGGCTTGGATATTGCCAGAGAAGAAATTTGGCTTTTTTTTTCTTAATGGACAAGAGACAGT  
TGCTGTTCTCATGTTCCAAGTCTGAGAGCAACAGACCCTCATCATCTGTGCCTGGAAGAGTT  
CACTGTCATTGAGCAGCACAGCCTGAGTGCTGGCCTCTGTCAACCCTTATTCCACTGCCTTA  
TTTGACAAGGGGTTACATGCTGCTCACCTTACTGCCCTGGGATTAAATCAGTTACAGGCCAG  
AGTCTCCTTGGAGGGCCTGGAAGTCTGAGTCCTCCTATGAACCTCTGTAGCCTAAATGAAAT  
TCTTAAATCACCGATGGAACCAAAAAAAAAAAAAAAAAAAGGGCGGCGCGACTCTAGAGTCG  
ACCTGCAGTAGGGATAACAGGGTAATAAGCTTGGCCGCCATGG

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**FIGURE 153**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50911

><subunit 1 of 1, 348 aa, 1 stop

><MW: 39711, pI: 8.70, NX(S/T): 1

MAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLLGSGQGPPQVGAGQTFEYLKREHSLSKPYQ  
GVGTGSSSLWNLMGNAMVMTQYIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKEIHGQGKKN  
LHGDGLAIWYTKDRMQPGPVFGNMDKFFVGLGVFVDTPNEEKQQQERVFPYISAMVNNGSLSY  
DHERDGRPTTELGGCTAIVRNLHYDTFLVIRYVKRHLTIMMDIDGKHEWRDCIEVPGVRLPRG  
YYFGTSSITGDLSDNHDVISLKLFEFTVERTPEEEKLHRDVFLPSVDNMKLPMTAPLPPLS  
GLALFLIVFFSLVFSVFAIVIGIILYNKWQEQSRKRFY

**Signal sequence:**

amino acids 1-38

**Transmembrane domain:**

amino acids 310-329



**FIGURE 154**

CCGAGCCGGGCGCGCAGCGACGGAGCTGGGGCCGGCCTGGGACCATGGGCGTGAGTGCAATCTACGGATCAGTCT  
CTGATGGTGGGTCGTTAACCTCAGTGGGGACTCCAAGATTTCCATGAAGAAAATCAGTTGTCTTCATTCAAGAAT  
TGGGGTCTGGCTCAGAATTCCTGCAGCTGGTGAAAATCTGTTTTCTAGAAGAGGTTTAATTAATGCCTGCAGTCT  
GACATGTTCCCGATTTGAGGTGAAACCATGAAGAGAAAATAGAATACTTAATAATGCTTTTCCGCAACCGCTTCT  
TGCTGCTGCTGGCCCTGGCTGCGCTGCTGGCCTTTGTGAGCCTCAGCCTGCAGTTCTTCCACCTGATCCCGGTGT  
CGACTCCTAAGAATGGAATGAGTAGCAAGAGTCGAAAGAGAATCATGCCCCGACCCTGTGACGGAGCCCCCTGTGA  
CAGACCCCGTTTATGAAGCTCTTTTGTACTGCAACATCCCCAGTGTGGCCGAGCGCAGCATGGAAGGTCATGCCC  
CGCATCATTTTAAGCTGGTCTCAGTGCATGTGTTTCATTGCGCACGGAGACAGGTACCCACTGTATGTTCATTCCCA  
AAACAAAGCGACCAGAAATTGACTGCACTCTGGTGGCTAACAGGAAACCGTATCACCCAAAATGGAAGCTTTCA  
TTAGTCACATGTCAAAGGATCCGGAGCCTCTTTCGAAAGCCCCCTGAACTCCTTGCCTCTTTACCCAAATCACC  
CATTGTGTGAGATGGGAGAGCTCACACAGACAGGAGTTGTGCAGCATTTGCAGAACGGTCAGCTGCTGAGGGATA  
TCTATCTAAAGAAACACAACTCCTGCCCAATGATTGGTCTGCAGACCAGCTCTATTTAGAGACCACTGGGAAAA  
GCCGGACCCTACAAAGTGGGCTGGCCTTGCTTTATGGCTTTCTCCAGATTTTGACTGGAAGAAGATTTATTTCA  
GGCACCAGCCAAGTGGCTGTCTGCTCTGGAAGCTGCTATTGCCCGGTAAAGAAACCAGTATCTGGAAAAGGAGC  
AGCGTCGTCAGTACCTCCTACGTTTGAAAAACAGCCAGCTGGAGAAGACCTACGGGGAGATGGCCAAGATCGTGG  
ATGTCCCCACCAAGCAGCTTAGAGCTGCCAACCCTATAGACTCCATGCTCTGCCACTTCTGCCACAATGTCAGCT  
TTCCCTGTACCAGAAATGGCTGTGTTGACATGGAGCACTTCAAGGTAATTAAGACCCATCAGATCGAGGATGAAA  
GGGAAAGACGGGAGAAGAAATTGACTTCGGGTATTCTCTCCTGGGTGCCACCCCATCCTGAACCAAAACCATCG  
GCCGGATGCAGCGTGCCACCGAGGGCAGGAAAGAAGAGCTCTTTGCCCTCTACTCTGCTCATGATGTCAGTCTGT  
CACCAGTTCTCAGTGCCTTGGGCTTTTCAAGAGCCAGGTTCCCAAGGTTTGCAGCCAGGTTGATCTTTGAGCTTT  
GGCAAGACAGAGAAAAGCCAGTGAACATTCCGTCCGGATTCTTTACAATGGCGTCGATGTCACATTCCACACCT  
CTTCTGCCAAGACCACCACAAGCGTTCTCCCAAGCCCATGTGCCCGCTTGAAAACCTTGGTCCGCTTTGTGAAAA  
GGGACATGTTTGTAGCCCTGGGTGGCAGTGGTACAAATTATTATGATGCATGTCACAGGGAAGGATTCTAAAGG  
TATGCAGTACAGCAGTATAGAATCCATGCCAATACAGAGCATAGGGAAAGGTCCACTTCTAGTTTTGTCTGTAC  
TAAGGGTAGAAGATTATTGCTTTTTAAAGGCTAAATATTGTTTGTGGGAACACAGATGGTTGGGGTTGAACACT  
AAGCACATTGCTGCAATGTGGTACGTGAATTGCTTGGTACAAAATGGCCAGTTCACAGAGGAATAGAAGGTACTT  
TATCATAGCCAGACTTCGCTTAGAATGCCAGAATAATATAGTTCAAGACCTGAAGTTGCCAATCCAAGTTTGCAC  
TCTTCTGGCCTGCCCCATGTTACTATGTGATGGAACCAGCACACCTCAACCAAAATTTTTTTAATCTTAGACATT  
TTTACCTTGTCTTGTGAAGAATTTCTTGAAGTGATTTATCTAAAATAAAGGTTGGCAAACCTTTTTCTGTAAAGG  
GCCAGATTGTAATATTTTCACTGTGTGGACCAAAAGGCCACATACAGTCTCTGTCATAACTACTCAACTCTGT  
TTCTGAAGCAGGAAAGCCACCACAGACAGTACATAAAGGAATATGTGTAGCTGGGTCCCAGGCCAGACAAAACA  
GATGGTGACCAGACTTGGCCCCCTGGGCTGTAGTTTGTCTGACCCCTCATCTAAAAAATAGGCTATACTACAATTGC  
ACTTCCAGCACTTTGAGAACGAGTTGAATACCAAGAATTATTCAATGGTTCTCCAGTAACCTTCTGCTAGAAACA  
CAGAATTTGGTCTGTATCTGACACTAGAACAAAATTTGAGGGTAAATAAACATTGAATTAGAATGAATCATAGAA  
AACTGATTAGAAGAATACTTGATGTTTATGATGATTGTGGTACAAGATAGTTTTAAGTATGTTCTAAATATTTGT  
CTGCTGTAGTCTATTTGCTGTATATGCTGAAATTTTTGTATGCCATTTAGTATTTTTATAGTTTAGGAAAATATT  
TTCTAAGACCAGTTTTAGATGACTCTTATTCCTGTAGTAATATTCAATTTGCTGTACCTGCTTGGTGGTTAGAAG  
GAGGCTAGAAGATGAATTCAGGCACCTTTCTTCCAATAAACTAATTATGGCTCATTCCCTTTGACAAGCTGTAGA  
ACTGGATTCATTTTTAAACCATTTTCATCAGTTTCAAATGGTAATTTCTGATTGATTTTTAAATGCGTTTTTGG  
AGAACTTTGCTATTAGGTAGTTTACAGATCTTTATAAGGTGTTTTATATATTAGAAGCAATTATAATTACATCTC  
TGATTTCTGAACTAATGGTGCTAATTCAGAGAAATGGAAAGTGAAAGTGAGATTCTCTGTTGTCATCGGCATTCC  
AACTTTTTCTCTTTGTTTTTGTCCAGTGTGTCATTTGAATATGTCTGTTTCTATAAATAAATTTTTTAAGAATAA

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**FIGURE 155**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48329

><subunit 1 of 1, 480 aa, 1 stop

><MW: 55240, pI: 9.30, NX(S/T): 2

MLFRNRFLLLLALAAALLAFVSLSLQFFHLIPVSTPKNGMSSKSRKRIMPDVTEPPVTDPVY  
EALLYCNIPPSVAERSMEGHAPHHFKLVSVHVFIRHGDRYPLYVIPKTKRPEIDCTLVANRKP  
YHPKLEAFISHMSKSGSGASFESPLNSLPLYPNHPLCEMGELTQTGVVQHLQNGQLLRDIYK  
KHKLLPNDWSADQLYLETTGKSRTLQSGLALLYGFLPDFDWKKIYFRHQPSALFCSGSCYCP  
VRNQYLEKEQRRQYLLRLKNSQLEKTYGEMAKIVDVPTKQLRAANPIDSMMLCHFCHNVSFPC  
TRNGCVDMEHFKVIKTHQIEDERERREKKLYFGYSLLGAHPILNQTIGRMQRATEGRKEELF  
ALYSAHDVTLSPVLSALGLSEARFPRFAARLIFELWQDREKPSHSVRILYNGVDVTFHTSF  
CQDHHKRSPKPMCPLNLVRFVKRDMFVALGGSGTNYYDACHREGF

**Signal sequence:**

amino acids 1-18

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**FIGURE 156**

AAAAAAGCTCACTAAAGTTTCTATTAGAGCGAATACGGTAGATTTCATCCCTTTTGAAGAACAGTACTGTGGA  
GCTATTTAAGAGATAAAAACGAAATATCCTTTCTGGGAGTTCAAGATTGTGCAGTAATTGGTTAGGACTCTGAGC  
GCCGCTGTTACCAATCGGGGAGAGAAAAGCGGAGATCCTGCTCGCCTTGACGCGCCTGAAGCACAAAGCAGAT  
AGCTAGGAATGAACCATCCCTGGGAGTATGTGGAAACAACGGAGGAGCTCTGACTTCCCAACTGTCCCATTCTAT  
GGGCGAAGGAACTGCTCCTGACTTCAGTGGTTAAGGGCAGAATTGAAAATAATTCTGGAGGAAGATAAGAATGAT  
TCCTGCGCGACTGCACCGGGACTACAAAGGGCTTGTCTGCTGGGAATCCTCCTGGGGACTCTGTGGGAGACCGG  
ATGCACCCAGATACGCTATTAGTTCGGGAAGAGCTGGAGAAAGGCTCTAGGGTGGGCGACATCTCCAGGGACCT  
GGGGCTGGAGCCCCGGGAGCTCGCGGAGCGCGGAGTCCGCATCATCCCCAGAGGTAGGACGCAGCTTTTCGCCCT  
GAATCCGCGCAGCGGCAGCTTGGTCACGGCGGGCAGGATAGACCGGGAGGAGCTCTGTATGGGGGCCATCAAGTG  
TCAATTAAATCTAGACATTCTGATGGAGGATAAAGTGAAAATATATGGAGTAGAAGTAGAAGTAAGGGACATTAA  
CGACAATGCGCCTTACTTTCTGTGAAAGTGAATTAGAAATAAAAATTAGTGAAAATGCAGCCACTGAGATGCGGTT  
CCCTCTACCCACGCTGGGATCCGGATATCGGGAAGAACTCTCTGCAGAGCTACGAGCTCAGCCCGAACACTCA  
CTTCTCCCTCATCGTGCAAAATGGAGCCGACGGTAGTAAGTACCCCGAATTGGTGCTGAAACGCGCCCTGGACCG  
CGAAGAAAAGGCTGCTCACCACCTGGTCTTACGGCCTCCGACGGGGCGACCCGGTGCGCACAGGCACCGCGCG  
CATCCGCGTGATGGTTCTGGATGCGAACGACAACGCACACAGCGTTTGTCTCAGCCCGAGTACCGCGCGAGCGTTCC  
GGAGAATCTGGCCTTGGGCACGCAGCTGCTTGTAGTCAACGCTACCGACCCTGACGAAGGAGTCAATGCGGAAGT  
GAGGTATTCCCTCCGGTATGTGGACGACAAGGCGGCCCAAGTTTTCAAAGTAGATTGTAATTGAGGGACAATATC  
AACAATAGGGGAGTTGGACCACGAGGAGTCAAGGATTCTACCAGATGGAAGTGCAAGCAATGGATAATGCAGGATA  
TTCTGCGCGAGCCAAAGTCTGATCACTGTTCTGGACGTGAACGACAATGCCCCAGAAGTGGTCTCACCTCTCT  
CGCCAGCTCGGTTCCCGAAAATCTCCAGAGGGACATTAATTGCCCTTTTAAATGTAAATGACCAAGATTCTGA  
GGAAAACGGACAGGTGATCTGTTTCATCCAAGGAAATCTGCCCTTTAAATTAGAAAATCTTACGGAAATTACTA  
TAGTTTAGTCAAGACATAGTCTTGGATAGGGAACAGGTTCTAGCTACAACATCACAGTGACCGCCACTGACCG  
GGGAACCCCGCCCTATCCACGGAACTCATATCTCGCTGAACGTGGCAGACACCAACGACAACCCGCGCGTCTT  
CCCTCAGGCCTCCTATTCCGCTTATATCCAGAGAACAATCCAGAGGAGTTTCCCTCGTCTCTGTGACCGCCCA  
CGACCCCGACTGTGAAGAGAACGCCAGATCACTTATTCCCTGGCTGAGAACACCATCCAAGGGGCAAGCCTATC  
GTCCTACGTGTCCATCAACTCCGACACTGGGGTACTGTATGCGCTGAGCTCCTTCGACTACGAGCAGTTCCGAGA  
CTTGCAAGTGAAAGTGATGGCGCGGGACAACGGGCACCCGCCCCCTCAGCAGCAACGTGTCGTTGAGCCTGTTCTG  
GCTGGACCAAGACGACAATGCGCCCGAGATCCTGTACCCCGCCCTCCCCACGGACGGTTCCACTGGCGTGGAGCT  
GGCTCCCCGCTCCGCAGAGCCCGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACAGAGACTCCGGCCAGAACGC  
CTGGCTGTCTACCGTCTGCTCAAGGCCAGCGAGCCGGGACTCTTCTCGGTGGGTCTGCACACGGGCGAGGTGCG  
CACGGCGCGAGCCCTGCTGGACAGAGACGCGCTCAAGCAGAGCCTCGTAGTGGCCGTCCAGGACCACGGCCAGCC  
CCCTCTCTCCGCCACTGTACGCTCACCGTGGCCGTGGCCGACAGCATCCCCAAGTCTTGGCGGACCTCGGCAG  
CCTCGAGTCTCCAGCTAACTCTGAAACCTCAGACCTCACTCTGTACCTGGTGGTAGCGGTGGCCGCGGTCTCCTG  
CGTCTTCTGGCCTTCGTCTCTTGTCTGCTGGCGCTCAGGCTGCGGCGCTGGCACAAGTCACGCCTGCTGCAGGC  
TTCAGGAGGCGGCTTGACAGGAGCGCGGCGTGCACCTTTGTGGGCGTGGACGGGGTGCAGGCTTTCCTGCAGAC  
CTATTCCCACGAGGTTTCCCTCACCACGGACTCGCGGAAGAGTCACTGATCTTCCCCCAGCCCACTATGCAGA  
CATGCTCGTCAGCCAGGAGAGCTTTGAAAAAAGCGAGCCCTTTTGTCTGTGAGGTGATTTCGGTATTTTCTAAAGA  
CAGTCATGGGTAAATTGAGGTGAGTTTATATCAAATCTTCTTTCTTTTCTTTTAAATTGCTCTGTCTCCCAAGC  
TGGAGTGACGCGGTACGATCATAGCTCACTGCGGCCTCAAACCTCCTAGGCTCAAGCAATTATCCACCTTTGCC  
CCGGTGTAACAGGGACTACAGGTGCAAGCCACCTACTGTCTGCCTATCTATCTATCTATCTATCTATCTATCTAT  
CTATCTATCTATCTATCTATTACTTTCTTGTACAGACGGGAGTCTCAGCCTGTAATCCCAGTACTTTGGGAGGC  
CGAGGCGGGTGGATCACCTGAGGTTGGGAGTTTGAGACCAGCCTGACCAACATGGAGAAACCCGCTCTATACTAA  
AAAAATACAAATTAGCCGGGCGTGGTGGTGCATGTCTGTAATCCCAGCTACTTGGGAGGCTGAGTCAGGAGAAT  
TGCTTTAACCTGGGAGGTGGAGGTTGCAATGAGCTGAGATTGTGCCATTGCACTCCAGCCTGGGCAACAAGAGTG  
AAACTCTATCTCA

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**FIGURE 157**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48306

><subunit 1 of 1, 916 aa, 1 stop

><MW: 100204, pI: 4.92, NX(S/T): 4

MIPARLHRDYKGLVLLGILLGTLWETGCTQIRYSVP EELEKGSRVGDISRDLGLEPRELAER  
GVRIIPRGRTQLFALNPRSGSLVTAGRIDREELCMGAIKCQLNLDILMEDKVKIYGVEVEVR  
DINDNAPYFRESELEIKISENAATEMRFP LPHAWDPDIGKNSLQSYELSPNTHFSLIVQNGA  
DGSKYPELV LKRALDREEKAAHHLVLTASDGGDPVRTGTARIRVMVLDANDNAPAFAPQPEYR  
ASVPENLALGTQLLV V NATDPDEGVNAEVRYSFYVDDKAAQVFKLDCNSGTISTIGELDHE  
ESGFYQMEVQAMDNAGYSARAKVLITVLDVNDNAPEVVLTS LASSVPENSPRGTLIALLVN  
DQDSEENGQVICFIQGNLPFKLEKSYGNYYSLVTDIVLDREQVPSYNITVTATDRGTPPLST  
ETHISLVNADTNDNPPVFPQASYSAYIPENNPRGVSLVSVTAHDPDCEENAQITYSLAENTI  
QGASLSSYVSINS DTGVLYALSSFDYEQFRDLQVKVMARDNGHPPLSSNVSLSLFVLDQNDN  
APEILYPALPTDGSTGV ELAPRSAEPGYLVTKVVAVDRDSGQNAWLSYRLLKASEPGLFSVG  
LHTGEVRTARALLDRDALKQSLVVAVQDHGQPPLSATVTLTVAVADSIPQVLADLGSLESPA  
NSETSDLTLYLVVAVAAVSCVFLAFVILL LALRLRRWHKSRL LQASGGGLTGAPASHFVGVD  
GVQAFLQTY SHEVSLTTDSRKSHLIFPQPNYADMLVSQESFEKSEPLLLSGDSVFSKDSHGL  
IEVSLYQIFFLFFFNCSVSQAGVQRYDHSSLRPQTPRLKQLSHLCLRCNRD YRCKPPTVCLS  
IYLSIYLSIYLSIYLLLSCTDGS LTPVIPVLWEAEAGGSPEVGSLRPA

**Signal sequence:**

amino acids 1-30

**Transmembrane domains:**

amino acids 693-711, 809-823, 869-888

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**FIGURE 158**

CCCAGGCTCTAGTGCAGGAGGAGAAGGAGGAGGAGCAGGAGGTGGAGATTCCCAGTTAAAAG  
GCTCCAGAATCGTGTACCAGGCAGAGAACTGAAGTACTGGGGCCTCCTCCACTGGGTCCGAA  
TCAGTAGGTGACCCCGCCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGT  
GCGGCCAAGACGTGGATGTTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGC  
ACAGGAGGACAAGGTGCTGGGGGGTCAAGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG  
CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAAGGTGGCAACTGGGTCTT  
ACAGCTGCCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTACAGAA  
TAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTTCAAGTCCATCCCACACCCCTGCTACAACA  
GCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCATCC  
CTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTGGCCAGAAGTG  
CACCGTCTCAGGCTGGGGCACTGTCACCAGTCCCCGAGAGAATTTTCCTGACACTCTCAACT  
GTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACA  
GATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAGG  
CCCCCTGGTGTGTGATGGTGCACCTCCAGGGCATCACATCCTGGGGCTCAGACCCCTGTGGGA  
GGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACCTGGACTGGATCAAGAAGATC  
ATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCTCCCTTAATAAACTCACAACTCT  
CTGGTTC

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**FIGURE 159**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48336

<subunit 1 of 1, 260 aa, 1 stop

<MW: 28048, pI: 7.87, NX(S/T): 1

MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAALFQGQQLLCGGVL  
VGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPVVQSIPHPCYNSSDVEDHNHDLMLL  
QLRDQASLGSKVKPISLADHCTQPGQKCTVSGWGTVTSPRENFDTLNCAEVKIFPQKKCED  
AYPGQITDGMVCAGSSKGADTCQGDSSGGLVCDGALQGITSWGS DPCGRSDKPGVYTNICRY  
LDWIKKIIGSKG

**Important Features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 51-71

**N-glycosylation site.**

amino acids 110-113

**Serine proteases, trypsin family, histidine active site.**

amino acids 69-74 and 207-217

**Tyrosine kinase phosphorylation site.**

amino acids 182-188

**Kringle domain proteins motif**

amino acids 205-217

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**FIGURE 160**

GGCGCCGGTGCACCGGGCGGGCTGAGCGCCTCCTGCGGCCCGGCCTGCGCGCCCCGGCCCCGC  
CGCGCCGCCCACGCCCCAACCCCGGCCCGCGCCCCCTAGCCCCCGCCCCGGGCCCGCGCCCCGC  
GCCCGCGCCAGGTGAGCGCTCCGCCCGCCGCGAGGCCCGCCCCGGCCCCGCCCCCGCCCCG  
CCCCGGCCGGCGGGGGAACCGGGCGGATTCTCGCGCGTCAAACACCTGATCCCATAAAAC  
ATTCATCCTCCCGGCGGCCCGCGCTGCGAGCGCCCCGCCAGTCCGCGCCGCGCCGCCCTCG  
CCCTGTGCGCCCTGCGCGCCCTGCGCACCCCGCGGCCCGAGCCAGCCAGAGCCGGGCGGAGC  
GGAGCGCGCCGAGCCTCGTCCCGCGGCCCGGGCCGGGGCCGCTAGCGGCGGCGCCTGGA  
TGCGGACCCGGCCGCGGGGAGACGGGCGCCCCGCCCCGAAACGACTTTCAGTCCCCGACGCGC  
CCCGCCCAACCCCTACGATGAAGAGGGCGTCCGCTGGAGGGAGCCGGCTGCTGGCATGGGTG  
CTGTGGCTGCAGGCCTGGCAGGTGGCAGCCCCATGCCAGGTGCCTGCGTATGCTACAATGA  
GCCCAAGGTGACGACAAGCTGCCCCCAGCAGGGCCTGCAGGCTGTGCCCGTGGGCATCCCTG  
CTGCCAGCCAGCGCATCTTCCTGCACGGCAACCGCATCTCGCATGTGCCAGCTGCCAGCTTC  
CGTGCCCTGCCGCAACCTCACCATCCTGTGGCTGCACTCGAATGTGCTGGCCCGAATTGATGC  
GGCTGCCTTCACTGGCCTGGCCCTCCTGGAGCAGCTGGACCTCAGCGATAATGCACAGCTCC  
GGTCTGTGGACCCTGCCACATTCCACGGCCTGGGCCGCCTACACACGCTGCACCTGGACCGC  
TGCGGCCTGCAGGAGCTGGGCCCGGGGCTGTTCCGCGGCCTGGCTGCCCTGCAGTACCTCTA  
CCTGCAGGACAACGCGCTGCAGGCACTGCCTGATGACACCTTCCGCGACCTGGGCAACCTCA  
CACACCTCTTCCTGCACGGCAACCGCATCTCCAGCGTGCCCGAGCGCGCCTTCCGTGGGCTG  
CACAGCCTCGACCGTCTCCTACTGCACCAGAACCGCGTGCCCCATGTGCACCCGCGATGCCTT  
CCGTGACCTTGGCCGCCTCATGACACTCTATCTGTTTGCCAACAATCTATCAGCGCTGCCCA  
CTGAGGCCCTGGCCCCCTGCGTGCCCTGCAGTACCTGAGGCTCAACGACAACCCCTGGGTG  
TGTGACTGCCGGGCACGCCCCTCTGGGCCTGGCTGCAGAAGTTCGCGGGCTCCTCCTCCGA  
GGTGCCCTGCAGCCTCCCGCAACGCCTGGCTGGCCGTGACCTCAAACGCCTAGCTGCCAATG  
ACCTGCAGGGCTGCGCTGTGGCCACCGGCCCTTACCATCCCATCTGGACCGGCAGGGCCACC  
GATGAGGAGCCGCTGGGGCTTCCCAAGTGCTGCCAGCCAGATGCCGCTGACAAGGCCTCAGT  
ACTGGAGCCTGGAAGACCAGCTTCGGCAGGCAATGCGCTGAAGGGACGCGTGCCGCCCGGTG  
ACAGCCCGCCGGGCAACGGCTCTGGCCACGGCACATCAATGACTCACCCCTTGGGACTCTG  
CCTGGCTCTGCTGAGCCCCCGCTCACTGCAGTGCGGCCCGAGGGCTCCGAGCCACCAGGGTT  
CCCCACCTCGGGCCCTCGCCGGAGGCCAGGCTGTTACGCAAGAACCGCACCCGCGAGCCACT  
GCCGTCTGGGCCAGGCAGGCAGCGGGGGTGGCGGGACTGGTGACTCAGAAGGCTCAGGTGCC  
CTACCCAGCCTCACCTGCAGCCTCACCCCCCTGGGCCTGGCGCTGGTGCTGTGGACAGTGCT  
TGGGCCCTGCTGAACCCCCAGCGGACACAAGAGCGTGCTCAGCAGCCAGGTGTGTGTACATAC  
GGGGTCTCTCTCCACGCCGCCAAGCCAGCCGGGCGGCCGACCCGTGGGGCAGGCCAGGCCAG  
GTCCTCCCTGATGGACGCCTGCCGCCCGCCACCCCCATCTCCACCCCATCATGTTTACAGGG  
TTCGGCGGCAGCGTTTGTTCAGAACGCCGCTCCACCCAGATCGCGGTATATAGAGATAT  
GCATTTTATTTTACTTGTGTAAAAATATCGGACGACGTGGAATAAAGAGCTCTTTTCTTAA  
AAAA

7671237



**FIGURE 161**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44184

><subunit 1 of 1, 473 aa, 1 stop

><MW: 50708, pI: 9.28, NX(S/T): 6

MKRASAGGSRL LAWVLWLQAWQVAAPCPGACVCYNEPKVTTSCPQQGLQAVPVGIP AASQRI  
FLHGNRISHVPAASFRACRNLTILWLHSNVLARIDAAFTGLALLEQLDLSDNAQLRSVDPA  
TFHGLGRLHTLHLDRCLQELGPGLFRGLAALQYLYLQDNALQALPDDTFRDLGNLTHLFLH  
GNRISSVPERAFRGLHSLDRLLLHQNRVAHVHHPHAFRDLGRLMTLYLFANNLSALPTEALAP  
LRALQYLRLNDNPWVCD CRARPLWAWLQKFRGSSSEVPCSLPQRLAGRDLKRLAANDLQGCA  
VATGPYHPIWTGRATDEEPLGLPKCCQPDAA DKASVLEPGRPASAGNALKGRVPPGDSPPGN  
GSGPRHINDSPFGTLPGSAEPPLTAVRPEGSEPPGFPTSGPRRRPGCSRKNRTRSHCRLGQA  
GSGGGGTGDSEGGALPSLTCSLTPLGLALVLWTVLGPC

**Important features:****Signal peptide:**

amino acids 1-26

**Leucine zipper pattern.**

amino acids 135-156

**Glycosaminoglycan attachment site.**

amino acids 436-439

**N-glycosylation site.**

amino acids 82-85, 179-183, 237-240, 372-375 and 423-426

**VWFC domain**

amino acids 411-425

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FIGURE 162

GGAAGTCCACGGGGAGCTTGGATGCCAAAGGGAGGACGGCTGGGTCTCTGGAGAGGACTAC  
TCACTGGCATATTTCTGAGGTATCTGTAGAATAACCACAGCCTCAGATACTGGGGACTTTAC  
AGTCCCACAGAACCGTCTCTCCAGGAAGCTGAATCCAGCAAGAACA**ATG**GAGGGCCAGCGGGA  
AGCTCATTTGCGAGACAAAGGCAAGTCCTTTTTTCTCTTTTGGGCTTATCTCTGGCG  
GGCGCGGCGGAACCTAGAAGCTATTCTGTGGTGGAGGAACTGAGGGCAGCTCCTTTGTCAC  
CAATTTAGCAAAGGACCTGGGTCTGGAGCAGAGGGAATTCTCCAGGCGGGGGGTTAGGGTTG  
TTTCCAGAGGGGAACAACTACATTTGCGAGCTCAATCAGGAGACCGCGGATTGTGTTGCTAAAT  
GAGAAATTGGACCGTGAGGATCTGTGCGGTCAACACAGAGCCCTGTGTGCTACGTTTCCAAGT  
GTTGCTAGAGAGTCCCTTCGAGTTTTTTCAAGCTGAGCTGCAAGTAATAGACATAAACGACC  
ACTCTCCAGTATTTCTGGACAAACAAATGTTGGTGAAAGTATCAGAGAGCAGTCCTCCTGGG  
ACTACGTTTCCTCTGAAGAATGCCGAAGACTTAGATGTAGGCCAAAACAATATTGAGAACTA  
TATAATCAGCCCCAACTCCTATTTTCGGGTCTCACCCGCAAACGCAGTGATGGCAGGAAAT  
ACCCAGAGCTGGTGCTGGACAAAGCGCTGGACCGAGAGGAAGAAGCTGAGCTCAGGTTAACA  
CTCACAGCACTGGATGGTGGCTCTCCGCCCAGATCTGGCACTGCTCAGGTCTACATCGAAGT  
CCTGGATGTCAACGATAATGCCCCCTGAATTTGAGCAGCCTTTCTATAGAGTGCAGATCTCTG  
AGGACAGTCCGGTAGGCTTCCTGGTTGTGAAGGTCTCTGCCACGGATGTAGACACAGGAGTC  
AACGGAGAGATTTCTTATTCACTTTTCCAAGCTTCAGAAGAGATTGGCAAACCTTTAAGAT  
CAATCCCTTGACAGGAGAAATTGAACTAAAAAAACAACCTCGATTTCGAAAACTTCAGTCCT  
ATGAAGTCAATATTGAGGCAAGAGATGCTGGAACCTTTTCTGGAAAATGCACCGTTCTGATT  
CAAGTGATAGATGTGAACGACCATGCCCCAGAAGTTACCATGTCTGCATTTACCAGCCCAAT  
ACCTGAGAACGCGCCTGAACTGTGGTTGCACTTTTTCAGTGTTTCAGATCTTGATTTCAGGAG  
AAAATGGGAAAATTAGTTGCTCCATTCAGGAGGATCTACCCTTCCTCCTGAAATCCGCGGAA  
AACTTTTACACCCTACTAACGGAGAGACCACTAGACAGAGAAAGCAGAGCGGAATACAACAT  
CACTATCACTGTCACTGACTTGGGGACCCCTATGCTGATAACACAGCTCAATATGACCGTGC  
TGATCGCCGATGTCAATGACAACGCTCCCGCCTTCACCCAAACCTCCTACACCCTGTTTCGTC  
CGCGAGAACAAACAGCCCCGCCCTGCACATCCGCAGCGTCAGCGCTACAGACAGAGACTCAGG  
CACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCCAGGACCCGCACCTGCCCTCACAT  
CCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTCTCTGGACTACGAG  
GCCCTGCAGGGGTTCCAGTTCCGCGTGGGCGCTTCAGACCACGGCTCCCCGGCGCTGAGCAG  
CGAGGCGCTGGTGCGCGTGGTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACC  
CGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGCCGGGCTAC  
CTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCCTGGCTGTTCGTACCA  
GCTGCTCAAGGCCACGGAGCTCGGTCTGTTTCGGCGTGTGGGCGCACAAATGGCGAGGTGCGCA  
CCGCCAGGCTGCTGAGCGAGCGCGACGCGGCCAAGCACAGGCTGGTGGTGCTGGTCAAGGAC  
AATGGCGAGCCTCCGCGCTCGGCCACCGCCACGCTGCACGTGCTCCTGGTGGACGGCTTCTC  
CCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCCGACCCAGGCCAGGCCGACTTGCTCACCG  
TCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCTTTTCGGTGCTCCTGTTT  
GTGGCGGTGCGGCTGTGTAGGAGGAGCAGGGCGGCCCTCGGTGGGTGCTGCTTGGTGCCCGA  
GGGCCCCCTTCCAGGGCATCTTGTGGACATGAGCGGCACCAGGACCCCTATCCCAGAGCTACC  
AGTATGAGGTGTGTCTGGCAGGAGGCTCAGGGACCAATGAGTTCAAGTTCCTGAAGCCGATT  
ATCCCCAACTTCCCTCCCCAGTGCCCTGGGAAAGAAATACAAGGAAATTCTACCTTCCCCAA  
TAACTTTGGGTTCAATATTCAG**TGA**CCATAGTTGACTTTTACATTCCATAGGTATTTTATTT  
TGTGGCATTTCATGCCAATGTTTATTTCCCCCAATTTGTGTGTATGTAATATTGTACGGAT  
TTACTCTTGATTTTTCTCATGTTCTTTCTCCCTTTGTTTTAAAGTGAACATTTACCTTTATT  
CCTGGTTCTT

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**FIGURE 163**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48314

<subunit 1 of 1, 798 aa, 1 stop

<MW: 87552, pI: 4.84, NX(S/T): 5

MEASGKLICRQRQVLFSFLLLGLSLAGAAEPRSYSVVEETEGSSFVTNLAKDLGLEQREFSR  
RGVRVVSARGNKLHLQLNQETADLLLNEKLDREDLCGHTEPCVLRQVLLSPFEFFQAELOV  
IDINDHSPVFLDKQMLVKVSESSPPGTTFPLKNAEDLDVGQNNIENYIISPNSYFRVLTRKR  
SDGRKYPELVLDKALDREEEAELRLTLTALDGGSPPRSGTAQVYIEVLDVNDNAPEFEQPFY  
RVQISEDSPVGFLVVKVSATDVDTGNGEISYSLFQASEEIGKTFKINPLTGEIELKKQLDF  
EKLQSYEVNIEARDAGTFSGKCTVLIQVIDVNDHAPEVTMSAFTSPIPENAPETVVALFSVS  
DLDSGENGKISCSIQEDLPFLLKSAENFYTLTLLTERPLDRESRAEYNITITVTDLGTPLMLITQ  
LNMTVLIADVNDNAPAFQTQTSYTLFVRENNSPALHIRSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLTSLVSINADNGHLFALRSLDYEALQGFQFRVGASDHGSPALSSEALVRVVVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDGQNAWLSYQLLKATELGFLGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHVLLVDGFSQPYLPLPEAAPTQAQ  
ADLLTVYLVVALASVSSLFLFSVLLFVAVRLCRRSRAASVGRCLVPEGPLPGHLVDMSGTRT  
LSQSYQYEVCLAGGSGTNEFKFLKPIIPNFPQCPGKEIQGNSTFPNNFGFNIQ

**Important features:****Signal peptide:**

amino acids 1-26

**Transmembrane domain:**

amino acids 685-712

**Cadherins extracellular repeated domain signature.**

amino acids 122-132, 231-241, 336-346, 439-449 and 549-559

**ATP/GTP-binding site motif A (P-loop).**

amino acids 285-292

**N-glycosylation site.**

amino acids 418-421, 436-439, 567-570 and 786-789

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**FIGURE 164**

ACCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCCCACGCGTCCGCGCGTAGCCGTGC  
GCCGATTGCCTCTCGGCCTGGGCAATGGTCCCGGCTGCCGGTCGACGACCGCCCCGCGTCAT  
GCGGCTCCTCGGCTGGTGGCAAGTATTGCTGTGGGTGCTGGGACTTCCCGTCCGCGGCGTGG  
AGGTTGCAGAGGAAAGTGGTCGCTTATGGTCAGAGGAGCAGCCTGCTCACCTCTCCAGGTG  
GGGGCTGTGTACCTGGGTGAGGAGGAGCTCCTGCATGACCCGATGGGCCAGGACAGGGCAGC  
AGAAGAGGCCAATGCGGTGCTGGGGCTGGACACCCAAGGCGATCACATGGTGATGCTGTCTG  
TGATTCCTGGGGAAGCTGAGGACAAAGTGAGTTCAGAGCCTAGCGGCGTCACCTGTGGTGCT  
GGAGGAGCGGAGGACTCAAGGTGCAACGTCCGAGAGAGCCTTTTCTCTCTGGATGGCGCTGG  
AGCACACTTCCCTGACAGAGAAGAGGAGTATTACACAGAGCCAGAAGTGGCGGAATCTGACG  
CAGCCCCGACAGAGGACTCCAATAACACTGAAAGTCTGAAATCCCCAAAGGTGAACTGTGAG  
GAGAGAAACATTACAGGATTAGAAAATTTCACTCTGAAAATTTTAAATATGTCACAGGACCT  
TATGGATTTTCTGAACCCAAACGGTAGTGACTGTACTCTAGTCCTGTTTTACACCCCGTGGT  
GCCGCTTTTCTGCCAGTTTGGCCCCCTCACTTTAACTCTCTGCCCCGGGCATTTCCAGCTCTT  
CACTTTTTTGGCACTGGATGCATCTCAGCACAGCAGCCTTTCTACCAGGTTTGGCACCGTAGC  
TGTTCCCTAATATTTTATTATTTCAAGGAGCTAAACCAATGGCCAGATTTAATCATAACAGATC  
GAACACTGGAAACACTGAAAATCTTCATTTTTTAATCAGACAGGTATAGAAGCCAAGAAGAAT  
GTGGTGGTAACTCAAGCCGACCAAATAGGCCCTCTTCCCAGCACTTTGATAAAAAGTGTGGA  
CTGGTTGCTTGTATTTTCCTTATTCTTTTTTAATTAGTTTTATTATGTATGCTACCATTCGAA  
CTGAGAGTATTCGGTGGCTAATTCAGGACAAGAGCAGGAACATGTGGAGTAGTGATGGTCT  
GAAAGAAGTTGGAAAGAGGAACTTCAATCCTTCGTTTCAGAAATTAGTGCTACAGTTTCATA  
CATTTTCTCCAGTGACGTGTTGACTTGAACTTCAGGCAGATTAAAAGAATCATTTGTTGAA  
CAACTGAATGTATAAAAAAATTATAAACTGGTGTTTTAACTAGTATTGCAATAAGCAAATGC  
AAAAATATTCAATAG

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**FIGURE 165**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48333

><subunit 1 of 1, 360 aa, 1 stop

><MW: 39885, pI: 4.79, NX(S/T): 7

MVPAAGRPPRVMRLLGWWQVLLWVLGLPVRGVEVAEESGRLWSEEQPAHPLQVGAVYLGEE  
ELLHDPMGQDRAAEEANAVLGLDTQGDHVMVLSVIPGEAEDKVSSEPSGVTCGAGGAEDSRC  
NVRESLFSLDGAGAHFPDREEEYYTEPEVAESDAAPTEDSNNTESLKSPKVNCEERNITGLE  
NFTLKILNMSQDLMDFLNPNNGSDCTLVLFYTPWCRFSASLAPHFNSLPRAFPALHFLALDAS  
QHSSLSTRFGTVAVPNILLFQGAKPMAFNFHTDRTLETCLKIFIFNQTGIEAKKNVVVTQADQ  
IGPLPSTLIKSVDWLLVFSLFFLISFIMYATIRTESIRWLIPGQEQEHVE

**Important features:****Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 321-340

**Homologous region to dilsufide isomerase**

amino acids 212-302

**N-glycosylation site.**

amino acids 165-168, 181-184, 187-190, 194-197, 206-209, 278-281  
and 293-296

**Thioredoxin domain**

amino acids 211-227

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**FIGURE 166**

CCCGGCTCCGCTCCCTCTGCCCCCTCGGGGTCGCGCGCCACGATGCTGCAGGGGCCCTGGCT  
CGCTGCTGCTGCTCTTCCTCGCCTCGCACTGCTGCCTGGGCTCGGCGCGCGGGCTCTTCCTC  
TTTGGCCAGCCCGACTTCTCCTACAAGCGCAGCAATTGCAAGCCCATCCCGGTCAACCTGCA  
GCTGTGCCACGGCATCGAATACCAGAACATGCGGCTGCCAACCTGCTGGGCCACGAGACCA  
TGAAGGAGGTGCTGGAGCAGGCCGGCGCTTGGATCCCGCTGGTCATGAAGCAGTGCCACCCG  
GACACCAAGAAGTTCCTGTGCTCGCTCTTCGCCCCCGTCTGCCTCGATGACCTAGACGAGAC  
CATCCAGCCATGCCACTCGCTCTGCGTGCAAGGTGAAGGACCGCTGCGCCCCGGTCATGTCCG  
CCTTCGGCTTCCCCTGGCCCGACATGCTTGAGTGCGACCGTTTCCCCCAGGACAACGACCTT  
TGCATCCCCCTCGCTAGCAGCGACCACCTCCTGCCAGCCACCGAGGAAGCTCCAAAGGTATG  
TGAAGCCTGCAAAAATAAAAATGATGATGACAACGACATAATGGAAACGCTTTGTAAAAATG  
ATTTTGCACTGAAAATAAAAGTGAAGGAGATAACCTACATCAACCGAGATACCAAATCATC  
CTGGAGACCAAGAGCAAGACCATTTACAAGCTGAACGGTGTGTCCGAAAGGGACCTGAAGAA  
ATCGGTGCTGTGGCTCAAAGACAGCTTGCAGTGCACCTGTGAGGAGATGAACGACATCAACG  
CGCCCTATCTGGTCATGGGACAGAAACAGGGTGGGGAGCTGGTGATCACCTCGGTGAAGCGG  
TGGCAGAAGGGGCAGAGAGAGTTCAAGCGCATCTCCCGCAGCATCCGCAAGCTGCAGTGCTTA  
GTCCCCGGCATCCTGATGGCTCCGACAGGCCTGCTCCAGAGCACGGCTGACCATTTCTGCTCC  
GGGATCTCAGCTCCCGTTCCCCAAGCACACTCCTAGCTGCTCCAGTCTCAGCCTGGGCAGCT  
TCCCCCTGCCTTTTGCACGTTTGCATCCCCAGCATTTCTGAGTTATAAGGCCACAGGAGTG  
GATAGCTGTTTTACCTAAAGGAAAAGCCCACCCGAATCTTGTAGAAATATTCAAACATAA  
AAATCATGAATATTTTAA

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**FIGURE 167**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50920

><subunit 1 of 1, 295 aa, 1 stop

><MW: 33518, pI: 7.74, NX(S/T): 0

MLQGPGSLLLLFLASHCCLGSARGLFLFGQPDFS YKRSNCKPIPVNLQLCHGIEYQNMRLPN  
LLGHETMKEVLEQAGAWIPLVMKQCHPDTKKFLCSLFAPVCLDDLD ETIQPCHSLCVQVKDR  
CAPVMSAFGFPWPDMLECDRFPQDNDLCIPLASSDHLLPATEEAPKVCEACKNKNDNDNDIM  
ETLCKNDFALKIKVKEITYINRDTKIILETKSKTIYKLNGVSE RDLKKSVLWLKDSLQCTCE  
EMNDINAPYLVMGQKQG GELVITSVKRWQKGQREFKRISRSIRKLQC

**Important features:****Signal peptide:**

amino acids 1-20

**Cysteine rich domain, homologous to frizzled N terminus**

amino acids 6-153

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**FIGURE 168**

GTGGAGGCCGCCGACGATGGCGGGGCCGACGGAGGCCGAGACGGGGTTGGCCGAGCCCCGGG  
CCCTGTGCGCGCAGCGGGGCCACCGCACCTACGCGCGCCGCTGGGTGTTCTGTCTCGCGATC  
AGCCTGCTCAACTGCTCCAACGCCACGCTGTGGCTCAGCTTTGCACCTGTGGCTGACGTCAT  
TGCTGAGGACTTGGTCCTGTCCATGGAGCAGATCAACTGGCTGTCACTGGTCTACCTCGTGG  
TATCCACCCCATTTGGCGTGGCGGCCATCTGGATCCTGGACTCCGTCGGGCTCCGTGCGGGC  
ACCATCCTGGGTGCGTGGCTGAACTTTGCCGGGAGTGTGCTACGCATGGTGCCCTGCATGGT  
TGTTGGGACCCAAAACCCATTTGCCTTCCTCATGGGTGGCCAGAGCCTCTGTGCCCTTGCCC  
AGAGCCTGGTCATCTTCTCTCCAGCCAAGCTGGCTGCCTTGTGGTTCCCAGAGCACCAGCGA  
GCCACGGCCAACATGCTCGCCACCATGTCGAACCCTCTGGGCGTCCTTGTGGCCAATGTGCT  
GTCCCCTGTGCTGGTCAAGAAGGGTGAGGACATTCCGTTAATGCTCGGTGTCTATAACCATCC  
CTGCTGGCGTCGTCTGCCTGCTGTCCACCATCTGCCTGTGGGAGAGTGTGCCCCCACC  
CCCTCTGCCGGGGCTGCCAGCTCCACCTCAGAGAAGTTCCTGGATGGGCTCAAGCTGCAGCT  
CATGTGGAACAAGGCCTATGTCATCCTGGCTGTGTGCTTGGGGGGAATGATCGGGATCTCTG  
CCAGCTTCTCAGCCCTCCTGGAGCAGATCCTCTGTGCAAGCGGCCACTCCAGTGGGTTTTCC  
GGCCTCTGTGGCGCTCTCTTCATCACGTTTGGGATCCTGGGGGCACTGGCTCTCGGCCCCTA  
TGTGGACCGGACCAAGCACTTCACTGAGGCCACCAAGATTGGCCTGTGCCTGTTCTCTCTGG  
CCTGCGTGCCCTTTGCCCTGGTGTCCAGCTGCAGGGACAGACCCTTGCCCTGGCTGCCACC  
TGCTCGCTGCTCGGGCTGTTTGGCTTCTCGGTGGGCCCCGTGGCCATGGAGTTGGCGGTCTGA  
GTGTTCTTCCCCGTGGGGGAGGGGGCTGCCACAGGCATGATCTTTGTGCTGGGGCAGGCCG  
AGGGAATACTCATCATGCTGGCAATGACGGCACTGACTGTGCGACGCTCGGAGCCGTCCTTG  
TCCACCTGCCAGCAGGGGGAGGATCCACTTGACTGGACAGTGTCTCTGCTGCTGATGGCCGG  
CCTGTGCACCTTCTTCAGCTGCATCCTGGCGGTCTTCTTCCACACCCCATACCGGCGCCTGC  
AGGCCGAGTCTGGGGAGCCCCCTCCACCCGTAACGCCGTGGGCGGCGCAGACTCAGGGCCG  
GGTGTGGACCGAGGGGGAGCAGGAAGGGCTGGGGTCCTGGGGCCCAGCACGGCGACTCCGGA  
GTGCACGGCGAGGGGGGCTCGCTAGAGGACCCAGAGGGCCCCGGGAGCCCCACCCAGCCT  
GCCACCGAGCGACTCCCCGTGCGCAAGGCCAGCAGCCACCGACGCGCCCTCCCGCCCCGGC  
AGACTCGCAGGCAGGGTCCAAGCGTCCAGGTTTATTGACCCGGCTGGGTCTCACTCCTCCTT  
CTCCTCCCCGTGGGTGATCACGTAGCTGAGCGCCTTGTAAGTCCAGGTTGCCCGCCACATCGA  
TGGAGGCGAACTGGAACATCTGGTCCACCTGCGGGCGGGGGCGAAAGGGCTCCTTGCGGGCT  
CCGGGAGCGAATTACAAGCGCGCACCTGAAAA

7691237

**FIGURE 169**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50988

><subunit 1 of 1, 560 aa, 1 stop

><MW: 58427, pI: 6.86, NX(S/T): 2

MAGPTEAETGLAEPRALCAQRGHRTYARRWVFLLAISLLNCSNATLWLSFAPVADVIAEDLV  
LSMEQINWLSLVYLVVSTPFGVAAIWILDSVGLRAATILGAWLNFAGSVLRMVPCMVGTON  
PFAFLMGGQSLCALAQSLVIFSPAKLAALWFPEHQRTANMLATMSNPLGVLVANVLSPVLV  
KKGEDIPLMLGVYTIPAGVVCLLSTICLWESVPPTPPSAGAASSTSEKFLDGLKLQLMWNKA  
YVILAVCLGGMIGISASFSALLEQILCASGHSSGFSGLCGALFITFGILGALALGPYVDRTK  
HFTEATKIGLCLFSLACVPFALVSQQLQGQTLALAATCSLLGLFGFSVGPVAMELAVECSFPV  
GEGAATGMIFVLGQAEGILIMLMTALTVRRSEPSLSTCQQGEDPLDWTVSLLLMAGLCTFF  
SCILAVFFHTPYRRLQAESGEPSTRNAVGGADSGPGVDRGGAGRAGVLGPSTATPECTARG  
ASLEDPRGPGSPHPACHRATPRAQGPAATDAPSRPGRLAGRVQASRFIDPAGSHSSFSSPWVIT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 61-79, 98-112, 126-146, 169-182, 201-215, 248-268,  
280-300, 318-337, 341-357, 375-387, 420-441

**N-glycosylation site.**

amino acids 40-43 and 43-46

**Glycosaminoglycan attachment site.**

amino acids 468-471

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**FIGURE 170**

GTCCCACATCCTGCTCAACTGGGTCAGGTCCCTCTTAGACCAGCTCTTGTECATCATTTGCTGAAGTGGACCAAC  
TAGTTCCCCAGTAGGGGGTCTCCCCTGGCAATTCTTGATCGGCGTTTGGACATCTCAGATCGCTTCCAATGAAGA  
TGGCCTTGCCCTGGGGTCCTGCTTGTTTCATAATCATCTAACTATGGGACAAGGTTGTGCCGGCAGCTCTGGGGG  
AAGGAGCACGGGGCTGATCAAGCCATCCAGGAAACACTGGAGGACTTGTCCAGCCTTGAAAGAACTCTAGTGGT  
TCTGAATCTAGCCCACTTGGCGGTAAGCATGATGCAACTTCTGCAACTTCTGCTGGGGCTTTTGGGGCCAGGTGG  
CTACTTATTTCTTTTAGGGGATTGTGAGGAGGTGACCACTCTCACGGTGAAATACCAAGTGTGAGAGGAAGTGCC  
ATCTGGTACAGTGATCGGGAAGCTGTCCCAGGAACTGGGCGGGAGGAGAGGGCGGAGGCAAGCTGGGGCCGCCTT  
CCAGGTGTTGCAGCTGCCTCAGGCGCTCCCCATTAGGTGGACTCTGAGGAAGGCTTGCTCAGCACAGGCAGGCG  
GCTGGATCGAGAGCAGCTGTGCCGACAGTGGGATCCCTGCCTGGTTTCTTTGATGTGCTTGCCACAGGGGATTT  
GGCTCTGATCCATGTGGAGATCCAAGTGTGGACATCAATGACCACCAGCCACGGTTTCCCAAAGGCGAGCAGGA  
GCTGGAAATCTCTGAGAGCGCCTCTCTGCGAACC CGGATCCCCCTGGACAGAGCTCTTGACCCAGACACAGGCC  
TAACACCCTGCACACCTACACTCTGTCTCCCAGTGAGCACTTTGCCTTGATGTGCTTGTGGGCCCTGATGAGAC  
CAAACATGCAGAACTCATAGTGGTGAAGGAGCTGGACAGGGAAATCCATTCAATTTTTTATGCTGCTGTTAACTGC  
CTATGACAATGGGAACCCCCCAAGTCAGGTACCAGCTTGGTCAAGGTCAACGTCTTGGAATCCAATGACAATAG  
CCCTGCGTTTGCTGAGAGTTCAGTGGCACTGGAAATCCAAGAAGATGCTGCACCTGGTACGCTTCTCATAAACT  
GACCGCCACAGACCCTGACCAAGGCCCAATGGGGAGGTGGAGTTCTTCCCTCAGTAAGCACATGCCTCCAGAGGT  
GCTGGACACCTTCAGTATTGATGCCAAGACAGGCCAGGTCACTTCTGCGTGCACCTCTAGACTATGAAAAGAACC  
TGCTTACGAGGTGGATGTTGAGGCAAGGGACCTGGGTCCCAATCCTATCCCAGCCATTGCAAAGTTCTCATCAA  
GGTTCTGGATGTCAATGACAACATCCCAAGCATCCACGTACATGGGCCTCCCAGCCATCACTGGTGTGAGAAGC  
TCTTCCCAAGGACAGTTTTATTGCTCTTGTCATGGCAGATGACTTGGAATCAGGACACAATGGTTTGGTCCACTG  
CTGGCTGAGCCAAGAGCTGGGCCACTTCAGGCTGAAAAGAACTAATGGCAACACATACATGTTGCTAACCAATGC  
CACACTGGACAGAGAGCAGTGGCCCCAATATACCCTCACTCTGTTAGCCCCAAGACCAAGGACTCCAGCCCTTATC  
AGCCAAGAAACAGCTCAGCATTGAGATCAGTGACATCAACGACAATGCACCTGTGTTTGAGAAAAGCAGGTATGA  
AGTCTCCACGCGGGGAAAACAACCTTACCCTCTCTTACCTCATTACCATCAAGGCTCATGATGCAGACTTGGGCAT  
TAATGGAAAAGTCTCATACCGCATCCAGGACTCCCCAGTTGCTCACTTAGTAGCTATTGACTCCAACACAGGAGA  
GGTCACTGCTCAGAGGTCACTGAACATATGAAGAGATGGCCGGCTTTGAGTTCCAGGTGATCGCAGAGGACAGCGG  
GCAACCCATGCTTGCATCCAGTGTCTGTGTGGGTGAGCCTCTTGATGCCAATGATAATGCCCCAGAGGTGGT  
CCAGCCTGTGCTCAGCGATGGAAAAGCCAGCCTCTCCGTGCTTGTGAATGCCTCCACAGGCCACCTGCTGGTGCC  
CATCGAGACTCCCAATGGCTTGGGCCAGCGGGCACTGACACACCTCCACTGGCCACTCACAGCTCCCGGCCATT  
CCTTTTGACAACCATTGTGGCAAGAGATGCAGACTCGGGGGCAAATGGAGAGCCCCCTCTACAGCATCCGCAATGG  
AAATGAAGCCCACCTCTTCATCCTCAACCCTCATACGGGGCAGCTGTTGTCATGTCAATGTCAACCAATGCCAGCAGCCT  
CATTGGGAGTGAGTGGGAGCTGGAGATAGTAGTAGAGGACCAGGGAAGCCCCCCTTACAGACCCGAGCCCTGTT  
GAGGGTCATGTTTGTCAACAGTGTGGACCACCTGAGGGACTCAGCCCGCAAGCCTGGGGCCTTGAGCATGTGAT  
GCTGACGGTGATCTGCCTGGCTGTACTGTTGGGCATCTTCGGGTGATCCTGGCTTTGTTTATGTCCATCTGCCG  
GACAGAAAAGAAGGACAACAGGGCCTACAACCTGTGCGGAGGCGGAGTCCACCTACCGCCAGCAGCCCAAGAGGCC  
CCAGAAACACATTGAGAAGGCAGACATCCACCTCGTGCTGTGCTCAGGGGTGAGGCAGGTGAGCCTTGTGAAGT  
CGGGCAGTCCCAAAAGATGTGGACAAGGAGGCGATGATGGAAGCAGGCTGGGACCCCTGCCTGCAGGCCCCCTT  
CCACCTCACCCCGACCCTGTACAGGACGCTGCGTAATCAAGGCAACCAGGGAGCACC GGCGGAGAGCCGAGAGGT  
GCTGCAAGACACGGTCAACCTCCTTTTCAACCATCCCAGGCAGAGGAATGCCTCCCGGGAGAACCTGAACCTTCC  
CGAGCCCCAGCCTGCCACAGGCCAGCCACGTTCCAGGCCCTCTGAAGGTTGCAGGCAGCCCCACAGGGAGGCTGGC  
TGGAGACCAGGGCAGTGAGGAAGCCCCACAGAGGCCACCAGCCTCCTCTGCAACCCTGAGACGGCAGCGACATCT  
CAATGGCAAAGTGTCCCCTGAGAAAGAATCAGGGCCCCGTCAGATCCTGCGGAGCCTGGTCCGGCTGTCTGTGGC  
TGCCTTCCCGAGCGGAACCCCGTGGAGGAGCTCACTGTGGATTCTCCTCCTGTTGAGCAATCTCCCAGCTGCT  
GTCCTTGCTGCATCAGGGCCAATTCCAGCCCCAAACCAACCCAGGGAATAAGTACTTGGCCAAGCCAGGAGG  
CAGCAGGAGTGCAATCCCAGACACAGATGGCCCCAAGTGAAGGGCTGGAGGCCAGACAGACCAGAACAGGAGGA  
AGGGCCTTTGGATCCTGAAGAGGACCTCTCTGTGAAGCAACTGCTAGAAGAAGAGCTGTCAAGTCTGCTGGACCC  
CAGCACAGGTCTGGCCCTGGACCGGCTGAGCGCCCCCTGACCGGCCCTGGATGGCGAGACTCTCTTTGCCCTCAC  
CACCAACTACCGTGACAATGTGATCTCCCCGGATGCTGCAGCCACGGAGGAGCCGAGGACCTTCCAGACGTTCCG  
CAAGGCAGAGGCACCAGAGCTGAGCCCAACAGGCACGAGGCTGGCCAGCACCTTTGTCTCGGAGATGAGCTCACT  
GCTGGAGATGCTGCTGGAACAGCGCTCCAGCATGCCCGTGGAGGCGCCTCCGAGGCGCTGCGGCGGCTCTCGGT  
CTGCGGGAGGACCCCTCAGTTTAGACTTGGCCACCAGTGCAGCCTCAGGCATGAAAGTGCAAGGGGACCCAGGTGG  
AAAGACGGGGACTGAGGGCAAGAGCAGAGGCAGCAGCAGCAGCAGGTCCTGTGAACATACCTCAGACGCCT  
CTGGATCCAAGAACCAGGGGCCTGAGGATCTGTGGACAAGAGCTGGTTTCTAAAATCTTGTAACCTCACTAGCTAG  
CGGCGGCCTGAGAACTTTAGGGTGACTGATGCTACCCCCACAGAGGAGGCAAGAGCCCCAGGACTAACAGCTGAC  
TGACCAAAGCAGCCCTTGTAAAGCAGCTCTGAGTCTTTTGGAGGACAGGGACGGTTTGTGGCTGAGATAAGTGTT  
TCCTGGCAAACATATGTGGAGCACAAAGGGTCAGTCTCTGGCAGAACAGATGCCACGGAGTATCACAGGCAGG  
AAAGGGTGGCCTTCTTGGGTAGCAGGAGTCAGGGGGCTGTACCCTGGGGGTGCCAGGAAATGCTCTCTGACCTAT  
CAATAAAGGAAAAGCAGTAAAAA

**FIGURE 171**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48331

<subunit 1 of 1, 1184 aa, 1 stop

<MW: 129022, pI: 5.20, NX(S/T): 5

MMQLLQLLLGLLGPGGYLFLLGDCQEVTTLTVKYQVSEEVPSGTVIGKLSQELGREERRRQA  
GAAFQVLQLPQALPIQVDSEEGLLSTGRRLDREQLCRQWDPCLVSFVLDLATGDLALIHVEIQ  
VLDINDHQPRFPKGEQELEISESASLRTRIPLDRALDPDTGPNTLHTYTLSPSEHFALDVIV  
GPDETKHAELIVVKELDREIHSFFDLVLTAYDNGNPPKSGTSLVKVNVLDSDNDNSPAFAESS  
LALEIQEDAAPGTLLIKLTATDPDQGPNGEVEFFLSKHMPEVLDTFSIDAKTGQVILRRPL  
DYEKNPAYEVDVQARDLGPNPIPAHCKVLIKVLVDVNDNIPSIHVTWASQPSLVSEALPKDSF  
IALVMADDLDSGHNGLVHCWLSQELGHFRLKRTNGNTYMLLTNATLDREQWPKYTLTLLAQD  
QGLQPLSAKKQLSIQISDINDNAPVFEKSRYEVSTRENNLPSLHLITIKAHADLGINGKVS  
YRIQDSPVAHLVAIDSNTGEVTAQRSLNYYEEMAGFEFQVIAEDSGQPMLASSVSVWVSLDA  
NDNAPEVVQPVLSDGKASLSVLVNASTGHLLVPIETPNGLGPAGTDTPLATHSSRPFLTT  
IVARDADSGANGEPLYSRNGNEAHLFILNPHTGQLFVNVTNASSLIGSEWELEIVVEDQGS  
PPLQTRALLRVMFVTSVDHLRDSARKPGALSMSMLTVICLAVLLGIFGLILALFMSICRTEK  
KDNRAYNCREAESTYRQQPKRPQKHIOKADIHLVPVLRGQAGEPCEVGQSHKDVDKEAMMEA  
GWDPCLOAPFHLTPTLYRTLNRNQGNGAPAESREVLQDTVNLLFNHPRQRNASRENLNLP  
QPATGQPRSRPLKVAGSPTGRLAGDQGSEEAPQRPPASSATLRRQRHLNGKVSPEKESGPRQ  
ILRSLVRLSVAFAERNPVEELTVDSPPVQQISQLLSLLHQGQFQPKPNHRGNKYLAKEGGS  
RSAIPDPTDGPSARAGGQTDPEQEEGPLDPEEDLSVKQLLEEELSSLLDPSTGLALDRLSAPD  
PAWMARLSLPLTTNYRDNVISPDAAATEEPRTFQTFGKAEAPELSPTGTRLASTFVSEMSSL  
LEMLLEQRSSMPVEAASEALRRLSVCGRTLSDLATSAASGMKVQGDPPGKTGTGEGKSRGSS  
SSSRCL

**Important features:****Signal peptide:**

amino acids 1-13

**Transmembrane domain:**

amino acids 719-739

**N-glycosylation site.**

amino acids 415-418, 582-585, 659-662, 662-665 and 857-860

**Cadherins extracellular repeated domain signature.**

amino acids 123-133, 232-242, 340-350, 448-458 and 553-563

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**FIGURE 172**

CGGACGCGTGGGCGGACGCGTGGGGGAGAGCCGCGAGTCCCGGCTGCAGCACCTGGGAGAAGG  
CAGACCGTGTGAGGGGGCCTGTGGCCCCAGCGTGCTGTGGCCTCGGGGAGTGGGAAGTGGAG  
GCAGGAGCCTTCCTTACACTTCGCCATGAGTTTCCTCATCGACTCCAGCATCATGATTACCT  
CCCAGATACTATTTTTTGGATTTGGGTGGCTTTTCTTCATGCGCCAATTGTTTAAAGACTAT  
GAGATACGTCAGTATGTTGTACAGGTGATCTTCTCCGTGACGTTTGCATTTTCTTGCACCAT  
GTTTGAGCTCATCATCTTTGAAATCTTAGGAGTATTGAATAGCAGCTCCCGTTATTTTCACT  
GGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTTTTCATGGTGCCTTTTTTACATTGGC  
TATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTTCTGTCTCTT  
ATGGCTGACCTTTATGTATTTCTTCTGGAACTAGGAGATCCCTTTCCCATTCCTCAGCCCAA  
AACATGGGATCTTATCCATAGAACAGCTCATCAGCCGGGTGGTGTGATTGGAGTGACTCTC  
ATGGCTCTTCTTTCTGGATTTGGTGCTGTCAACTGCCCATACACTTACATGTCTTACTTCCT  
CAGGAATGTGACTGACACGGATATTCTAGCCCTGGAACGGCGACTGCTGCAAACCATGGATA  
TGATCATAAGCAAAAAGAAAAGGATGGCAATGGCACGGAGAACAATGTTCCAGAAGGGGGAA  
GTGCATAACAAACCATCAGGTTTCTGGGGAATGATAAAAAGTGTTACCACTTCAGCATCAGG  
AAGTGAAAATCTTACTCTTATTCAACAGGAAGTGGATGCTTTGGAAGAATTAAGCAGGCAGC  
TTTTTCTGGAAACAGCTGATCTATATGCTACCAAGGAGAGAATAGAATACTCCAAAACCTTC  
AAGGGGAAATATTTTAATTTTCTTGGTTACTTTTTCTCTATTTACTGTGTTTGGAAAATTTT  
CATGGCTACCATCAATATTGTTTTTGATCGAGTTGGGAAAACGGATCCTGTCACAAGAGGCA  
TTGAGATCACTGTGAATTATCTGGGAATCCAATTTGATGTGAAGTTTTGGTCCCAACACATT  
TCCTTCATTCTTGTTGGAATAATCATCGTCACATCCATCAGAGGATTGCTGATCACTCTTAC  
CAAGTTCTTTTATGCCATCTCTAGCAGTAAGTCCTCCAATGTCATTGTCCTGCTATTAGCAC  
AGATAATGGGCATGTACTTTGTCTCCTCTGTGCTGCTGATCCGAATGAGTATGCCTTTAGAA  
TACCGCACCATAATCACTGAAGTCCTTGGAGAACTGCAGTTCAACTTCTATCACCGTTGGTT  
TGATGTGATCTTCCTGGTCAGCGCTCTCTCTAGCATACTCTTCCTCTATTTGGCTCACAAAC  
AGGCACCAGAGAAGCAAATGGCACCTTGAACTTAAGCCTACTACAGACTGTTAGAGGCCAGT  
GGTTTCAAATTTAGATATAAGAGGGGGGAAAAATGGAACCAGGGCCTGACATTTTATAAAC  
AAACAAAATGCTATGGTAGCATTTTTTACCTTCATAGCATACTCCTTCCCCGTCAGGTGATA  
CTATGACCATGAGTAGCATCAGCCAGAACATGAGAGGGAGAACTAACTCAAGACAATACTCA  
GCAGAGAGCATCCCGTGTGGATATGAGGCTGGTGTAGAGGCGGAGAGGAGCCAAGAACTAA  
AGGTGAAAAATACACTGGAACCTCTGGGGCAAGACATGTCTATGGTAGCTGAGCCAAACACGT  
AGGATTTCCGTTTTAAGGTTACATGGAAAAGGTTATAGCTTTGCCTTGAGATTGACTCATT  
AAAATCAGAGACTGTAACAAAAAAGGGCGGCGGCGACTCTAGAGTCG  
ACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATG

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**FIGURE 173**

MSFLIDSSIMITSQILFFGFGWLFFMRQLFKDYEIRQYVVQVIFSVTFAFSCTMFELIIFEI  
LGVLNSSSRYPFWKMNLCVILLILVFMVPFYIGYFIVSNIRLLHKQRLLFSCLLWLTFMYFF  
WKLGDPPFPLSPKHGILSIEQLISRVGVIQVTLMAALLSGFGAVNCPYTYMSYFLRNVTDTDI  
LALERRLLQTMDMIISKKKRMAMARRTMFQKGEVHNKPSGFWGMIKSVTTSASGSENLTLIQ  
QEVDAALEELSRQLFLETADLYATKERIEYSKTFKGKYFNFLGYFFSIYCVWKIFMATINIVF  
DRVGKTDVPVTRGIEITVNYLGIQFDVKFWSQHISFILVGIIIVTSIRGLLITLTKEFFYAIS  
SKSSNVIVLLLAQIMGYFVSSVLLIRMSMPLEYRTIITEVLGELQFNFYHRWFDVIFLVSA  
LSSILFLYLAHKQAPEKQMAP

**Important features:****Signal peptide:**

amino acids 1-23

**Potential transmembrane domains:**

amino acids 37-55, 81-102, 150-168, 288-311, 338-356, 375-398,  
425-444

**N-glycosylation sites.**

amino acids 67-70, 180-183 and 243-246

**Eukaryotic cobalamin-binding proteins**

amino acids 151-160

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**FIGURE 174**

CATGGGAAGTGGAGCCGGAGCCTTCCTTACACTCGCCATGAGTTTCCTCATCGACTCCAGCA  
TCATGATTACCTCCCNGANACTATTTTTTGGATTGTTGGGTGGCTTTTCTTCNGCGCCAATGTT  
TAAAGACTATGAGATACGTCAGTATGTTGTACNNGGTGATCTTCTCCGTGACGTTTGCCATTT  
CTTGCACCATGTTTGAGCTCATCATCTTTGAAATCTTNGGAGTATTGAATAGCAGCTCCCGT  
TATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATCCTGGTTNTCATGGTGCCTTT  
TTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCATAAACAACGACTGCTTTTTT  
CCTGTCTCTTATGGCTGACCTTTATGTATTTCCAG

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**FIGURE 175**

GTGTTGCCCTTGGGGAGGGGAAGGGGAGCCNGGCCCTTTCCTAAAATTTGGCCAAGGGTTTC  
TTTNTTGAATTCCGGGTNNNGNATACCTTCCCAGAAAATATTTTTTGGATTGGGGTAGNTT  
TTTTTCATGCGCCAATTGTTTAAAGACTATGAGATACGTCAGTATGTTGTACAGGTGATNTT  
NTCCGTGACGTTTGCATTTTCTTGCACCATGTTTGAGCTCATCATNTTTGAAATNTTAGGAG  
TATTGAATAGCAGCTCCCGTTATTTTCACTGGAAAATGAACCTGTGTGTAATTCTGCTGATC  
CTGGTTTTTCATGGTGCCTTTTTTACATTGGCTATTTTATTGTGAGCAATATCCGACTACTGCA  
TAAACAACGACTGCTTTTTTTCCTGTCTNTTATGGCTGACCTTTATGTATTTNTTNTGGAAAN  
TAGGAGATCCCTTTCCCATTC

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**FIGURE 176**

CTCGCGCAGGGATCGTCCC**ATG**GCCGGGGCTCGGAGCCGCGACCCTTGGGGGGGCTCCGGGATTTGCTACCTTTT  
TGGCTCCCTGCTCGTCGAACTGCTCTTCTCACGGGCTGTGCGCTTCAATCTGGACGTGATGGGTGCCTTGCGCAA  
GGAGGGCGAGCCAGGCAGCCTCTTCGGCTTCTCTGTGGCCCTGCACCGGCAGTTGCAGCCCCGACCCAGAGCTG  
GCTGCTGGTGGGTGCTCCCCAGGCCCTGGCTCTTCCTGGGCAGCAGGCGAATCGCACTGGAGGCCTCTTCGCTTG  
CCCGTTGAGCCTGGAGGAGACTGACTGCTACAGAGTGGACATCGACCAGGGAGCTGATATGCAAAAGGAAAGCAA  
GGAGAACCAGTGGTTGGGAGTCAGTGTTCGGAGCCAGGGGCTGGGGGCAAGATTGTTACCTGTGCACACCGATA  
TGAGGCAAGGCAGCGAGTGGACCAGATCCTGGAGACGCGGGATATGATTGGTCGCTGCTTTGTGCTCAGCCAGGA  
CCTGGCCATCCGGGATGAGTTGGATGGTGGGGAATGGAAGTTCTGTGAGGGACGCCCCAAGGCCATGAACAATT  
TGGGTTCTGCCAGCAGGGCACAGCTGCCGCCCTTCTCCCTGATAGCCACTACCTCCTCTTTGGGGCCCCAGGAAC  
CTATAATTGGAAGGGCACGGCCAGGGTGGAGCTCTGTGCACAGGGCTCAGCGGACCTGGCACACCTGGACGACGG  
TCCCTACGAGGCGGGGGGAGAGAAGGAGCAGGACCCCCGCTCATCCCGGTCCTGCCAACAGCTACTTTGGCTT  
CTCTATTGACTCGGGGAAAGGTCTGGTGCCTGCAGAAGAGCTGAGCTTTGTGGCTGGAGCCCCCGCGCCAACCA  
CAAGGGTGCTGTGGTCATCCTGCGCAAGGACAGCGCCAGTCCGCTGGTGCCGAGGTTATGCTGTCTGGGGAGCG  
CCTGACCTCCGGCTTTGGCTACTCACTGGCTGTGGCTGACCTCAACAGTGATGGCTGGCCAGACCTGATAGTGGG  
TGCCCCCTACTTCTTTGAGCGCCAAGAAGAGCTGGGGGGTGTGTGTATGTGTACTTGAACCAGGGGGGCTCACTG  
GGCTGGGATCTCCCTCTCCGGCTCTGCGGCTCCCTGACTCCATGTTCCGGATCAGCCTGGCTGTCTGGGGGA  
CCTCAACCAAGATGGCTTTCCAGATATTGCAGTGGGTGCCCCCTTTGATGGTGATGGGAAAGTCTTCATCTACCA  
TGGGAGCAGCCTGGGGGTTGTGCGCAAACCTTCACAGGTGCTGGAGGGCGAGGCTGTGGGCATCAAGAGCTTCGG  
CTACTCCCTGTCAGGCAGCTTGGATATGGATGGGAACCAATACCCTGACCTGCTGGTGGGCTCCCTGGCTGACAC  
CGCAGTGCTCTTCAGGGCCAGACCCATCCTCCATGTCTCCCATGAGGTCTCTATTGCTCCACGAAGCATCGACCT  
GGAGCAGCCCAACTGTGCTGGCGGGCCACTCGGTCTGTGTGGACCTAAGGGTCTGTTTCAGCTACATTGCAGTCCC  
CAGCAGCTATAGCCCTACTGTGGCCCTGGACTATGTGTTAGATGCGGACACAGACCGGAGGCTCCGGGGCCAGGT  
TCCCCGTGTGACGTTCTGAGCCGTAACCTGGAAGAACCAAGCACCAGGCCTCGGGCACCCTGTGGCTGAAGCA  
CCAGCATGACCGAGTCTGTGGAGACGCCATGTTCCAGCTCCAGGAAAATGTCAAAGACAAGCTTCGGGCCATTGT  
AGTGACCTTGTCTACAGTCTCCAGACCCCTCGGCTCCGGCGACAGGCTCCTGGCCAGGGGCTGCCTCCAGTGGC  
CCCCATCCTCAATGCCCACCAGCCAGCACCAGCGGGCAGAGATCCACTTCTGAAGCAAGGCTGTGGTGAAGA  
CAAGATCTGCCAGAGCAATCTGCAGCTGGTCCACGCCCCGCTTCTGTACCCGGGTGAGCGACACGGAATTCACACC  
TCTGCCCATGGATGTGGATGGAACAACAGCCCTGTTTGCAGTGAAGTGGGCAGCCAGTCAATTGGCTGGAGCTGAT  
GGTCACCAACCTGCCATCGGACCCAGCCAGCCCCAGGCTGATGGGGATGATGCCCATGAAGCCCAGCTCCTGGT  
CATGCTTCTGACTCACTGCACTACTCAGGGGTCCGGGCCCTGGACCCTGCGGAGAAGCCACTCTGCCTGTCCAA  
TGAGAATGCCTCCCATGTTGAGTGTGAGCTGGGGAACCCCATGAAGAGAGGTGCCAGGTACCTTCTACCTCAT  
CCTTAGCACCTCCGGGATCAGCATTGAGACCACGGAACCTGGAGGTAGAGCTGCTGTTGGCCACGATCAGTGAGCA  
GGAGCTGCATCCAGTCTCTGCACGAGCCCGTGTCTTCATTGAGCTGCCACTGTCCATTGCAGGAATGGCCATTCC  
CCAGCAACTCTTCTTCTCTGGTGTGGTGGAGGGGCGAGAGAGCCATGCAGTCTGAGCGGGATGTGGGCAGCAAGGT  
CAAGTATGAGGTACGGTTTCCAACCAAGGCCAGTCCGCTCAGAACCTGGGCTCTGCCTTCTCAACATCATGTG  
GCCTCATGAGATTGCCAATGGGAAGTGGTTGCTGTACCCAATGCAGGTTGAGCTGGAGGGCGGGCAGGGGCCTGG  
GCAGAAAGGGCTTTGCTCTCCAGGCCCAACATCCTCCACCTGGATGTGGACAGTAGGGATAGGAGGCGGGCGGA  
GCTGGAGCCACCTGAGCAGCAGGAGCCTGGTGGAGCGGCAGGAGCCAGCATGTCTGGTGGCCAGTGTCTCTGC  
TGAGAAGAAGAAAAACATCACCTGGACTGCGCCCCGGGGCACGGCCAACCTGTGTGGTGTTCAGCTGCCACTCTA  
CAGCTTTGACCGCGCGGCTGTGCTGCATGTCTGGGGCCGTCTCTGGAACAGCACCTTTCTGGAGGAGTACTCAGC  
TGTGAAGTCCCTGGAAGTGATTGTCCGGGCCAACATCACAGTGAAGTCCCTCCATAAAGAACTTGATGCTCCGAGA  
TGCCTCCACAGTGATCCAGTGATGGTATACTTGGACCCCATGGCTGTGGTGGCAGAAGGAGTGCCTGGTGGGT  
CATCCTCCTGGCTGTACTGGCTGGGCTGCTGGTGTAGCACTGCTGCTGCTCCTGTGGAAGATGGGATTCTT  
CAAACGGGCGAAGCACCCCGAGGCCACCGTGCCCCAGTACCATGCGGTGAAGATTCTCGGGAAGACCGACAGCA  
GTTCAAGGAGGAGAAGACGGGCACCATCCTGAGGAACAACCTGGGGCAGCCCCCGGGGAGGGCCCCGGATGCACA  
CCCCATCCTGGCTGCTGACGGGCATCCCGAGCTGGGCCCCGATGGGCATCCAGGGCCAGGCACCGCCT**AGG**TTCC  
CATGTCCAGCCTGGCCTGTGGCTGCCCTCCATCCCTTCCCCAGAGATGGCTCCTTGGGATGAAGAGGGTAGAGT  
GGGCTGCTGGTGTGCATCAAGATTGTCAGGATCGGCTTCTCAGGGGCACAGACCTCTCCACCCACAAGAAC  
TCCTCCACCCAACTTCCCTTAGAGTGTGTGAGATGAGAGTGGGTAAATCAGGGACAGGGCCATGGGGTAGGG  
TGAGAAGGGCAGGGGTGTCTGATGCAAAGGTGGGGAGAAGGGATCCTAATCCCTTCTCTCCATTACCCCTGT  
GTAACAGGACCCCAAGGACCTGCCTCCCCGGAAGTGCCTTAACCTAGAGGGTGGGGAGGAGGTTGTGTCACTGA  
CTCAGGCTGCTCCTTCTCTAGTTTCCCTCTCATCTGACCTTAGTTTGCTGCCATCAGTCTAGTGGTTTCGTGGT  
TTCGTCTATTTATTAAAAATATTTGAGAACAACAAAAA

777/237

**FIGURE 177**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL  
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMOKESKENQWL  
GVSVRSQGPGGKIIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDEL DGGGEWKFC EG  
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKG TARVELCAQGSADLAHLDDGPYEA  
GGEKEQDPRLIPVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV  
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVYVYLNQGGHWAGI  
SPLRLCGSPDSMFGISLAVLGDLNQGDFPDIAVGAPFDGDGKVFYIHGSSSLGVVAKPSQVLE  
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGSLADTAVLFRARPILHVSHEVSIAPRSIDLEQ  
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRRLRGQVPRVTFLSRNLEEPK  
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSSLSLQTPRLRRQAPGQGLPPVAP  
ILNAHQ PSTQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA  
LSGQPVIGLELMVTNLPSPDPAQPQADGDDAHEAQLLVMLPDSLHYSGVRALDPAEKPLCLSN  
ENASHVECELGNPMKRGAQVTFYLILSTSGISIIETTELEV ELLLATISEQELHPVSARARVF  
IELPLSIAGMAIPQQ LFFSGVVRGERAMQSERDVGSKVKYEVT VSNQGSRLTLGSAFLNIM  
WPHEIANGKWLLYPMQVELEGGQGPGQKGLCSRP RNILHLDVDSRDRRRRELEPPEQQEPGE  
RQEPSMSWVPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY  
SAVKSLEVIVRANITVKSSIKNLMRLDASTVIPVMVYLDPM AVVAEGVPWWVILLAVLAGLL  
VLALLVLLLWKMGFFKRAKHPEATVPQYHAVKIPREDRQQFKEEKTGTILRNNWGSPRREGP  
DAHPIAADGHPELGPDPGHPPGTA

**Important features:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 1040-1062

**N-glycosylation sites.**

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

**Integrins alpha chain proteins.**

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-  
407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408  
and 1031-1047

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**FIGURE 178**

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGGCGCGTGCAGCAGCTCCAGA  
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT  
CACAACAAGATGCTCAAGGTGTCAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA  
GTCTCTCGCAGCTGCCGCGGGCGGTGGCTGCAGCCGGGGGGCGGTGCGACGGCGGTAATTTTC  
TGGATGATAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC  
AAATTCCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCCTTCGA  
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT  
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG  
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG  
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA  
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC  
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT  
GGAGTTCAGGGAAGTGGCAAACAGATTGCGGGACTGGTTCAAGGCCCTTCATGAAAGTGGAA  
GTCAAAACAAGAAGACAAAAACATTGCTGAGGCCTGAGAGAAGCAGATTTCGATACCAGCATC  
TTGCCAATTTGCAAGGACTCACTTGGCTGGATGTTTAAACAGACTTGATACAAACTATGACCT  
GCTATTGGACCAGTCAGAGCTCAGAAGCATTACCTTGATAAGAATGAACAGTGTACCAAGG  
CATTCTTCAATTCTTGTGACACATACAAGGACAGTTTAATATCTAATAATGAGTGGTGCTAC  
TGCTTCCAGAGACAGCAAGACCCACCTTGCCAGACTGAGCTCAGCAATATTCAGAAGCGGCA  
AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC  
CAACACAATGTCATGGCAGTGTGGACAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC  
ATGGGATCCAGAATAAATGGTGTGTCAGATTGTGCTATAGATTTTGAGATCTCCGGAGATTT  
TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG  
ATGAAGATGAAATTGAAGATGATGATGAAGATGAAGGGGATGATGATGATGGTGGTGTGAC  
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATTCTACATTTCTAATATTTA  
CAAAAATGATAGCCTATTTAAAATTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA  
CATATATTTTGTATAATTATTTGAAAAATTGCAGCTAAAGTTATAGAACTTTATGTTTAAAT  
AAGAATCATTTGCTTTGAGTTTTTATATTCCTTACACAAAAGAAAATACATATGCAGTCTA  
GTCAGACAAAATAAAGTTTTGAAGTGCTACTATAATAAATTTTTTCACGAGAACAACTTTGT  
AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTAAATTTTTTGAAAG  
ATAATTCTAAGTGAAATTTAAAATAAATAAATTTTAAATGACCTGGGTCTTAAGGATTTAGG  
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG  
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

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**FIGURE 179**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA49829

><subunit 1 of 1, 436 aa, 1 stop

><MW: 49429, pI: 4.80, NX(S/T): 0

MLKVSAVLCVCAAAWCSQSLAAAAVAAAGGRSDGGNFLDDKQWLTTISQYDKEVGQWNKFR  
DEVEDDYFRTWSPGKPFQALDPAKDPCLKMKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA  
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP  
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESGSQNKKTLLRPERSRFDTSILPI  
CKDSLGMFNRDLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ  
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCDEDGYKPTQCHGSVGQCWCVDRYGNEVMGS  
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDDIMNDEDEIEDDDDEDEGDDDDGGDDHDVYI

**Important features:****Signal peptide:**

amino acids 1-16

**Leucine zipper pattern.**

amino acids 246-267

**N-myristoylation sites.**

amino acids 357-362, 371-376 and 376-381

**Thyroglobulin type-1 repeat proteins**

amino acids 353-365 and 339-352

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**FIGURE 180**

CAGACTCCAGATTTCCCTGTCAACCACGAGGAGTCCAGAGAGGAAACGCGGAGCGGAGACAACAGTACCTGACGC  
CTCTTTTCAGCCCGGGATCGCCCCAGCAGGGATGGGCGACAAGATCTGGCTGCCCTTCCCCGTGCTCCTTCTGGCC  
GCTCTGCCCTCCGGTGCTGCTGCCTGGGGCGGGCGGCTTCACACCTTCCCTCGATAGCGACTTCACCTTTACCCTT  
CCCGCCGGCCAGAAGGAGTGCTTCTACCAGCCCATGCCCTGAAGGCCCTCGCTGGAGATCGAGTACCAAGTTTGA  
GATGGAGCAGGATTAGATATTGATTTCCATCTTGCCTCTCCAGAAGGCCAAAACCTTAGTTTTTGAACAAAGAAAA  
TCAGATGGAGTTCACACTGTAGAGACTGAAGTTGGTGATTACATGTTCTGCTTTGACAATACATTTCAGCACCATT  
TCTGAGAAGGTGATTTTCTTTGAATTAATCCTGGATAATATGGGAGAACAGGCACAAGAACAAGAAGATTGGAAG  
AAATATATTACTGGCACAGATATATTGGATATGAACTGGAAGACATCCTGGAATCCATCAACAGCATCAAGTCC  
AGACTAAGCAAAAGTGGGCACATACAAATTTCTGCTTAGAGCATTGGAAGCTCGTGATCGAAACATACAAGAAAGC  
AACTTTGATAGAGTCAATTTCTGGTCTATGGTTAATTTAGTGGTTCATGGTGGTGGTGTGAGCCATTCAAGTTTAT  
ATGCTGAAGAGTCTGTTTGAAGATAAGAGGAAAAGTAGAACTTAAACTCCAAACTAGAGTACGTAACATTGAAA  
AATGAGGCATAAAAATGCAATAAACTGTTACAGTCAAGACCATTAAATGGTCTTCTCCAAAATATTTTGAGATATA  
AAAGTAGGAAACAGGTATAATTTTAAATGTGAAAATTAAGTCTTCACTTTCTGTGCAAGTAATCCTGCTGATCCAG  
TTGTAAGTGTGTAACAGGAATATTTTGCAGAATATAGGTTTAACTGAATGAAGCCATATTAATAACTGCAT  
TTTCCTAACTTTGAAAAATTTTGCAATGTCTTAGGTGATTTAAATAAATGAGTATTGGGCCTAATTGCAACACC  
AGTCTGTTTTTAACAGGTTCTATTACCCAGAATTTTGTAAATGCGGCAGTTACAAATTAAGTGTGGAAGTTT  
TCAGTTTTAAGTTATAAATCACCTGAGAATTACCTAATGATGGATTGAATAAATCTTTAGACTACAAAAGCCCAA  
CTTTTCTCTATTACATATGCATCTCTCCTATAATGTAAATAGAATAATAGCTTTGAAATACAATTAGGTTTTTG  
AGATTTTTATAACCAAATACATTTTCAGTGTAAACATATTAGCAGAAAGCATTAGTCTTTGTAAGTTGCTTACATTC  
CCAAAAGCTGACATTTTCACGATTCTTAAAAACACAAAGTTACACTTACTAAAATTAGGACATGTTTTCTCTTG  
AAATGAAGAATATAGTTTTAAAGCTTCCCTCCATAGGGACACATTTTCTCTAACCCTTAAGTGTAGGA  
TTTTAAATTAATGTGAGGTAAAATAAGTTTATTTTAAATAGTATCTGTCAAGTTAATATCTGTCAACAGTTAA  
TAATCATGTTATGTTAATTTTAACATGATTGCTGACTTGGATAATTCATTATTACCAGCAGTTATGAAGGAAATA  
TTGCTAAAATGATCTGGGCCTACCATAAATAAATATCTCCTTTTCTGAGCTCTAAGAATTATCAGAAAACAGGAA  
AGAATTTAGAAAACTTGAGAAAACCTAATCCAAAATAAATTCACTTAAGTAGAACTATAAATAAATATCTAGA  
ATCTGACTGGCTCATCATGACATCCTACTCATAACATAAATCAAAGGAGATGATTAATTTCCAGTTAGCTGGAAG  
AACTTTGGCTGTAGGTTTTTATTTTCTACAAGAATTCTGGTTTGAATTATTTTGTAGCAGGTACATTTTATA  
AAATGTAAGCCCTACTGTAAGGTTTAGCACTGGGTGTACATATTTATTAAAAATTTTATTATAACAACCTTTTAT  
TAAAATGGCCTTTCTGAACACTTTATTTATTGATGTTGAAGTAAGGATTAGAAACATAGACTCCCAAGTTTTAAA  
CACCTAAATGTGAATAACCCATATATACAACAAAGTTTCTGCCATCTAGCTTTTGAAGTCTATGGGGGTCTTAC  
TCAAGTACTAGTAATTTAACTTCATCATGAATGAACATAATTTTAAAGTTATGCCCATTTATAACGTTGTTTAT  
GACTACATTGTGAGTTAGAAACAACTTAAATTTGGGGTATAGAACCCCTCAACAGGTTAGTAATGCTGGAATT  
CTTGATGAGCAATAATGATAACCAGAGAGTGATTTTCACTTACACTCATAGTAGTATAAAAAGAGATACATTTCCC  
TCTTAGGCCCCCTGGGAGAAGAGCAGCTTAGATTTCCCTACTGGCAAGGTTTAAAAATGAGGTAAATGCCGTAT  
ATGATCAATTACCTTAATTGGCCAAGAAAATGCTTCAGGTGTCTAGGGGTATCCTCTGCAACACTTGCAGAACAA  
AGGTCAATAAGATCCTTGCCTATGAATACCCCTCCCTTTTGGCGCTGTTAAATTTGCAATGAGAAGCAAATTTACA  
GTACCATAACTAATAAAGCAGGGTACAGATATAAACTACTGCATCTTTTCTATAAACTGTGATTAAGAATTCTA  
CCTCTCCTGTATGGCTGTTACTGTACTGTACTCTCTGACTCCTTACCTAACAATGAATTTGTTACATAATCTTCT  
ACATGTATGATTTGTGCCACTGATCTTAAACCTATGATTCAGTAACCTTCTTACCATATAAAAACGATAATTGCTT  
TATTTGGAAAAGAATTTAGGAATACTAAGGACAATTATTTTATAGACAAAGTAAAAAGACAGATATTTAAGAGG  
CATAACCAAAAAGCAAACTTGTAACAGAGTAAAAATCTTTAATATTTCTAAAGACATACTGTTTATCTGCTT  
CATATGCTTTTTTTAATTTCACTATTCCATTTCTAAATTAAGTTATGCTAAATTGAGTAAGCTGTTTATCACTT  
AACAGCTCATTTTGTCTTTTCAATATACAAATTTTAAAAATACTACAATATTTAACTAAGGCCCAACCGATTTT  
CATAATGTAGCAGTTACCGTGTTTACCTCACACTAAGGCCTAGAGTTTGTCTGTATGCATTTGGATGATTAAT  
GTTATGCTGTTCTTTCATGTGAATGTCAAGACATGGAGGGTGTTTGTAAATTTTATGGTAAAATTAATCCTTCTTA  
CACATAATGGTGTCTTAAATTGACAAAAAATGAGCACTTACAATTGTATGTCTCCTCAATGAAGATTCTTTAT  
GTGAAATTTTAAAAGACATTGATTCCGCATGTAAGGATTTTTCATCTGAAGTACAATAATGCACAATCAGTGTG  
CTCAAACTGCTTTATACTTATAAACAGCCATCTTAAATAAGCAACGTATTGTGAGTACTGATATGTATATAATAA  
AAATTATCAAAGGAAAA

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**FIGURE 181**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52196

><subunit 1 of 1, 229 aa, 1 stop

><MW: 26017, pI: 4.73, NX(S/T): 0

MGDKIWLPEFPVLLLAALPPVLLPGAAGFTPSLSDFTFTLPAGQKECFYQPMPLKASLEIEY

QVLDGAGLDIDFHLASPEGKTLVFEEQRKSDGVHTVETEVGDYMFCDNTFSTISEKVIFEL

ILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLRAFEARDN

IQESNFDRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT

**Important features:****Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 195-217

**N-myristoylation site.**

amino acids 43-48

**Tyrosine kinase phosphorylation site.**

amino acids 55-62

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**FIGURE 182**

CCATCCCTGAGATCTTTTTATAAAAAACCCAGTCTTTGCTGACCAGACAAAGCATAACCAGAT  
CTCACCAGAGAGTGCAGACACTATGCTGCCTCCCATGGCCCTGCCAGTGTGTCCTGGATG  
CTGCTTTCCTGCCTCATTCTCCTGTGTCAGGTTCAAGGTGAAGAAACCCAGAAGGAACTGCC  
CTCTCCACGGATCAGCTGTCCCAAAGGCTCCAAGGCCTATGGCTCCCCCTGCTATGCCTTGT  
TTTTGTACCAAAATCCTGGATGGATGCAGATCTGGCTTGCCAGAAGCGGCCCTCTGGAAAA  
CTGGTGTCTGTGCTCAGTGGGGCTGAGGGATCCTTCGTGTCTCCTGGTGAGGAGCATTAG  
TAACAGCTACTCATACATCTGGATTGGGCTCCATGACCCACACAGGGCTCTGAGCCTGATG  
GAGATGGATGGGAGTGGAGTAGCACTGATGTGATGAATTACTTTGCATGGGAGAAAAATCCC  
TCCACCATCTTAAACCCTGGCCACTGTGGGAGCCTGTCAAGAAGCACAGGATTTCTGAAGTG  
GAAAGATTATAACTGTGATGCAAAGTTACCCTATGTCTGCAAGTTCAAGGACTAGGGCAGGT  
GGGAAGTCAGCAGCCTCAGCTTGGCGTGCAGCTCATCATGGACATGAGACCAGTGTGAAGAC  
TCACCCTGGAAGAGAATATTCTCCCCAACTGCCCTACCTGACTACCTTGTCATGATCCTCC  
TTCTTTTTCCTTTTTCTTCACCTTCATTCAGGCTTTTCTCTGTCTTCCATGTCTTGAGATC  
TCAGAGAATAATAATAAAAATGTTACTTTATAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 183**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56965

<subunit 1 of 1, 175 aa, 1 stop

<MW: 19330, pI: 7.25, NX(S/T): 1

MLPPMALPSVSWMLLSCLILLCQVQGEETQKELPSPRISCPKGSKAYGSPCYALFLSPKSWM  
DADLACQKRPSGKLVSVLSGAEGSFVSSLVRSISNSYSYIWIGLHDPTQGSEPDGDGWEWSS  
TDVMNYFAWEKNPSTILNPGHCGSLSRSTGFLKWKDYNCDAKLPYVCKFKD

**Important features:**

**Signal peptide:**

amino acids 1-26

**C-type lectin domain signature.**

amino acids 146-171

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**FIGURE 184**

CCAGTCTGTCGCCACCTCACTTGGTGTCTGCTGTCCCCGCCAGGCAAGCCTGGGGTGAGAGC  
ACAGAGGAGTGGGCCGGGACCATGCGGGGGACGCGGCTGGCGCTCCTGGCGCTGGTGCTGGC  
TGCCTGCGGAGAGCTGGCGCCGGCCCTGCGCTGCTACGTCTGTCCGGAGCCCACAGGAGTGT  
CGGACTGTGTCACCATCGCCACCTGCACCACCAACGAAACCATGTGCAAGACCACACTCTAC  
TCCCGGGAGATAGTGTACCCCTTCCAGGGGGACTCCACGGTGACCAAGTCCTGTGCCAGCAA  
GTGTAAGCCCTCGGATGTGGATGGCATCGGCCAGACCCTGCCCCGTGTCCTGCTGCAATACTG  
AGCTGTGCAATGTAGACGGGGCGCCCGCTCTGAACAGCCTCCACTGCGGGGGCCCTCACGCTC  
CTCCCCTCTTGAGCCTCCGACTGTAGAGTCCCCGCCCACCCCCATGGCCCTATGCGGCCCA  
GCCCCGAATGCCTTGAAGAAGTGCCCCCTGCACCAGGAAAAAAAAAAAAAAAAAAAA

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## FIGURE 185

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56405

<subunit 1 of 1, 125 aa, 1 stop

<MW: 13115, pI: 5.90, NX(S/T): 1

MRGTRLALLALVLAACGELAPALRCYVCPEPTGVSDCVTIATCTTNETMCKTTLYSREIVYP  
FQGDSTVTKSCASKCKPSDVGIGQTLPVSCCNTELCNVDGAPALNSLHCGALTLLPLLSLRL

**Important features:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation site.**

amino acids 46-49

7861237

**FIGURE 186**

CTGCAGTCAGGACTCTGGGACCGCAGGGGGCTCCCGGACCCTGACTCTGCAGCCGAACCGGC  
ACGGTTTCGTGGGGACCCAGGCTTGCAAAGTGACGGTCATTTTCTCTTTCTTTCTCCCTCTT  
GAGTCCTTCTGAGATGATGGCTCTGGGCGCAGCGGGAGCTACCCGGGTCTTTGTGCGGATGG  
TAGCGGCGGCTCTCGGCGGCCACCCTCTGCTGGGAGTGAGCGCCACCTTGAACCTCGGTTCTC  
AATTCCAACGCTATCAAGAACCTGCCCCACCGCTGGGCGGCGCTGCGGGGCACCCAGGCTC  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ACTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGACGCAGGCGTGCAAATCTGTCTCGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCACGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTCTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGGTATTCCAGAAGAACCACCTTGTCTTCAAAAATGTATCACACCAA  
AGGACAAGAAGGTTCTGTTTGTCTCCGGTCATCAGACTGTGCCTCAGGATTGTGTTGTGCTA  
GACACTTCTGGTCCAAGATCTGTAAACCTGTCCTGAAAGAAGGTCAAGTGTGTACCAAGCAT  
AGGAGAAAAGGCTCTCATGGACTAGAAATATTCCAGCGTTGTTACTGTGGAGAAGGTCTGTC  
TTGCCGGATACAGAAAGATCACCATCAAGCCAGTAATTCTTCTAGGCTTCACACTTGTGCTA  
GACACTAAACCAGCTATCCAAATGCAGTGAACCTCTTTTATATAATAGATGCTATGAAAACC  
TTTTATGACCTTCATCAACTCAATCCTAAGGATATAACAAGTTCTGTGGTTTCAGTTAAGCAT  
TCCAATAACACCTTCCAAAAACCTGGAGTGTAAGAGCTTTGTTTCTTTATGGAACTCCCCTG  
TGATTGCAGTAAATTACTGTATTGTAAATTCTCAGTGTGGCACTTACCTGTAAATGCAATGA  
AACTTTTAATTATTTTTCTAAAGGTGCTGCACTGCCTATTTTTCTCTTGTATGTAAATTT  
TTGTACACATTGATTGTTATCTTGACTGACAAATATTCTATATTGAACTGAAGTAAATCATT  
TCAGCTTATAGTTCTTAAAAGCATAACCCTTTACCCCATTTAATTCTAGAGTCTAGAACGCA  
AGGATCTCTTGGAATGACAAATGATAGGTACCTAAAATGTAACATGAAAATACTAGCTTATT  
TTCTGAAATGTACTATCTTAATGCTTAAATTATATTTCCCTTTAGGCTGTGATAGTTTTTGA  
AATAAAATTTAACATTTAAAAA

**FIGURE 187**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57530

<subunit 1 of 1, 266 aa, 1 stop

<MW: 28672, pI: 8.85, NX(S/T): 1

MMALGAAGATRVFVAMVAAALGGHPLLGVSATLNSVLNSNAIKNLPPPLGGAAGHPGSAVSA  
APGILYPGGNKYQTIIDNYQPYPCAEDEECGTDEYCASPTRGGDAGVQICLACRKRKRCMRH  
AMCCPGNYCKNGICVSSDQNHFRGEIEETITESFGNDHSTLDGYSRRTLSSKMYHTKGQEG  
SVCLRSSDCASGLCCARHFWSKICKPVLKEGQVCTKHRRKGSHGLEIFQRCYCGEGLSCRIQ  
KDHHQASNSSLHTCQRH

**Important features:****Signal peptide:**

amino acids 1-23

**N-glycosylation site.**

amino acids 256-259

**Fungal Zn(2)-Cys(6) binuclear cluster domain**

amino acids 110-126

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**FIGURE 188**

TGTGTTTCCCTGCAGTCAGAATTTGGGACNGCAGGGGTTCCTGGACCTGATTTTGCAGCGGA  
ACGGGAAGGTTTTGTGGGACCCAGGTTGAAATGACGGTCATTTTTTTTTCTTTCTCCTTCNG  
GAGTCCTTNTGAGANGATGGTTTTGGGCGCAGCGGGAGCTAACCCGGTTTTTTGTNGCGATG  
GTAGCGGCGGTTTTTCGGCGGCCACCTTNTGCTGGGAGTGAGCGCCACCTTGAATCGGTTTTTC  
AATTCCAACGNTATCAAGAACCTGCCCCCACCNTGGGCGGCGCTGCGGGGCACCCAGGNTT  
TGCAGTCAGCGCCGCGCCGGGAATCCTGTACCCGGGCGGGAATAAGTACCAGACCATTGACA  
ATTACCAGCCGTACCCGTGCGCAGAGGACGAGGAGTGCGGCACTGATGAGTACTGCGCTAGT  
CCCACCCGCGGAGGGGGANGCGGGCGTGCAAATNTGTNTNGCCTGCAGGAAGCGCCGAAAACG  
CTGCATGCGTCANGCTATGTGCTGCCCCGGGAATTACTGCAAAAATGGAATATGTGTGTNTT  
CTGATCAAAATCATTTCCGAGGAGAAATTGAGGAAACCATCACTGAAAGCTTTGGTAATGAT  
CATAGCACCTTGGATGGG

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**FIGURE 189**

GAGGAACCTACCGGTACCGGCCGCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCCGTGCGCCGCGG  
CTGGGCCGTGCGGAGAGTGCCTGTGCTTCTCTCCTGCACGCGGTGCTTGGGCTCGGCCAGGCGGGGTCCGCCGCCA  
GGGTTTGAGGATGGGGGAGTAGCTACAGGAAGCGACCCCGCGATGGCAAGGTATATTTTTGTGGAATGAAAAGGA  
AGTATTAGAAATGAGCTGAAGACCATTACAGATTAAATATTTTTGGGGACAGATTGTGATGCTTGATTACCCCT  
TGAAGTAATGTAGACAGAAGTTCTCAAATTTGCATATTACATCAACTGGAACCAGCAGTGAATCTTAATGTTTAC  
TTAAATCAGAACTTGCATAAGAAAGAGAAATGGGAGTCTGGTTAAATAAAGATGACTATATCAGAGACTTGAAAAG  
GATCATTCTCTGTTTTCTGATAGTGTATATGGCCATTTTAGTGGGCACAGATCAGGATTTTACAGTTTACTTGG  
AGTGTCCAAAACCTGCAAGCAGTAGAGAAATAAGACAAGCTTTCAAGAAATTGGCATTGAAGTTACATCCTGATAA  
AAACCCGAATAACCCAAATGCACATGGCGATTTTTTAAAAATAAATAGAGCATATGAAGTACTCAAAGATGAAGA  
TCTACGGAAAAAGTATGACAAATATGGAGAAAAGGACTTGAGGATAATCAAGGTGGCCAGTATGAAAGCTGGAA  
CTATTATCGTTATGATTTTTGGTATTTATGATGATGATCCTGAAATCATAACATTGGAAAGAAGAGAATTTGATGC  
TGCTGTTAATTCTGGAGAACTGTGGTTTGTAAATTTTTACTCCCCAGGCTGTTCACTGCCATGATTTAGCTCC  
CACATGGAGAGACTTTGCTAAAGAAGTGGATGGGTACTTCGAATTGGAGCTGTTAACTGTGGTGATGATAGAAT  
GCTTTGCCGAATGAAAGGAGTCAACAGCTATCCCAGTCTCTTCATTTTTTCGGTCTGGAATGGCCCCAGTGAAATA  
TCATGGAGACAGATCAAAGGAGAGTTTAGTGAGTTTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTTG  
GACAGGAAATTTTGTCACTCCATACAACTGCTTTTGCTGCTGGTATTGGCTGGCTGATCACTTTTTGTTCAA  
AGGAGGAGATTGTTTGACTTCACAGACACGACTCAGGCTTAGTGGCATGTTGTTTCTCACTCATTGGATGCTAA  
AGAAATATATTTGGAAGTAATACATAATCTTCCAGATTTTGAAGTACTTTCGGCAAACACACTAGAGGATCGTTT  
GGCTCATCATCGGTGGCTGTTATTTTTTCACTTTTGGAAAAATGAAATTCAAATGATCCTGAGCTGAAAAACT  
AAAACTCTACTTAAAAATGATCATATTCAAGTTGGCAGGTTTGAAGTCTCTCTGCACCAGACATCTGTAGTAA  
TCTGTATGTTTTTCAGCCGTCTCTAGCAGTATTTAAAGGACAAGGAACCAAAGAATATGAAATTCATCATGGAAA  
GAAGATTCTATATGATATACTTGCTTTGCCAAAGAAAGTGTGAATTCTCATGTTACCACGCTTGACCTCAAAA  
TTTTCTGCCAATGACAAAGAACCATGGCTTGTTGATTTCTTTGCCCCCTGGTGTCCACCATGTGAGCTTTACT  
ACCAGAGTTACGAAGAGCATCAAATCTTCTTATGGTCAGCTTAAGTTTGGTACACTAGATTGTACAGTTCATGA  
GGGACTCTGTAAATGTATAACATTGAGGCTTATCCAACAACAGTGGTATTCAACCAGTCCAACATTGATGAGTA  
TGAAGGACATCACTCTGCTGAACAAATCTTGGAGTTCATAGAGGATCTTATGAATCCTTCAGTGGTCTCCCTTAC  
ACCCACCACCTTCAACGAAGTACACAAAGAAAACACAACGAAGTCTGGATGGTTGATTTCTATTCTCCGTG  
GTGTCATCCTTGCCAAGTCTTAATGCCAGAATGGAAAAGAAATGGCCCGGACATTAAGTGGACTGATCAACGTGGG  
CAGTATAGATTGCCAACAGTATCATTCTTTTTGTGCCAGGAAAACGTTCAAAGATACCCTGAGATAAGATTTTT  
TCCCCCAAATCAAATAAGCTTATCAGTATCACAGTTACAATGGTTGGAATAGGGATGCTTATCCCTGAGAAT  
CTGGGGTCTAGGATTTTTACCTCAAGTATCCACAGATCTAACACCTCAGACTTTTCAAGTGAAGAAAGTTCTACAAG  
GAAAAATCATTGGGTGATTGATTTCTATGCTCCTTGGTGTGGACCTTGCCAGAATTTGCTCCAGAATTTGAGCT  
CTTGGCTAGGATGATTAAAGGAAAAGTGAAGCTGGAAAAGTAGACTGTGAGGCTTATGCTCAGACATGCCAGAA  
AGCTGGGATCAGGGCCTATCCAAGTGTAAAGTTTTATTTCTACGAAAGAGCAAAGAGAAATTTTCAAGAAAGCA  
GATAAATACCAGAGATGCAAAAGCAATCGCTGCCTTAATAAGTGAAGAAATTTGGAAGTCTCCGAAATCAAGGCAA  
GAGGAATAAGGATGAAGTTTGAATAATGTTGAAGATGAAGAAAAAGTTTAAAGAAATTTCTGACAGATGACATCAG  
AAGACACCTATTTAGAATGTTACATTTATGATGGGAATGAATGAACATTATCTTAGACTTGCAGTTGTACTGCCA  
GAATTATCTACAGCACTGGTGTAAAAGAAGGGTCTGCAAACTTTTTCTGTAAAGGGCCGGTTTATAAATATTTTA  
GACTTTGCAGGCTATAATATATGGTTTACACATGAGAACAAAGAAATAGAGTCAATCATGATTTCTTTGTTATTTGCT  
TTTAAACACCTTTAAAAAATATTTAAACGATTCTTAGCTCAGAGCCATACAAAAGTAGGCTGGATTGAGTCCATG  
GACCATAGATTGCTGTCCCCCTCGACGGACTTATAATGTTTTCAGGTGGCTGGCTTGAACATGAGTCTGCTGTGCT  
ATCTACATAAATGTCTAAGTTGTATAAAGTCCACTTTCCCTTCAGTTTTTTGGCTGACCTGAAAAGAGGTAAGT  
TAGTTTTTGGTCACTTGTTCTCCTAAAAATGCTATCCCTAACCATATATTTATATTTCTGTTTTAAAAACACCCAT  
GATGTGGCACAGTAAACAAACCCTGTTATGCTGTATTATTATGAGGAGATTCTTCATTGTTTTCTTTCTTCTCA  
AAGGTTGAAAAAATGCTTTTAAATTTTTTACAGCCGAGAAACAGTGCAGCAGTATATGTGCACACAGTAAGTACAC  
AAATTTGAGCAACAGTAAGTGCACAAATTTCTGTAGTTTGTGTATCATCCAGGAAACCTGAGGGAAAAAATTA  
TAGCAATTAAGTGGCATTGTAGAGTATCCTAAATATGTTATCAAGTATTTAGAGTTCTATATTTTAAAGATATA  
TGTGTTTATGATTTTTCTGAAATTGCTTTTATAGAAATTTTCCCACTGATAGTTGATTTTTGAGGCATCTAATAT  
TTACATATTTGCCTTCTGAAGTTTGTTTTGAAGTGTATCCTTTATTTACATTGGGTTTTTCTTTTATAGTTTTGG  
TTTTTCACTCCTGTCCAGTCTATTTATTTTCAAATAGGAAAAATTTACTTTACAGGTTGTTTTACTGTAGCTTAT  
AATGATACTGTAGTTATTCCAGTTACTAGTTTACTGTGAGAGGGCTGCCTTTTTTCAAGATAAATATTGACATAATA  
ACTGAAGTTATTTTTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTTCTAGTTTCTGTGTTGTTTGA  
CTCAAAGAATCACAAATTTGTGAGTAACATGTAGTTGTTTAGTTATAATTGAGAGTGTACAGAATGGTAAAAATTT  
CCAATCAGTCAAAGAGGTCATGAATTAAAGGGCTTGCAACTTTTTTCAAAAAA

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**FIGURE 190**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56439

<subunit 1 of 1, 747 aa, 1 stop

<MW: 86127, pI: 7.46, NX(S/T): 2

MGVWLNKDDYIRDLKRIILCFLIVYMAILVGTDQDFYSLLGVSKTASSREIRQAFKKLALKL  
HPDKNPNPNNAHGDFLKNRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYRYDFGI  
YDDDPEIITLERREFDAAVNSGELWFVNFYSPGCSHCHDLAPTWRDFAKEVDGLLRIGAVNC  
GDDRMLCRMKGVNSYPSLFI FRSGMAPVKYHGDRSKESLVSFAMQHVRSTVTELWTGNFVNS  
IQTAFAGIGWLITFCSKGGDCLTSQTRLRLSGMLFLNSLDAKEIYLEVIHNLPDFELLSAN  
TLEDRLAHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLYVFQP  
SLAVFKGQGTKEYEIHGKKILYDILAFAKESVNSHVTTLGPQNFPANDKEPWLVDFFAPWC  
PPCRALLPELRRASNLLYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVVFNQSNIEYEGHHS  
AEQILEFIEDLMNPSVVS LTPTTFNELVTQRKHNEVWMVDFYSPWCHPCQVLMPEWKRMART  
LTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPPKSNKAYQYHSYNGWNRDAYSLRIWGLG  
FLPQVSTD LTPQTFSEKVLQGKNHWVIDFYAPWCGPCQNFAPFELLARMIKGKVKAGKVDC  
QAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAI AALISEKLETLRNQGKRNDKDEL

**Important features:**

**Endoplasmic reticulum targeting sequence.**

amino acids 744-747

**Cytochrome c family heme-binding site signature.**

amino acids 158-163

**Nt-dnaJ domain signature.**

amino acids 77-96

**N-glycosylation site.**

amino acids 484-487

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**FIGURE 191**

AGACAGTACCTCCTCCCTAGGACTACACAAGGACTGAACCAGAAGGAAGAGGACAGAGCAAA  
GCCATGAACATCATCCTAGAAATCCTTCTGCTTCTGATCACCATCATCTACTCCTACTTGGG  
GTCGTTGGTGAAGTTTTTCATTCCTCAGAGGAGAAAATCTGTGGCTGGGGAGATTGTTCTCA  
TACTGGAGCTGGGCATGGAATAGGCAGGCAGACTACTTATGAATTTGCAAAACGACAGAGC  
ATATTGGTTCTGTGGGATATTAATAAGCGCGGTGTGGAGGAACTGCAGCTGAGTGCCGAAA  
ACTAGGCGTCACTGCGCATGCGTATGTGGTAGACTGCAGCAACAGAGAAGAGATCTATCGCT  
CTCTAAATCAGGTGAAGAAAGAAGTGGGTGATGTAACAATCGTGGTGAATAATGCTGGGACA  
GTATATCCAGCCGATCTTCTCAGCACCAAGGATGAAGAGATTACCAAGACATTTGAGGTCAA  
CATCCTAGGACATTTTTTGGATCACAAAAGCACTTCTTCCATCGATGATGGAGAGAAATCATG  
GCCACATCGTCACAGTGGCTTCAGTGTGCGGCCACGAAGGGATTCCCTTACCTCATCCCATAT  
TGTTCCAGCAAATTTGCCGCTGTTGGCTTTCACAGAGGTCTGACATCAGAACTTCAGGCCTT  
GGGAAAAACTGGTATCAAAACCTCATGTCTCTGCCAGTTTTTGTGAATACTGGGTTCACCA  
AAAATCCAAGCACAAAGATTATGGCCTGTATTGGAGACAGATGAAGTCGTAAGAAGTCTGATA  
GATGGAATACTTACCAATAAGAAAATGATTTTTTGTTCATCGTATATCAATATCTTTCTGAG  
ACTACAGAAGTTTCTTCCTGAACGCGCCTCAGCGATTTTAAATCGTATGCAGAATATTCAAT  
TTGAAGCAGTGGTTGGCCACAAAATCAAAATGAAATTGAATAAATAAGCTCCAGCCAGAGATG  
TATGCATGATAATGATATGAATAGTTTTCGAATCAATGCTGCAAAGCTTTATTTTCACATTTTT  
TCAGTCCTGATAATATTAAAAACATTGGTTTGGCACTAGCAGCAGTCAAACGAACAAGATTA  
ATTACCTGTCTTCCTGTTTCTCAAGAATATTTACGTAGTTTTTTCATAGGTCTGTTTTTCCTT  
TCATGCCTCTTAAAAACTTCTGTGCTTACATAAACATACTTAAAAGGTTTTCTTTAAGATAT  
TTTATTTTTTCCATTTAAAGGTGGACAAAAGCTACCTCCCTAAAAGTAAATACAAAGAGAACT  
TATTTACACAGGGAAGGTTTAAGACTGTTCAAGTAGCATTCCAATCTGTAGCCATGCCACAG  
AATATCAACAAGAACACAGAATGAGTGCACAGCTAAGAGATCAAGTTTCAGCAGGCAGCTTT  
ATCTCAACCTGGACATATTTTAAGATTCAGCATTTGAAAGATTTCCCTAGCCTCTTCCTTTT  
TCATTAGCCCAAACGGTGCAACTCTATTCTGGACTTTATTACTTGATTCTGTCTTCTGTAT  
AACTCTGAAGTCCACCAAAGTGGACCCTCTATATTTCTCCCTTTTTTATAGTCTTATAAGA  
TACATTATGAAAGGTGACCGACTCTATTTTAAATCTCAGAATTTTAAGTTCTAGCCCCATGA  
TAACCTTTTTCTTTGTAATTTATGCTTTCATATATCCTTGGTCCCAGAGATGTTTAGACAAT  
TTTAGGCTCAAAAATTAAAGCTAACACAGGAAAAGGAACTGTACTGGCTATTACATAAGAAA  
CAATGGACCCAAGAGAAGAA

**FIGURE 192**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56409

<subunit 1 of 1, 300 aa, 1 stop

<MW: 33655, pI: 9.31, NX(S/T): 1

MNIILEILLLLITIIYSYLESLVKFFIPQRRKSVAGEIVLITGAGHGIGRQTTYEFAKRQSI  
LVLWDINKRGVEETAAECKRLGVTAHAYVVDCSNREEIYRSLNQVKKEVGDVTIVVNNAGTV  
YPADLLSTKDEEITKTFEVNILGHFWITKALLPSMMERNHGHIVTVASVCGHEGIPYLIPYC  
SSKFAAVGFHRGLTSELQALGKTGIKTSCLCPVFNVTGFTKNPSTRLWPVLETDEVVRSLID  
GILTNNKMIFVPSYINIFLRLQKFLPERASAILNRMQNIQFEAVVGHKIKMK

**Important features:**

**Signal peptide:**

amino acids 1-19

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 30-33 and 58-61

**Short-chain alcohol dehydrogenase family protein**

amino acids 165-202, 37-49, 112-122 and 210-219

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**FIGURE 193**

CGGCGGCGGCTGCGGGCGCGAGGTGAGGGGCGCGAGGTGAGGGGCGCGAGGTTCCCAGCAGG  
ATGCCCCGGCTCTGCAGGAAGCTGAAGTGAGAGGGCCCGGAGAGGGGCCAGCCCGCCCGGGGC  
AGGATGACCAAGGCCCGGCTGTTCCGGCTGTGGCTGGTGCTGGGGTCGGTGTTTCATGATCCT  
GCTGATCATCGTGTACTGGGACAGCGCAGGCGCCGCGCACTTCTACTTGCACACGTCCTTCT  
CTAGGCCGACACGGGGCCCGCTGCCCACGCCCGGGCCGGACAGGGACAGGGAGCTCACG  
GCCGACTCCGATGTCGACGAGTTTCTGGACAAGTTTCTCAGTGCTGGCGTGAAGCAGAGCGA  
CCTTCCCAGAAAGGAGACGGAGCAGCCGCCTGCGCCGGGGAGCATGGAGGAGAGCGTGAGAG  
GCTACGACTGGTCCCCGCGCGACGCCCGGCGCAGCCCAGACCAGGGCCGGCAGCAGGCGGAG  
CGGAGGAGCGTGCTGCGGGGCTTCTGCGCCAACTCCAGCCTGGCCTTCCCCACCAAGGAGCG  
CGCATTCGACGACATCCCCAACTCGGAGCTGAGCCACCTGATCGTGACGACCGGCACGGGG  
CCATCTACTGCTACGTGCCCAAGGTGGCCTGCACCAACTGGAAGCGCGTGATGATCGTGCTG  
AGCGGAAGCCTGCTGCACCGCGGTGCGCCCTACCGCGACCCGCTGCGCATCCCGCGCGAGCA  
CGTGCAACAACGCCAGCGCGCACCTGACCTTCAACAAGTTCTGGCGCCGCTACGGGAAGCTCT  
CCCGCCACCTCATGAAGGTCAAGCTCAAGAAGTACACCAAGTTCCTCTTCGTGCGCGACCCC  
TTCGTGCGCCTGATCTCCGCCTTCCGCAGCAAGTTCGAGCTGGAGAACGAGGAGTTCTACCG  
CAAGTTCGCCGTGCCCATGCTGCGGCTGTACGCCAACCACACCAGCCTGCCCGCCTCGGGCGC  
GCGAGGCCTTCCGCGCTGGCCTCAAGGTGTCCTTCGCCAACTTCATCCAGTACCTGCTGGAC  
CCGCACACGGAGAAGCTGGCGCCCTTCAACGAGCACTGGCGGCAGGTGTACCGCCTCTGCCA  
CCCGTGCCAGATCGACTACGACTTCGTGGGGAAGCTGGAGACTCTGGACGAGGACGCCGCGC  
AGCTGCTGCAGCTACTCCAGGTGGACCGGCAGCTCCGCTTCCCCCGAGCTACCGGAACAGG  
ACCGCCAGCAGCTGGGAGGAGGACTGGTTCGCCAAGATCCCCCTGGCCTGGAGGCAGCAGCT  
GTATAAACTCTACGAGGCCGACTTTGTTCTCTTCGGCTACCCCAAGCCCGAAAACCTCCTCC  
GAGACTGAAAGCTTTCGCGTTGCTTTTTCTCGCGTGCCTGGAACCTGACGCACGCGCACTCC  
AGTTTTTTTATGACCTACGATTTTGCAATCTGGGCTTCTTGTTCACTCCACTGCCTCTATCC  
ATTGAGTACTGTATCGATATTGTTTTTTAAGATTAAATATATTTTCAGGTATTTAATACGA

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**FIGURE 194**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56112

<subunit 1 of 1, 414 aa, 1 stop

<MW: 48414, pI: 9.54, NX(S/T): 4

MTKARLFRLWLVLGSVFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRELT  
DSDVDEFLLDKFLSAGVKQSDLPRKETEQPPAPGSMEESVRGYDWSPRDARRSPDQGRQQAER  
RSVLRGFCANSSLAFTKERAFDDIPNSELHLIVDDRHGAIYCYVPKVACTNWKRVMIIVLS  
GSLHHRGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKLKKYTKFLFVRDPF  
VRLISAFRSKFELNEEFYRKFAVPMLRLYANHTSLPASAREAFRAGLKVSFANFIQYLLDP  
HTEKLAPFNEHWRQVYRLCHPCQIDYDFVGKLETLDDEAAQLLQLLQVDRQLRFPPSYRNRT  
ASSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKPENLLRD

**Important features:****Signal peptide:**

amino acids 1-31

**N-glycosylation sites.**

amino acids 134-137, 209-212, 280-283 and 370-373

**TNFR/NGFR family cysteine-rich region protein**

amino acids 329-332

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**FIGURE 195**

TCGGGCCAGAATTCGGCACGAGGCGGCACGAGGGCGACGGCCTCACGGGGCTTTGGAGGTGA  
AAGAGGCCCAGAGTAGAGAGAGAGAGAGACCGACGTACACGGGATGGCTACGGGAACGCGCT  
ATGCCGGGAAGGTGGTGGTCGTGACCGGGGGCGGGCGCGGCATCGGAGCTGGGATCGTGCGC  
GCCTTCGTGAACAGCGGGGGCCCGAGTGGTTATCTGCGACAAGGATGAGTCTGGGGGCCGGGC  
CCTGGAGCAGGAGCTCCCTGGAGCTGTCTTTATCCTCTGTGATGTGACTCAGGAAGATGATG  
TGAAGACCCTGGTTTCTGAGACCATCCGCCGATTTGGCCGCCTGGATTGTGTTGTCAACAAC  
GCTGGCCACCACCCACCCCCACAGAGGCCTGAGGAGACCTCTGCCCAGGGATTCCGCCAGCT  
GCTGGAGCTGAACCTACTGGGGACGTACACCTTGACCAAGCTCGCCCTCCCCTACCTGCGGA  
AGAGTCAAGGGAATGTCATCAACATCTCCAGCCTGGTGGGGGCAATCGGCCAGGCCCAGGCA  
GTTCCCTATGTGGCCACCAAGGGGGCAGTAACAGCCATGACCAAAGCTTTGGCCCTGGATGA  
AAGTCCATATGGTGTCCGAGTCAACTGTATCTCCCCAGGAAACATCTGGACCCCGCTGTGGG  
AGGAGCTGGCAGCCTTAATGCCAGACCCTAGGGCCACAATCCGAGAGGGCATGCTGGCCACG  
CCACTGGGCCGCATGGGCCAGCCCGCTGAGGTCGGGGCTGCGGCAGTGTTCCCTGGCCTCCGA  
AGCCAACCTTCTGCACGGGCATTGAACTGCTCGTGACGGGGGGTGCAGAGCTGGGGTACGGGT  
GCAAGGCCAGTCGGAGCACCCCCGTGGACGCCCCCGATATCCCTTCCTGATTTCTCTCATTT  
CTACTTGGGGCCCCCTTCCTAGGACTCTCCACCCCCAACTCCAACCTGTATCAGATGCAGC  
CCCCAAGCCCTTAGACTCTAAGCCCAGTTAGCAAGGTGCCGGGTCACCCTGCAGGTTCCCAT  
AAAAACGATTTGCAGCC

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**FIGURE 196**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56045

<subunit 1 of 1, 270 aa, 1 stop

<MW: 28317, pI: 6.00, NX(S/T): 1

MATGTRYAGKVVVVTGGGRGIGAGIVRAFVNSGARVVICDKDESGGRALEQELPGAVFILCD  
VTQEDDVKTLVSETIRRFGRLLDCVVNNAGHHPPPQRPEETSAQGFRQLLELNLLGTYTLTKL  
ALPYLRKSQGNVINISLVLGAIGQAQAVPYVATKGAVTAMTKALALDESPYGVRVNCISPGN  
IWTPLWEELAALMPDPRATIREGMLAQPLGRMGQPAEVGAAVFLASEANFCTGIELLVTGG  
AELGYGCKASRSTPVDAPDIPS

**Important features:****N-glycosylation site.**

amino acids 138-141

**Short-chain alcohol dehydrogenase family protein**

amino acids 10-22, 81-91, 134-171 and 176-185

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**FIGURE 197**

AGGCGGGCAGCAGCTGCAGGCTGACCTTGCAGCTTGGCGGAATGGACTGGCCTCACAACCTG  
CTGTTTCTTCTTACCATTTCATCTTCCTGGGGCTGGGCCAGCCCAGGAGCCCCAAAAGCAA  
GAGGAAGGGGCAAGGGCGGCCTGGGCCCCCTGGCCCCCTGACCAGGTGCCACTGGACC  
TGGTGTACGGATGAAACCGTATGCCCCGCATGGAGGAGTATGAGAGGAACATCGAGGAGATG  
GTGGCCCAGCTGAGGAACAGCTCAGAGCTGGCCCAGAGAAAGTGTGAGGTCAACTTGCAGCT  
GTGGATGTCCAACAAGAGGAGCCTGTCTCCCTGGGGCTACAGCATCAACCACGACCCCAGCC  
GTATCCCCGTGGACCTGCCGGAGGCACGGTGCCCTGTGTCTGGGCTGTGTGAACCCCTTCACC  
ATGCAGGAGGACCGCAGCATGGTGAGCGTGCCGGTGTTTCAGCCAGGTTCCCTGTGCGCCGCCG  
CCTCTGCCCCGCCACCGCCCCGCACAGGGCCTTGCCGCCAGCGCGCAGTCATGGAGACCATCG  
CTGTGGGCTGCACCTGCATCTTCTGAATCACCTGGCCCAGAAGCCAGGCCAGCAGCCCGAGA  
CCATCCTCCTTGCACCTTTGTGCCAAGAAAGGCCTATGAAAAGTAAACACTGACTTTTGAAA  
GCAAG

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**FIGURE 198**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59294

<subunit 1 of 1, 180 aa, 1 stop

<MW: 20437, pI: 9.58, NX(S/T): 1

MDWPHNLLFLLTISIFLGLGQPRSPKSKRKGQGRPGPLAPGPHQVPLDLVSRMKPYARMEY  
ERNIEEMVAQLRNSSELAQRKCEVNLQLWMSNKRSLSPWGYSINHDPSPRIPVDLPEARCLCL  
GCVNPFTMQEDRSMVSVPVFSQVPVRRRLCPPPPRTGPCRQRAVMETIAVGCTCIF

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 75-78

**Homologous region to IL-17**

amino acids 96-180.

**FIGURE 199**

GCGCCGCCAGGCGTAGGCGGGGTGGCCCTTGCGTCTCCCGCTTCCTTGAAAAACCCGGCGGG  
CGAGCGAGGCTGCGGGCCGGCCGCTGCCCTTCCCCACACTCCCCGCCGAGAAGCCTCGCTCG  
GCGCCCAAC**ATG**GCGGGGTGGGCGCTGCGGCCCGCAGCTAACGGCGCTCCTGGCCGCCTGGAT  
CGCGGCTGTGGCGGCGACGGCAGGCCCGAGGAGGCCGCGCTGCCGCCGGAGCAGAGCCGGG  
TCCAGCCCATGACCGCCTCCAACCTGGACGCTGGTGATGGAGGGCGAGTGGATGCTGAAATTT  
TACGCCCCATGGTGTCATCCTGCCAGCAGACTGATTCAGAATGGGAGGCTTTTGCAAAGAA  
TGGTGAAATACTTCAGATCAGTGTGGGGAAGGTAGATGTCATTCAAGAACCAGGTTTGAGTG  
GCCGCTTCTTTGTCACTACTCTCCAGCATTTTTTTCATGCAAAGGATGGGATATTCCGCCGT  
TATCGTGGCCCAGGAATCTTCGAAGACCTGCAGAATTATATCTTAGAGAAGAAATGGCAATC  
AGTCGAGCCTCTGACTGGCTGGAAATCCCCAGCTTCTCTAACGATGTCTGGAATGGCTGGTC  
TTTTTAGCATCTCTGGCAAGATATGGCATCTTCACAACCTATTTACAGTGACTCTTGGAATT  
CCTGCTTGGTGTTCTTATGTGTTTTTCGTATAGCCACCTTGGTTTTTGGCCTTTTTATGGG  
TCTGGTCTTGGTGGTAATATCAGAATGTTTCTATGTGCCACTTCCAAGGCATTTATCTGAGC  
GTTCTGAGCAGAATCGGAGATCAGAGGAGGCTCATAGAGCTGAACAGTTGCAGGATGCGGAG  
GAGGAAAAAGATGATTCAAATGAAGAAGAAAACAAAGACAGCCTTGTAGATGATGAAGAAGA  
GAAAGAAGATCTTGGCGATGAGGATGAAGCAGAGGAAGAAGAGGAGGAGGACAACCTTGGCTG  
CTGGTGTGGATGAGGAGAGAAGTGAGGCCAATGATCAGGGGCCCCCAGGAGAGGACGGTGTG  
ACCCGGGAGGAAGTAGAGCCTGAGGAGGCTGAAGAAGGCATCTCTGAGCAACCCTGCCCAGC  
TGACACAGAGGTGGTGGAAAGACTCCTTGAGGCAGCGTAAAAGTCAGCATGCTGACAAGGGAC  
TG**TAG**ATTTAATGATGCGTTTTTCAAGAATACACACCAAAACAATATGTCAGCTTCCCTTTGG  
CCTGCAGTTTGTACCAAATCCTTAATTTTTTCCTGAATGAGCAAGCTTCTCTTAAAAGATGCT  
CTCTAGTCATTTGGTCTCATGGCAGTAAGCCTCATGTATACTAAGGAGAGTCTTCCAGGTGT  
GACAATCAGGATATAGAAAAACAAACGTAAGTGTGGGATCTGTTTGGAGACTGGGATGGGAA  
CAAGTTCATTTACTTAGGGGTCAGAGAGTCTCGACCAGAGGAGGCCATTCCCAGTCCTAATC  
AGCACCTTCCAGAGACAAGGCTGCAGGCCCTGTGAAATGAAAGCCAAGCAGGAGCCTTGGCT  
CCTGAGCATCCCCAAAGTGTAACGTAGAAGCCTTGCAATCCTTTTCTTGTTGTAAGTATTTAT  
TTTTGTCAAATTGCAGGAAACATCAGGCACCACAGTGCATGAAAAATCTTTCACAGCTAGAA  
ATTGAAAGGGCCTTGGGTATAGAGAGCAGCTCAGAAGTCATCCCAGCCCTCTGAATCTCCTG  
TGCTATGTTTTATTTCTTACCTTTAATTTTTTCCAGCATTTCCACCATGGGCATTCAGGCTCT  
CCACACTCTTCACTATTATCTCTTGGTCAGAGGACTCCAATAACAGCCAGGTTTACATGAAC  
TGTGTTTGTTCATTCTGACCTAAGGGGTTTAGATAATCAGTAACCATAACCCCTGAAGCTGT  
GACTGCCAAACATCTCAAATGAAATGTTGTGGCCATCAGAGACTCAAAGGAAGTAAGGATT  
TTACAAGACAGATTAAAAAAAATTGTTTTGTCCAAAATATAGTTGTTGTTGATTTTTTTTT  
AAGTTTTCTAAGCAATATTTTTCAAGCCAGAAGTCCTCTAAGTCTTGCCAGTACAAGGTAGT  
CTTGTGAAGAAAAGTTGAATACTGTTTTGTTTTTCATCTCAAGGGGTTCCTGGGTCTTGAAC  
TACTTTAATAATACTAAAAAACCCTTCTGATTTTCCTTCAGTGATGTGCTTTTGGTGAAA  
GAATTAATGAACCTCAGTACCTGAAAGTGAAAGATTTGATTTTGTTCATCTTCTGTAATC  
TTCCAAAGAATTATATCTTTGTAAATCTCTCAATACTCAATCTACTGTAAGTACCCAGGGAG  
GCTAATTTCTTT

**FIGURE 200**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56433

<subunit 1 of 1, 349 aa, 1 stop

<MW: 38952, pI: 4.34, NX(S/T): 1

MAGGRCGPQLTALLAAWIAAVAATAGPEEAALPPEQSRVQPMTASNWTLVMEGEWMLKFYAP  
WCPSCQQT DSEWEAFKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGI FRRYRG  
PGIFEDLQNYILEKKWQSVEPLTGWKSPASLTMSGMAGLFSISGKIWHLHNYFTVTLGIPAW  
CSYVFFVIATLVFGLFMGLVLVVISSECFYVPLPRHLSESEQNRRSEEAHRAEQLQDAEEEEK  
DDSNEEENKDSLVDDEEEKEDLGDEDEAEDEEDNLAAGVDEERSEANDQGPPGEDGV TRE  
EVEPEEAEEGISEQPCPADTEVVEDSLRQRKSQHADKGL

**Important features:****Signal peptide:**

amino acids 1-22

**Transmembrane domain:**

amino acids 191-211

**N-glycosylation site.**

amino acids 46-49

**Thioredoxin family proteins.** (homologous region to disulfide isomerase)

amino acids 56-72

**Flavodoxin proteins**

amino acids 173-187

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**FIGURE 201**

ATCTGGTTGAACTACTTAAGCTTAATTTGTTAAACTCCGGTAAGTACCTAGCCACATGATT  
TGACTCAGAGATTCTCTTTTGTCCACAGACAGTCATCTCAGGGGCAGAAAGAAAAGAGCTCC  
CAAATGCTATATCTATTCAGGGGCTCTCAAGAACA**ATG**GGAATATCATCCTGATTTAGAAAAT  
TTGGATGAAGATGGATATACTCAATTACACTTCGACTCTCAAAGCAATACCAGGATAGCTGT  
TGTTTCAGAGAAAGGATCGTGTGCTGCATCTCCTCCTTGGCGCCTCATTGCTGTAATTTTGG  
GAATCCTATGCTTGGTAATACTGGTGATAGCTGTGGTCCTGGGTACCATGGGGGTTCCTTCC  
AGCCCTTGTCTCCTAATTGGATTATATATGAGAAGAGCTGTTATCTATTCAGCATGTCACT  
AAATTCCTGGGATGGAAGTAAAAGACAATGCTGGCAACTGGGCTCTAATCTCCTAAAGATAG  
ACAGCTCAAATGAATTGGGATTTATAGTAAAACAAGTGTCTTCCCAACCTGATAATTCATTT  
TGGATAGGCCTTTCTCGGCCCCAGACTGAGGTACCATGGCTCTGGGAGGATGGATCAACATT  
CTCTTCTAACTTATTTTCAGATCAGAACCACAGCTACCCAAGAAAACCCATCTCCAAATTGTG  
TATGGATTCACGTGTCAGTCATTTATGACCAACTGTGTAGTGTGCCCTCATATAGTATTTGT  
GAGAAGAAGTTTTCAATG**TAA**GAGGAAGGGTGGAGAAGGAGAGAGAAATATGTGAGGTAGTA  
AGGAGGACAGAAAACAGAACAGAAAAGAGTAACAGCTGAGGTCAAGATAAATGCAGAAAATG  
TTTAGAGAGCTTGGCCAACTGTAATCTTAACCAAGAAATTGAAGGGAGAGGCTGTGATTTCT  
GTATTTGTGACCTACAGGTAGGCTAGTATTATTTTTTCTAGTTAGTAGATCCCTAGACATGG  
AATCAGGGCAGCCAAGCTTGAGTTTTTATTTTTTATTTATTTATTTTGTAGATAGGGTCT  
CACTTTGTTACCCAGGCTGGAGTGCAGTGGCACAATCTCGACTCACTGCAGCTATCTCTCGC  
CTCAGCCCCTCAAGTAGCTGGGACTACAGGTGCATGCCACCATGCCAGGCTAATTTTTTGGTG  
TTTTTTGTAGAGACTGGGTTTTTGCCATGTTGACCAAGCTGGTCTCTAACTCCTGGGCTTAAG  
TGATCTGCCCCGCTTGGCCTCCCAAAGTGCTGGGATTACAGATGTGAGCCACCACACCTGGC  
CCCAAGCTTGAATTTTCATTCTGCCATTGACTTGGCATTTACCTTGGGTAAGCCATAAGCGA  
ATCTTAATTTCTGGCTCTATCAGAGTTGTTTCATGCTCAACAATGCCATTGAAGTGCACGGT  
GTGTTGCCACGATTTGACCCTCAACTTCTAGCAGTATATCAGTTATGAACTGAGGGTGAAAT  
ATATTTCTGAATAGCTAAATGAAGAAATGGGAAAAAATCTTCACCACAGTCAGAGCAATTTT  
ATTATTTTCATCAGTATGATCATAATTATGATTATCATCTTAGTAAAAAGCAGGAACCTCCTA  
CTTTTTCTTTATCAATTAAATAGCTCAGAGAGTACATCTGCCATATCTCTAATAGAATCTTT  
TTTTTTTTTTTTTTTTTTTTTGTAGACAGAGTTTCGCTCTTGTGCCCAGGCTGGAGTGCAACGG  
CACGATCTCGGCTCACCGCAACCTCCGCCCCCTGGGTTCAAGCAATTCTCCTGCCTCAGCCT  
CCCAAGTAGCTGGGATTACAGTCAGGCACCACCACACCCGGCTAATTTTGTATTTTTTTTAGT  
AGAGACAGGGTTTCTCCATGTCGGTCAGGGTAGTCCCGAACTCCTGACCTCAAGTGATCTGC  
CTGCCTCGGCCTCCCAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCCAGCCTAGAATCT  
TGTATAATATGTAATTGTAGGGAAACTGCTCTCATAGGAAAGTTTTCTGCTTTTTTAAATACA  
AAAATACATAAAAATACATAAAATCTGATGATGAATATAAAAAAGTAACCAACCTCATTGGA  
ACAAGTATTAACATTTTGGAAATATGTTTTATTAGTTTTGTGATGTACTGTTTTACAATTTTT  
ACCATTTTTTTTTCAGTAATTACTGTAAAATGGTATTATTGGAATGAACTATATTTCTCATG  
TGCTGATTTGTCTTATTTTTTTTCTACTTTCCCACTGGTGCTATTTTTTATTTCCAATGGATA  
TTTCTGTATTACTAGGGAGGCATTTACAGTCCTCTAATGTTGATTAAATATGTGAAAAGAAAT  
TGTACCAATTTTACTAAATTATGCAGTTTAAAATGGATGATTTTATGTTATGTGGATTTTCAT  
TTCAATAAAAAAAACTCTTATCAAAAAAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTT

**FIGURE 202**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA53912

<subunit 1 of 1, 201 aa, 1 stop

<MW: 22563, pI: 4.87, NX(S/T): 1

MEYHPDLENLDEDGYTQLHFDSQSNTRIAVVSEKGS CAASPPWRLIAVILGILCLVILVIAV  
VLGTMGVLSSPCPPNWIIYEKSCYLFMSLSWDGSKRQCWQLGSNLLKIDSSNELGFIVKQ  
VSSQPDNSFWIGLSRPQTEVPWLWEDGSTFSSNLFQIRTTATQENPSPNCVWIHVSVIYDQL  
CSVPSYSICEKKFSM

**Important features:****Type II transmembrane domain:**

amino acids 45-65

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 197-200

**N-myristoylation sites.**

amino acids 35-40 and 151-156

**Homologous region to LDL receptor**

amino acids 34-67 and 70-200.

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**FIGURE 203**

GGAAGGGGAGGAGCAGGCCACACAGGCACAGGCCGGTGAGGGACCTGCCAGACCTGGAGGGTCTCGCTCTGTCA  
CACAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCATCGTAACCTCCACCTCCCGGGTTCAAGTGATTCTCATGCC  
TCAGCCTCCCGAGTAGCTGGGATTACAGGTGGTGACTTCCAAGAGTGACTCCGTCCGAGGAAAATGACTCCCCAG  
TCGCTGCTGCAGACGACACTGTTCTGCTGAGTCTGCTCTTCTGGTCCAAGGTGCCACGGCAGGGGCCACAGG  
GAAGACTTTCGCTTCTGCAGCCAGCGGAACCAGACACACAGGAGCAGCCTCCACTACAAACCCACACCAGACCTG  
CGCATCTCCATCGAGAACTCCGAAGAGGGCCCTCACAGTCCATGCCCCTTTCCTGCGAGCCACCCCTGCTTCCCGA  
TCCTTCCCTGACCCAGGGGCTCTACCACTTCTGCCTCTACTGGAACCGACATGCTGGGAGATTACATCTTCTC  
TATGGCAAGCGTGACTTCTTGCTGAGTGACAAAGCCTCTAGCCTCCTCTGCTTCCAGCACCAGGAGGAGAGCCTG  
GCTCAGGGCCCCCGCTGTTAGCCACTTCTGTACCTCCTGGTGGAGCCCTCAGAACATCAGCCTGCCAGTGCC  
GCCAGCTTACCTTCTCCTTCCACAGTCTCCCCACACGGCCGCTCACAATGCCTCGGTGGACATGTGCGAGCTC  
AAAAGGGACCTCCAGCTGCTCAGCCAGTTCTGAAGCATCCCCAGAAGGCCTCAAGGAGGCCCTCGGCTGCCCCC  
GCCAGCCAGCAGTTGCAGAGCCTGGAGTGCAGAACTGACCTCTGTGAGATTGATGGGGGACATGGTGTCTTTCGAG  
GAGGACCGGATCAACGCCACGGTGTGGAAGCTCCAGCCCACAGCCGGCCTCCAGGACCTGCACATCCACTCCCGG  
CAGGAGGAGGAGCAGAGCGAGATCATGGAGTACTCGGTGCTGCTGCCTCGAACACTCTTCCAGAGGACGAAAGGC  
CGGAGCGGGGAGGCTGAGAAGAGACTCCTCCTGGTGGACTTCAGCAGCCAAGCCCTGTTCCAGGACAAGAATTCC  
AGCCAAGTCTTGGGTGAGAAGGTCTTGGGGATTGTGGTACAGAACACCAAGTAGCCAACCTCACGGAGCCCCGTG  
GTGCTCACTTTCAGCACCAGCTACAGCCGAAGAATGTGACTCTGCAATGTGTGTTCTGGGTGAAGACCCCA  
TTGAGCAGCCCCGGGGCATTGGAGCAGTGCTGGGTGTGAGACCGTCAGGAGAGAAACCCAAACATCCTGCTTCTGC  
AACCACTTGACCTACTTTGCAGTGCTGATGGTCTCCTCGGTGGAGGTGGACGCCGTGCACAAGCACTACCTGAGC  
CTCCTCTCCTACGTGGGCTGTGTGCTCTCTGCCCTGGCCTGCCTTGTACCATTTGCCGCTACCTCTGCTCCAGG  
GTGCCCCCTGCCGTGCAGGAGGAAACCTCGGGACTACACCATCAAGGTGCACATGAACCTGCTGCTGGCCGTCTTC  
CTGCTGGACACGAGCTTCTGCTCAGCGAGCCGGTGGCCCTGACAGGCTCTGAGGCTGGCTGCCGAGCCAGTGCC  
ATCTTCTGCACTTCTCCCTGCTCACCTGCCTTTCTGGATGGGCCTCGAGGGGTACAACCTCTACCGACTCGTG  
GTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAAGCTGAGCGCCATGGGCTGGGGCTTCCCCATCTTT  
CTGGTGACGCTGGTGGCCCTGGTGGATGTGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAG  
GGCGTCATCTACCTTCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATCACCAACCTGGGCCTCTTCAGC  
CTGGTGTCTTCTGTTCAACATGGCCATGCTAGCCACCATGGTGGTGCAGATCCTGCGGCTGCGCCCCCACACCCAA  
AAGTGGTCACATGTGCTGACACTGCTGGGCCTCAGCCTGGTCCCTGGCCCTGCCCTGGGCCTTGATCTTCTTCTCC  
TTTGCTTCTGGCACCTTCCAGCTTGTGCTCCTCTACCTTTTCAGCATCATCACCTCCTTCCAAGGCTTCTCATC  
TTCATCTGGTACTGGTCCATGCGGCTGCAGGCCCGGGGTGGCCCCCTCCCCTCTGAAGAGCAACTCAGACAGCGCC  
AGGCTCCCCATCAGCTCGGGCAGCACCTCGTCCAGCCGCATCTAGGCCTCCAGCCCACCTGCCCATGTGATGAAG  
CAGAGATGCGGCCCTCGTCGCACACTGCCTGTGGCCCCCGAGCCAGGCCCCAGGCCCAGGCCAGTCAGCCGCAGACT  
TTGGAAGGCCCAACGACCATGGAGAGATGGGCCGTTGCCATGGTGGACGGACTCCCGGGCTGGGCTTTTGAATTG  
GCCTTGGGGACTACTCGGCTCTCACTCAGCTCCCACGGGACTCAGAAGTGCGCCGCCATGCTGCCTAGGGTACTG  
TCCCCACATCTGTCCCAACCCAGCTGGAGGCCTGGTCTCTCCTTACAACCCCTGGGCCAGCCCTCATTGCTGGG  
GGCCAGGCCTTGGATCTTGAGGGTCTGGCACATCCTTAATCCTGTGCCCTGCCTGGGACAGAAATGTGGCTCCA  
GTTGCTCTGTCTCTCGTGGTCACCCTGAGGGCACTCTGCATCCTCTGTCAATTTTAACCTCAGGTGGCACCCAGGG  
CGAATGGGGGCCAGGGCAGACCTTCAGGGCCAGAGCCCTGGCGGAGGAGAGGCCCTTTGCCAGGAGCACAGCAGC  
AGCTCGCCTACCTCTGAGCCCAGGCCCCCTCCCTCCCTCAGCCCCCAGTCCTCCCTCCATCTTCCCTGGGGTTC  
TCCTCCTCTCCAGGGCCTCCTTGCTCCTTCGTTACAGCTGGGGGTCCCCGATTTCCAATGCTGTTTTTTGGGGA  
GTGGTTTTCCAGGAGCTGCCTGGTGTCTGCTGTAAATGTTTGTCTACTGCACAAGCCTCGGCCTGCCCTGAGCCA  
GGCTCGGTACCGATGCGTGGGCTGGGCTAGGTCCCTCTGTCCATCTGGGCCTTTGTATGAGCTGCATTGCCCTTG  
CTCACCTGACCAAGCACACGCCTCAGAGGGGCCCTCAGCCTCTCCTGAAGCCCTCTTGTGGCAAGAACTGTGGA  
CCATGCCAGTCCCGTCTGGTTCCATCCCACTCCAAGGACTGAGACTGACCTCCTCTGGTGACACTGGCCTA  
GAGCCTGACACTCTCCTAAGAGGTTCTCTCCAAGCCCCCAAATAGCTCCAGGCGCCCTCGGCCGCCCATCATGGT  
TAATTCTGTCCAACAAACACACACGGGTAGATTGCTGGCCTGTTGTAGGTGGTAGGGACACAGATGACCGACCTG  
GTCACCTCCTCCTGCCAACATTAGTCTGGTATGTGAGGCGTGCGTGAAGCAAGAACTCCTGGAGCTACAGGGACA  
GGGAGCCATCATTCTGCCTGGGAATCCTGGAAGACTTCTGCAGGAGTCAGCCTTCAATCTTGACCTTGAAGAT  
GGGAAGGATGTTCTTTTACGTACCAATTCTTTTGTCTTTTGATATTAAGAAAGTACATGTTTATGTAGAGA  
ATTTGGAAACTGTAGAAGAGAATCAAGAAGAAAAATAAAAAATCAGCTGTTGTAATCGCCTAGCAAAAAAAAAAAAA  
AA

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**FIGURE 204**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA50921

<subunit 1 of 1, 693 aa, 1 stop

<MW: 77738, pI: 8.87, NX(S/T): 7

MTPQSLLQTTFLLSLLFLVQGAHGRGHREDFRSCQRNQTHRSSLHYKPTPDLRISIENSE  
EALTVHAPFPAAHPASRSFPDPRGLYHFCLYWNRHAGRLHLLYGKRDFLLSDKASSLLCFQH  
QEESLAQGPPLLATSVTSWWSPQNISLPSAASF TFSFHSPHTAAHNASVDMCELKRDLQLL  
SQFLKHPQKASRRPSAAPASQQQLQSLESKLT SVRFMGDMVSFEEDRINATVWKLQPTAGLQD  
LHIHSRQEEEQSEIMEYSVLLPRTL FQRTKGRSGEAEKRLLLVDFSSQALFQDKNSSQVLGE  
KVLGIVVQNTKVANLTEPVVLT FQHQLQPKNVT LQCVFWVEDPTLSSPGHWSSAGCETVRRE  
TQTSCFCNHLTYFAVLMVSSVEVDAVHKHYLSLLSYVGCVVVSALACLVTIAAYLCSRVP LPC  
RRKPRDYTIKVHNMNLLLAVFLLDTSELLSEPVALTGSEAGCRASAI FLHFSLLTCLSWMGLE  
GYNLYRLVVEVFGTYVPGYLLKLSAMGWGFPIFLVTLVALVDVDNYGPIILAVHRTPEGVIY  
PSMCWIRDSLVS YITNLGLFSLVFLFN MAMLATMVVQILRLRPHTQKWSHVL TLLGLSLVLG  
LPWALIFFSFASGTFQLVVLYLFSIITSFQGFLIFIWWSMRLQARGGPSPLKSN SDSARLP  
ISSGSTSSSRI

**Important features:****Signal peptide:**

amino acids 1-25

**Putative transmembrane domains:**

amino acids 382-398, 402-420, 445-468, 473-491, 519-537, 568-590  
and 634-657

**Microbodies C-terminal targeting signal.**

amino acids 691-693

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 198-201 and 370-373

**N-glycosylation sites.**

amino acids 39-42, 148-151, 171-174, 234-237, 303-306, 324-327  
and 341-344

**G-protein coupled receptors family 2 proteins**

amino acids 475-504

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**FIGURE 205**

TGCCTGGCCTGCCTTGTCAACAATGCCGCTTACTCTGCTTCCAGGTTGCCCTGCCTTGCAGA  
GGAAANCNTCGGGACTACACCNTCAAGTGCACATGAACCTGCTGCTGGCCGTCTTCCTGCTG  
GACACGAGCTTCCTGCTCAGCGNAGCCGGTGGCCCTGACAGGCTCTGAAGGCTGGCTGCCGA  
GCCAGTGCCATCTTCCTGCACTTCTCCTGCTCACCTGCCTTTCCTGGATGGGCCTCGAGGGG  
TACAACCTCTACCGACTCGTGGTGGAGGTCTTTGGCACCTATGTCCCTGGCTACCTACTCAA  
GCTGAGCGCCATGGGCTGGGGCTTCCCATCTTTCTGGTGACGCTGGTGGCCCTGGTGGATG  
TGGACAACTATGGCCCCATCATCTTGGCTGTGCATAGGACTCCAGAGGGCGTCATCTACCCT  
TCCATGTGCTGGATCCGGGACTCCCTGGTCAGCTACATACCAACCTGGGCCTCTTCAGCCT  
GGTGTTCCTGTTCAACATGG

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**FIGURE 206**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCTGCTTCAGGTCCAGGTTTTGCTTTGA  
TCCTTTTCAAAAAGTGGAGACACAGAAGAGGGCTCTAGGAAAAAGTTTTGGATGGGATTATGTGGAACTACCCT  
GCGATTCTCTGCTGCCAGAGCAGGCTCGGCGCTTCCACCCAGTGCAGCCTTCCCCTGGCGGTGGTGAAAGAGAC  
TCGGGAGTCGCTGCTTCCAAAGTGCCCGCCGTGAGTGAGCTCTCACCCAGTCAGCCAAATGAGCCTCTTCGGGC  
TTCTCCTGCTGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTAAATTCC  
AGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATG  
GAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAG  
AGGAAAATGTATGGATACAACCTTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGT  
ATGATTTTGTAGAAGTTGAGGAACCCAGTGATGGAACCTATATAGGGCGCTGGTGTGGTTCTGGTACTGTACCAG  
GAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAATATTTTCTTCTGAACCAGGGT  
TCTGCATCCACTACAACATTGTCTATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTT  
TGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGAAGACCTTATTCGATATCTTGAACCAG  
AGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAA  
GAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACTTCT  
CAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTG  
GTGGGAACTGTGCCTGTTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACC  
ACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTACCGACGTGGCCCTGGAGC  
ACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCCGCATCACCACCAGCAGCTCTTGCCCA  
GAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCT  
TCAAGGACCTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCA  
ACAGCTCTTTTGGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGTAT  
TAAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTTCTGTTCTTTC  
GATACGGCTTAGGGTAATGTGATACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAC  
TCTAAAGCTCCATGTCTTGGGCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGTCTCATATTCACAT  
ATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAACCTTGT  
GTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAATAATTTCTGCCATTAGAGAAGAGAACTACA  
TTCATGGTTTGGAAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTG  
TTTCATTGTGTACATTTTTTATATTCTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCT  
ATTTTTTACCAAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTCTAGCTTGGTAAATTTTCT  
AAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCA  
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTTAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAA  
GACTTTTTGAAAATAATTAAATTATCATATCTTCCATTCCCTGTTATTGGAGATGAAAATAAAAAGCACTTATGA  
AAGTAGACATTTCAGATCCAGCCATTACTAACCTATTCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACAT  
AAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCGTGCTGTGCTGTGCAGTAGGAACACATCCTATTTA  
TTGTGATGTTGTGGTTTTATTATCTTAAACTCTGTTCCATACACTTGTATAAATACATGGATATTTTTATGTACA  
GAAGTATGTCTCTTAACCAGTTCACTTATTGTACTCTGGCAATTTAAAAAGAAAATCAGTAAAATATTTTGCTTGT  
AAAATGCTTAATATNGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGA  
ATGTGGCTATTTTGGGGAGAAAATTAAAAAAGGTTTAGGGATAACAGGGTAATGCGGCC

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**FIGURE 207**

MSLFGLLLLT SALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHSPR  
FPHTYPRNTVLVWRLVAVEENVWQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTILGRWC  
GSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLL  
NNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLEEVRLY  
SCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQ  
LRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG

**Signal sequence:**

amino acids 1-14

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**FIGURE 208**

CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACATTCCATTTTGGAAGA  
AGACTAAAAATGGTGTTCCTAATGTGGACACTGAAGAGACAAATTCCTATCCTTTTAAACATAATCCTAATTTCC  
AAACTCCTTGGGGCTAGATGGTTTCCTAAACTCTGCCCTGTGATGTCACCTCTGGATGTTCCAAAGAACCATGTG  
ATCGTGGACTGCACAGACAAGCATTGACAGAAATTCCTGGAGGTATTCACGAAACACCACGAACCTCACCCCTC  
ACCATTAACCACATAACCAGACATCTCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTCAGA  
TGCAACTGTGTACCTATTCCACTGGGGTCAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCCAGAAGC  
TTTAGTGGACTCACTTATTTAAATCCCTTTACCTGGATGGAAACCAGCTACTAGAGATAACCGCAGGGCCTCCCG  
CCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACACATCTTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCC  
AACATAGAAATACTCTACCTGGGCCAAAACGTATTATTCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAA  
GATGCCTTCCTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTACAGCCGTCCTACTGTT  
TTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATCCAAGAAGATGATTTTAATAAC  
CTCAACCAATTACAAATTCCTTGACCTAAGTGGAAATTGCCCTCGTTGTTATAATGCCCCATTTCTTGTCGCGCCG  
TGTAATAATAATTCTCCCCTACAGATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTA  
CACAGTAACCTCTCTCAGCATGTGCCCCAAGATGGTTTAAAGAACATCAACAACTCCAGGAACTGGATCTGTCC  
CAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCCAGCCTCATCCAATTGGATCTG  
TCTTTCAATTTTGAACCTCAGGTCTATCGTGCATCTATGAATCTATCACAAGCATTTTCTTCACTGAAAAGCCTG  
AAAATTCTGCGGATCAGAGGATATGTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAA  
AATCTTGAAGTTCTTGATCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTTAAAAGA  
CTGAAAGTCATAGATCTTTCACTGAATAAAATATCACCTTCAGGAGATTCAAGTGAAGTTGGCTTCTGCTCAAT  
GCCAGAACTTCTGTAGAAAGTTATGAACCCCAAGTCTTGGAAACAATTACATTATTTTCAAGATATGATAAGTATGCA  
AGGAGTTGCAGATTCAAAAACAAAGAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACC  
TTGGATCTAAGTAAAAATAGTATATTTTTTGTCAAGTCTCTGATTTTTCAGCATCTTTCTTCTCCTCAAATGCCTG  
AATCTGTCAAGAAATCTCATTAGCCAACTCTTAATGGCAGTGAATTCACACCTTTAGCAGAGCTGAGATATTTG  
GACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACAGCATTGTAAGAGCTTCACAACTGGAAGTTCTGGAT  
ATAAGCAGTAATAGCCATTATTTTCAATCAGAAGGAATTACTCATATGCTAACTTTACCAAGAACCTAAAGGTT  
CTGCAGAACTGATGATGAACGACAATGACATCTCTTCTCCACCAGCAGGACCATGGAGAGTGAGTCTCTTAGA  
ACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAACAGATACTTACAATTATTCAAG  
AATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAATTCCTTAAGTTTCTTGCTTCTGGAGTTTTTGATGGT  
ATGCCCTCAAATCTAAAGAATCTCTCTTTGGCCAAAATGGGCTCAAATCTTTCAGTTGGAAGAACTCCAGTGT  
CTAAAGAACCTGGAACTTTGGACCTCAGCCACAACCACTGACCACTGTCCCTGAGAGATTATCCAAGTGTTC  
AGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAGTATTTTCTACAAGATGCCTTC  
CAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAGATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTC  
AACAACTCTGAAGATGTTGCTTTTGCATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGTTTGTCTGGTGG  
GTTAACCATACGGAGGTGACTATTCCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACACAAGGGC  
CAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTGATTCTGTTCTCACTTTCCATA  
TCTGTATCTCTCTTTCTCATGGTGTGATGATGACAGCAAGTACCTCTATTTCTGGGATGTGTGGTATATTTACCAT  
TTCTGTAAGGCCAAGATAAAGGGGTATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTAT  
GACACTAAAGACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAACTGGAAGACCCAAGAGAGAAA  
CATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTGGAAAACCTTTCCAGAGCATA  
CAGCTTAGCAAAAAGACAGTGTGTTGTGATGACAGACAAGTATGCAAAGACTGAAAATTTTAAGATAGCATTTTAC  
TTGTCCCATCAGAGGCTCATGGATGAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAG  
TCCAAGTTCCTCCAGCTCCGGAAGGGCTCTGTGGGAGTTCTGTCTTGTGAGTGGCCAAACAAACCCGCAAGCTCAC  
CCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCCTATAGTCAGGTGTTCAAGGAA  
ACGGTCTAGCCCTTCTTTGCAAAACACAACCTGCCTAGTTTACCAAGGAGAGGCCTGGC

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**FIGURE 209**

MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIPGG  
IPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRNCVPIPLGSKNNMCIKRLQIKPRSFS  
GLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLGQNCYR  
NPCYVSYSEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKIQEDDFNNL  
NQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSNSLQHVPFRWF  
KNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASMNLSQAFSSLKSL  
KILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQFKRLKVIDLSVNKIS  
PSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNKEASFMSVNESCYKYGO  
TLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQPLAELRYLDFSNNRLDLLH  
STAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQKLMMDNDISSSTSRTMESES  
LRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKNSLSFLPSGVFDGMPPNLKNLSL  
AKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSNCSRSKLNILKNNQIRSLTKYFLQ  
DAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLLHHNRFLCTCDAVWFVWWVNHTEVTIP  
YLATDVTVCVGPAGAHKGQSVISLDLYTCELDLTNLILFSLISISVSLFLMVMMTASHLYFWDVW  
YIYHFCKAKIKGYQRLISPDCCYDAFIVYDTKDPAVTEWVLAELVAKLEDPREKHFNLCLLEE  
RDWLPGQPVLNLSQSIQLSKKTVFVMTDKYAKTENFKIAFYLSHQRLMDEKVDVIILIFLE  
KPFQKSKFLQLRKRLCGSSVLEWPTNPQAHFYFWQCLKNALATDNHVAYSQVFKETV

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 840-860

**FIGURE 210**

GGGTACCATTTCTGCGCTGCTGCAAGTTACGGAATGAAAAATTAGAACACAGAAACATGGAAAACATGTTCCCTTC  
AGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGTTCCCTGTGAGTTATGCGCCGAAGAAAATTTTCTA  
GAAGCTATCCTTGTGATGAGAAAAAGCAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAG  
TTCCCCAAACGGTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTTCATCACACACATAACGAATGAAT  
CATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTACAGCACCAGAACGGAAATC  
CCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCATTCCCTCAACCTAAAAACCTAAGGGAGTTACTGC  
TTGAAGACAACCAGTTACCCCAAATACCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACA  
ATATATACAACATAACTAAAGAGGGCATTTCAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAGTGT  
ATTTTAACAAAGTTTGGGAGAACTAACATAGAAGATGGAGTATTTGAAACGCTGACAAATTTGGAGTTGCTAT  
CACTATCTTTCAATTCTCTTTACACGCTGCCACCCAACTGCCAAGCTCCCTACGCAAACTTTTTCTGAGCAACA  
CCCAGATCAAATACATTAGTGAAGAAGATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAAGT  
GTCCGAGGTGCTTCAATGCCCAATTTCCATGCGTGCCTTGTGATGGTGGTGTCTCAATTAATATAGATCGTTTTG  
CTTTTCAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGGAAGATTAATGCTGCCTGGT  
TTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATCAACTATTTAGTGGGAGAAATAGTCTCTGGGGCAT  
TTTTAACGATGCTGCCCCGCTTAGAAATACTTGACTTGTCTTTAACTATATAAAGGGGAGTTATCCACAGCATA  
TTAATATTTCCAGAACTTCTCTAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAGGAAC  
TCAGAGAAGATGATTTCCAGCCCCGTGATGCAGCTTCCAACTTATCGACTATCAACTGGGTATTAATTTTATTA  
AGCAAATCGATTTCAAACCTTTTCCAAATTTCTCCAATCTGGAAATTATTTACTTGTGAGAAAACAGAATATCAC  
CGTTGGTAAAAGATACCCGGCAGAGTTATGCAAATAGTTCTCTTTTCAACGTCATATCCGGAAACGACGCTCAA  
CAGATTTTGAGTTTGACCCACATTCGAACTTTTATCATTTACCCGTCCTTTAATAAAGCCACAATGTGCTGCTT  
ATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAATTTGAAATCTTCTGACA  
TTGCTGTTTAAATCTGTCTGCAAATAGCAATGCTCAAGTGTTAAGTGGAACTGAATTTTCAGCCATTCCTCATG  
TCAAATATTTGGATTGACAAACAATAGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGG  
AAGTTCTAGATCTCAGCTATAATTCACACTATTTCAAGATAGCAGGCGTAACACATCATCTAGAATTTATTCAA  
ATTTCACAAATCTAAAAGTTTAACTTGAGCCACAACAACATTTATACTTTAACAGATAAGTATAACCTGGAAA  
GCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTTGACATTTTGTGGAATGATGATGACAACAGGTATA  
TCTCCATTTTCAAAGGTCTCAAGAATCTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATG  
AAGCATTCCTTAATTTGCCAGCGAGTCTCACTGAACATATAAATGATAATATGTTAAAGTTTTTTAACTGGA  
CATTACTCCAGCAGTTTCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAACTACTCTTTTAACTGATAGCC  
TATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGTCATAACAGGATTTCCACCTACCCTCTGGCTTTC  
TTTCTGAAGTCAGTAGTCTGAAGCACCTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTG  
AACTAAGACCACCACCAAAATTATCTATGTTGGAACACACGGAACCCCTTTGAATGCACCTGTGACATTGGAG  
ATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAATTTCCAGACTGGTAGATGTCATTTGTGCCAGTCCTG  
GGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACAACTTGTGTTTCAGATGTCAGTGCAGTGATATTAT  
TTTTCTTCACGTTCTTTATCACCACCATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTTACTGGGATGTTT  
GGTTTATATATAATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAACCTTTCTATGATG  
CTTACATTTCTTATGACACCAAAGATGCCTCTGTACTGACTGGGTGATAAATGAGCTGCGCTACCACCTTGAAG  
AGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGGGATTGGGACCCGGGATTGGCCATCATCGACAACC  
TCATGCAGAGCATCAACCAAAGCAAGAAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACCTTTA  
AAACAGCTTTTTACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTGGAGC  
CAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCCATCCTCCAGTGGCCTGACA  
ACCCGAAGGCAGAAGGCTTGTGTTTGGCAAACCTCTGAGAAATGTGGTCTTGACTGAAAATGATTACGGGTATAACA  
ATATGTATGTGATTCCATTAAGCAATACTAACTGACGTTAAGTCATGATTTTCGCGCCATAATAAAGATGCAAAG  
GAATGACATTTCTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAACCTTAGTGGTTTAAACAACACA  
TTTGCTGGCCACAGTTTTTGGGGTCAGGAGTCCAGGCCAGCATAACTGGGTCTCTGCTCAGGGTGTCTCAG  
AGGCTGCAATGTAGGTGTTTACCAGAGACATAGGCATCACTGGGGTCACACTCATGTGGTTGTTTTCTGGATTCA  
ATTCTCCTGGGCTATTGGCCAAAGGCTATACTCATGTAAGCCATGCGAGCCTCTCCACAAGGCAGCTTGCTTC  
ATCAGAGCTAGCAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAAATCGAATCAAAAAGTGAT  
ATCTCATCACTTTGGCCATATTCTATTTGTTAGAAAGTAAACCACAGGTCCCACCAGCTCCATGGGAGTGACCACC  
TCAGTCCAGGGAAACAGCTGAAGACCAAGATGGTGAAGCTCTGATTGCTTCAGTTGGTCATCAACTATTTTCCCT  
TGACTGCTGTCTGGGATGGCCTGCTATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACC  
ATCTTAGCAGTTGACCTAACACATCTTCTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCTAATA  
TTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTGTGGTTGCGTTCCGTTTTAT  
TTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTTCTAAGGTTTAGATGCCATTTAAGAACTGAGATGG  
ATAGCTTTTAAAGCATCTTTTACTTCTTACCATTTTTTAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATA  
TTGTTAATTGCCATTGCTGTAAATCTTAAATGAATGAATAAAATGTTTCATTTTACAAAAA

**FIGURE 211**

MENMFLOSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQND SVIAECSNRRLQEVPTVG  
KYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHONGNPGIQSNGLNITDGAFLNL  
KNLRELLLEDNQLPQIPSGLPESLTEL SLIQNNIYNITKEGISRLINLKNLYLAWNCYFNKV  
CEKTNIEDGVFETLTNLELLSLSENSLSHVPPKLPSSLRKLFSLNTQIKYISEEDFKGLINL  
TLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNL TQLRYLNLSSLSLRKINA AWFKNM  
PHLKVLDLEFN YLVGEIVSGAFLTMLPRLEILDLSFN YIKGSYPQHINISRNF SKLLSLRAL  
HLRGYVFQELREDDFQPLMQLPNLSTINLGINF IKQIDFKLFQNF SNLEIIYLS ENRISPLV  
KDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCAAYGKALDLSLNSIFFI  
GPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNNRLDFDNASALTELS DLEV  
LDLSYN SHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYT LT DKYNLESKSLVELVFSGNRL  
DILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFLNLPASLTE LHINDNMLKFFNWT  
LLQQFPRLLELLDLRGNKLLFLTDSLSDFTSSLRTLLLSHNRISHLPSGFLSEVSSLKHL DLS  
SNLLKTINKSALETKTTTKLSMLELHG NPFECTCDIGDFRRWMDEHLNVKIPRLVDVICASP  
GDQRGKSIVSLELTTCVSDVTAVILFFFTFFITTMVMLAALAHHLFYWDVWFIYNVCLAKVK  
GYRSLSTSQT FYDAYISYDTKDASVTDWVINELRYHLEESRDKNVLLCLEERDWD PGLAIID  
NMQSINQSKKT VFLTKKYAKSWNFKTA FYLALQRLMDENMDVII FILL EPVLQHSQYLRL  
RQRICKSSILQWPDNPKA EGLFWQTLRNVVLTENDSRYNNMYVDSIKQY

**Signal sequence:**

amino acids 1-26

**Transmembrane domain:**

amino acids 826-848

**FIGURE 212**

CCAGGTCCAACCTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCT  
CGACCTCGACCCACGCGTCCGCCAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGA  
CAGGCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGC  
AAGGGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGC  
TCCAGCAGCATCAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGA  
GCAGCTCCTGCCCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAA  
GGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTT  
CTGGTGTTGGCAGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGT  
CCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCA  
CCACCTGCGACGGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGC  
CGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGAC  
CAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGA  
GCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCA  
GATGTGGATGAATGCAGTGCTAGGAGGGGCGGCTGTCCCCAGCGCTGCATCAACACCGCCGG  
CAGTTACTGGTGCCAGTGTTGGGAGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGC  
CCAAGGGAGGGCCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAA  
GAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGC  
CCCCTGCACAGCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCC  
TGGTGCACCTCCTTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCTCTG  
GAGGAGCAGCTGGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTG  
GACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAG  
AAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCC  
TTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCAC  
CCCTGGCTACCCCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTG  
AGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAG  
GCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACAATAAAAATGAAACGTGA  
AAGGGCGGCCGCGACTCTAGAGT  
CGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAAT

**FIGURE 213**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19



**FIGURE 214**

GCCAGGCAGGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAG  
GGCTAGGGTCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCC  
AGCAGCATCAGAGCAGCCCCCTGTGGTTGGCAGCAAAGTTTCTAGCTTGGCTGGGCCCCGCTGTGA  
GGGGCTTCGCGCTACGCCCTGCGGTGTCCCGAGGGGCTGAGGTCTCCTCATCTTCTCCCTAGC  
AGTGGATGAGCAACCCAACGGGGGGCCCCGGGGAGGGGAACTGGCCCCGAGGGAGAGGAACCCC  
AAAGCCACATCTGTAGCCAGGATGAGCAGTGTGAATCCAGGCAGCCCCCAGGACCGGGGAGG  
CACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGCCCTGTCCGGGGGATGACTGATTC  
TCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGCCTGGAGGCACAGGCCATGAGGGGC  
TCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTGGCAGTGGGCGGCACAGAGCACGCCTA  
CCGGCCCCGGCCGTAGGGTGTGTGCTGTCCGGGCTCACGGGGACCCTGTCTCCGAGTCGTTCC  
TGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGACGGGGACCGGGCCTGCAGCACCTAC  
CGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGGGCTGGCCCCCTGCCAGGCCTCGCTA  
CGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTCCTGGGGCCTGTGGAGCAGCAATAT  
GCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAGCCTGGCCGCTGCCGCTGCCCTGCA  
GGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGAATGCAGTGCTAGGAGGGGGCGGCTG  
TCCCCAGCGCTGCATCAACACCGCCGGCAGTTACTGGTGCCAGTGTTGGGAGGGGGCACAGCC  
TGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGGCCCCCCCCAGGGTGGCCCCCAACCCG  
ACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAGGCTGCAGTCCAGGGTGGACCTGCT  
GGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACAGCCTGGCCTCGCAGGCACTGGAGC  
ATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCCTTCCAGCAGCTCGGCCGCATCGAC  
TCCCTGAGCGAGCAGATTTCTTCTCCTGGAGGAGCAGCTGGGGTCTGCTCCTGCAAGAAAGA  
CTCGTGACTGCCCAGCGCTCCAGGCTGGACTGAGCCCCCTCACGCCGCCCTGCAGCCCCCATG  
CCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCGGGGTGACTGAGCGGAAGGCCAGGC  
AGGGCCTTCCTCCTCTTCTCCTCCCCTTCCTCGGGAGGCTCCCCAGACCCTGGCATGGGAT  
GGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACCCCCACCCTGGCTACCCCAACGGCA  
TCCCAAGGCCAGGTGGACCCTCAGCTGAGGGAAGGTACGAGCTCCCTGCTGGAGCCTGGGAC  
CCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGGCCTCAGTGGGGGCTGCTGCCTGAC  
CCCCAGCACAATAAAAATGAAACGTG



**FIGURE 215**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDVSESFVQRVYQPFLTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPGGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

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**FIGURE 216**

CCCACGCGTCCGAAGCTGGCCCTGCACGGCTGCAAGGGAGGCTCCTGTGGACAGGCCAGGCA  
GGTGGGCCTCAGGAGGTGCCTCCAGGCGGCCAGTGGGCCTGAGGCCCCAGCAAGGGCTAGGG  
TCCATCTCCAGTCCCAGGACACAGCAGCGGCCACCATGGCCACGCCTGGGCTCCAGCAGCAT  
CAGCAGCCCCCAGGACCGGGGAGGCACAGGTGGCCCCCACCACCCGGAGGAGCAGCTCCTGC  
CCCTGTCCGGGGGATGACTGATTCTCCTCCGCCAGGCCACCCAGAGGAGAAGGCCACCCCGC  
CTGGAGGCACAGGCCATGAGGGGGCTCTCAGGAGGTGCTGCTGATGTGGCTTCTGGTGTTGGC  
AGTGGGCGGCACAGAGCACGCCTACCGGCCCGGCCGTAGGGTGTGTGCTGTCCGGGGCTCACG  
GGGACCCTGTCTCCGAGTCGTTTCGTGCAGCGTGTGTACCAGCCCTTCCTCACCACCTGCGAC  
GGGCACCGGGCCTGCAGCACCTACCGAACCATCTATAGGACCGCCTACCGCCGCAGCCCTGG  
GCTGGCCCCCTGCCAGGCCTCGCTACGCGTGCTGCCCCGGCTGGAAGAGGACCAGCGGGCTTC  
CTGGGGCCTGTGGAGCAGCAATATGCCAGCCGCCATGCCGGAACGGAGGGAGCTGTGTCCAG  
CCTGGCCGCTGCCGCTGCCCTGCAGGATGGCGGGGTGACACTTGCCAGTCAGATGTGGATGA  
ATGCAGTGCTAGGAGGGGGCGGCTGTCCCCAGCGCTGCGTCAACACCGCCGGCAGTTACTGGT  
GCCAGTGTTGGGAGGGGGCACAGCCTGTCTGCAGACGGTACACTCTGTGTGCCCAAGGGAGGG  
CCCCCAGGGTGGCCCCCAACCCGACAGGAGTGGACAGTGCAATGAAGGAAGAAGTGCAGAG  
GCTGCAGTCCAGGGTGGACCTGCTGGAGGAGAAGCTGCAGCTGGTGCTGGCCCCACTGCACA  
GCCTGGCCTCGCAGGCACTGGAGCATGGGCTCCCGGACCCCGGCAGCCTCCTGGTGCACTCC  
TTCCAGCAGCTCGGCCGCATCGACTCCCTGAGCGAGCAGATTTCTTCCTGGAGGAGCAGCT  
GGGGTCCTGCTCCTGCAAGAAAGACTCGTGACTGCCCAGCGCCCCAGGCTGGACTGAGCCCC  
TCACGCCGCCCTGCAGCCCCCATGCCCCTGCCCAACATGCTGGGGGTCCAGAAGCCACCTCG  
GGGTGACTGAGCGGAAGGCCAGGCAGGGCCTTCCTCCTCTTCCTCCTCCCCTTCCTCGGGAG  
GCTCCCCAGACCCTGGCATGGGATGGGCTGGGATCTTCTCTGTGAATCCACCCCTGGCTACC  
CCCACCCTGGCTACCCCAACGGCATCCCAAGGCCAGGTGGGCCCTCAGCTGAGGGAAGGTAC  
GAGCTCCCTGCTGGAGCCTGGGACCCATGGCACAGGCCAGGCAGCCCGGAGGCTGGGTGGGG  
CCTCAGTGGGGGCTGCTGCCTGACCCCCAGCACATAAAAATGAAACGTG

**FIGURE 217**

MRGSQEVLLMWLLVLAVGGTEHAYRPGRRCVAVRAHGDPVSESEFVQRVYQPFELTTCDGHRAC  
STYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRRCR  
CPAGWRGDTQCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPGGGPPRVA  
PNPTGVDSAMKEEVQRLQSRVDLLEEKQLQLVLAPLHSLASQALEHGLPDPGSLLVHSFQQLG  
RIDSLSEQISFLEEQLGSCSCKKDS

**Signal sequence:**

1-19

**FIGURE 218**

GGTTGCCACAGCTGGTTTAGGGCCCCGACCACTGGGGCCCCCTTGT CAGGAGGAGACAGCCTCCCGGCCCGGGGAG  
GACAAGTCGCTGCCACCTTTGGCTGCCGACGTGATTCCTGGGACGGTCCGTTTCCTGCCGT CAGCTGCCGGCCG  
AGTTGGGTCTCCGTGTTTCAGGCCGGCTCCCCCTTCCTGGTCTCCCTTCTCCCGCTGGGCCGGTTTATCGGGAGG  
AGATTGTCTTCCAGGGCTAGCAATTGGACTTTTGATGATGTTTGACCCAGCGGCAGGAATAGCAGGCAACGTGAT  
TTCAAAGCTGGGCTCAGCCTCTGTTTCTTCTCTCGTGAATCGCAAAACCCATTTTGGAGCAGGAATTCCAATCA  
TGTCTGTGATGGTGGTGAGAAAGAAGGTGACACGGAAATGGGAGAACTCCCAGGCAGGAACACCTTTTGCTGTG  
ATGGCCGCGTCATGATGGCCCGGCAAAAGGGCATTTCCTACCTGACCCTTTTCCTCATCCTGGGGACATGTACAC  
TCTTCTTCGCCTTTGAGTGCCGCTACCTGGCTGTT CAGCTGTCTCCTGCCATCCCTGTATTTGCTGCCATGCTCT  
TCCTTTTCTCCATGGCTACACTGTTGAGGACCAGCTTCAGTGACCCTGGAGTGATTCCCTCGGGCGCTACCAGATG  
AAGCAGCTTTCATAGAAATGGAGATAGAAGCTACCAATGGTGCGGTGCCCGAGGGCCAGCGACCACCGCCTCGTA  
TCAAGAATTTCCAGATAAACAACCAGATTGTGAAACTGAAATACTGTTACACATGCAAGATCTTCGGCCTCCCC  
GGCCTCCCATTTGCAGCATCTGTGACAACTGTGTGGAGCGCTTCGACCATCACTGCCCTGGGTGGGGAATTGTG  
TTGGAAAGAGGAACTACCGCTACTTCTACCTCTTCATCCTTTCTCTCCTCCTCACAATCTATGTCTTCGCCT  
TCAACATCGTCTATGTGGCCCTCAAATCTTTGAAAATTGGCTTCTTGGAGACATTGAAAGAACTCCTGGAACCTG  
TTCTAGAAGTCCTCATTTGCTTCTTTACACTCTGGTCCGTCGTGGGACTGACTGGATTTTCATACTTTCTCGTGG  
CTCTCAACCAGACAACCAATGAAGACATCAAAGGATCATGGACAGGGAAGAATCGCGTCCAGAATCCCTACAGCC  
ATGGCAATATTGTGAAGAAGTGTGTGAAGTGTGTGTGGCCCTTGCCCCCAGTGTGCTGGATCGAAGGGGTA  
TTTTGCCACTGGAGGAAAGTGGAAAGTCGACCTCCAGTACTCAAGAGACCAGTAGCAGCCTCTTGCCACAGAGCC  
CAGCCCCACAGAACACCTGAACTCAAATGAGATGCCGGAGGACAGCAGCACTCCCGAAGAGATGCCACCTCCAG  
AGCCCCCAGAGCCACCACAGGAGGCAGCTGAAGCTGAGAAGTAGCCTATCTATGGAAGAGACTTTTGTGTTGTGTT  
TAATTAGGGCTATGAGAGATTT CAGGTGAGAAGTTAAACCTGAGACAGAGAGCAAGTAAGCTGTCCCTTTTAACT  
GTTTTTCTTTGGTCTTTAGTCAACCAGTTGCACACTGGCATTTTCTTGCTGCAAGCTTTTTTAAATTTCTGAACT  
CAAGGCAGTGGCAGAAGATGT CAGTCACCTCTGATAACTGGAAAATGGGTCTCTTGGGCCCTGGCACTGGTTCT  
CCATGGCCTCAGCCACAGGGTCCCCTTGGAACCCCTCTCTTCCCTCCAGATCCCAGCCCTCCTGCTTGGGGTCAC  
TGGTCTCATTCTGGGGCTAAAAGTTTTTGGAGACTGGCTCAAATCCTCCCAAGCTGCTGCACGTGCTGAGTCCAGA  
GGCAGTCACAGAGACCTCTGGCCAGGGGATCCTAACTGGGTCTTGGGGTCTTCAGGACTGAAGAGGAGGGAGAG  
TGGGGTCAGAAGATTCTCCTGGCCACCAAGTGCCAGCATTGCCACAAATCCTTTTAGGAATGGGACAGGTACCT  
TCCACTTGTTGTANNNNNNNNNNNNNNNNNNNNNNNNNNNNTGTTTTTCTTTTACTCCTGCTCCCATTAGGAG  
CAGGAATGGCAGTAATAAAAGTCTGCACTTTGGTCATTTCTTTTCTCAGAGGAAGCCCGAGTGCTCACTTAAAC  
ACTATCCCCTCAGACTCCCTGTGTGAGGCCTGCAGAGGCCCTGAATGCACAAATGGGAAACCAAGGCACAGAGAG  
GCTCTCCTCTCCTCTCCTCTCCCCGATGTACCCTCAAAAAAAAAAAATGCTAACCAGTTCTTCCATTAAAGCCT  
CGGCTGAGTGAGGGAAAGCCCAGCACTGCTGCCCTCTCGGGTAACTCACCTAAGGCTCGGCCACCTCTGGCT  
ATGGTAACCACACTGGGGGCTTCCTCCAAGCCCCGCTCTTCCAGCACTTCCACCGGCAGAGTCCCAGAGCCACTT  
CACCTGGGGGTGGGCTGTGGCCCCCAGTCAGCTCTGCTCAGGACCTGCTCTATTT CAGGGAAGAAGATTTATGT  
ATTATATGTGGCTATATTTCTAGAGCACCTGTGTTTTCTCTTTCTAAGCCAGGGTCCTGTCTGGATGACTTAT  
GCGGTGGGGAGTGTAACCGGAACCTTTTCATCTATTTGAAGGCGATTAACTGTGTCTAATGCA

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**FIGURE 219**

MSVMVVRKKVTRKWEKLPGRNTFCCDGRVMMARQKGIFYLTFLILGTCTLFFAFECRYLAV  
QLSPAIPVFAAMLFLFSMATLLRTSFSDPGVIPRALPDEAAFIEMEIEATNGAVPQGQRPPP  
RIKNFQINNQIVKLKCYTCKIFRPPRASHCSICDNCVERFDHHCPWVGNCVGKRNYRYFYL  
FILSLSLTIYVFAFNIVYVALKSLKIGFLETLKETPGTVLEVLCFFTLWSVVGLTGFHTF  
LVALNQTTNEDIKGSWTGKNRVQNPYSHGNIVKNCCEVLCGPLPPSVLDRRGILPLEESGSR  
PPSTQETSSSLLPQSPAPTEHLNSNEMPEDSSTPEEMPPEPPEPPQEAAEA EK

**Putative transmembrane domains:**

amino acids 36-55 (type II TM), 65-84, 188-208, 229-245

**FIGURE 220**

AAAACCCTGTATTTTTTACAATGCAAATAGACAATNANCCTGGAGGTCTTTGAATTAGGTAT  
TATAGGGATGGTGGGGTTGATTTTTNTTCCTGGAGGCTTTTGGCTTTGGACTCTCNCTTTCT  
CCCACAGAGCNCTTCGACCATCACTGCCCCTGGGTGGGGAATTGTGTTGGAAAGAGGAACTA  
CCGCTANTTCTACCTCTTCATCCTTTNTCTCTCCCNCTCACAATCTATGTCTTCGCCTTCA  
ACATCGT



**FIGURE 221**

GTTGTGTCCTTCAGCAAAACAGTGGATTAAATCTCCTTGCACAAGCTTGAGAGCAACACAA  
TCTATCAGGAAAGAAAGAAAGAAAAAACCGAACCTGACAAAAAGAAGAAAAAGAAGA  
AAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTCAC  
GGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTTCC  
CCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTATT  
GACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAATGA  
CAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCATCG  
AGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACAAC  
CACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATTTC  
TTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGAC  
CAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAGCGGTTGGCTTTGTGAGTGAAGAC  
GAATACTTGGAATTTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTC  
CAATGACGTGGCCGCGCCCGTGGTACGGAGAGTAAAGGTCACCGTGAACCTATCCACCATACA  
TTTCAGAAGCCAAGGGTACAGGTGTCCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCC  
TCAGCAGTCCCCTCAGCAGAATTCCAGTGGTACAAGGATGACAAAAGACTGATTGAAGGAAA  
GAAAGGGGTGAAAGTGGAAAACAGACCTTTCCTCTCAAACTCATCTTCTTCAATGTCTCTG  
AACATGACTATGGGAACTACACTTGCGTGGCCTCCAACAAGCTGGGCCACACCAATGCCAGC  
ATCATGCTATTTGGTCCAGGCGCCGTCAGCGAGGTGAGCAACGGCACGTGAGGAGGGCAGG  
CTGCGTCTGGCTGCTGCCTCTTCTGGTCTTGCACCTGCTTCTCAAATTTTGATGTGAGTGCC  
ACTTCCCCACCCGGGAAAGGCTGCCGCCACCACCACCAACACAACAGCAATGGCAACAC  
CGACAGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGA  
AATTTGAGGGAGGGGAACAAAGAATACTTTGGGGGGAAAAGAGTTTTAAAAAAGAAATTGAA  
AATTGCCTTGCAGATATTTAGGTACAATGGAGTTTTCTTTTCCCAAACGGGAAGAACACAGC  
ACACCCGGCTTGGACCCACTGCAAGCTGCATCGTGCAACCTCTTTGGTGCCAGTGTGGGCAA  
GGGCTCAGCCTCTCTGCCACAGAGTGCCCCCACGTGGAACATTCTGGAGCTGGCCATCCCA  
AATTCAATCAGTCCATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCGTGGCGCTGCGG  
GCACTTTGGTAGACTGTGCCACCACGGCGTGTGTTGTGAAACGTGAAATAAAAAGAGCAAAA  
AAAAA

**FIGURE 222**

MKTIQPKMHNSISWAI FTGLAALCLFQGV PVRSGDATFPKAMDNVTVRQGESATLRCTIDNR  
VTRVAWLNRSTILYAGNDKWCLDPRVLLSNTQTQYSIEIQNV DVYDEGPYTCSVQTDNHPK  
TSRVHLIVQVSPKIVEISSDISINEGNNISLT CIATGRPEPTVTWRHISPKAVGFVSEDEYL  
EIQGITREQSGDYEC SASNDVAAPVVRVKVTVNYPPYISEAKGTGVPVGQKGTLOCEASAV  
PSAEFQWYKDDKRLIEGKKGVKVENRPFLSKLIFFNVSEHDYGN YTCVASNKLGH TNASIML  
FGPGAVSEVSNGTSRRAGCVWLLPLLVLHLLLKF

**Signal peptide:**

amino acids 1-28

**FIGURE 223**

GAAAAAAATCATGAAAACCATCCAGCCAAAAATGCACAATTCTATCTCTTGGGCAATCTTC  
ACGGGGCTGGCTGCTCTGTGTCTCTTCCAAGGAGTGCCCGTGCGCAGCGGAGATGCCACCTT  
CCCCAAAGCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGCGCCACCCTCAGGTGCACTA  
TTGACAACCGGGTCACCCGGGTGGCCTGGCTAAACCGCAGCACCATCCTCTATGCTGGGAAT  
GACAAGTGGTGCCTGGATCCTCGCGTGGTCCTTCTGAGCAACACCCAAACGCAGTACAGCAT  
CGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGACA  
ACCACCCAAAGACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAATTGTAGAGATT  
TCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAG  
ACCAGAG

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**FIGURE 224**

ATGGCTGGTGACGGCGGGGCGGGCAGGGGACCGGGGCGCGGGCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGA  
ATCACCGCCTGGCCCGACTCCACCATGAACGTCGCGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAG  
AAGGGGACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTACTGCTGGCT  
GCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCATCCCACAGCACCTGCCTTACA  
GAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCTGGACCGAGGGGTGAGCCCTGTGAGGACTTTTAC  
CAGTTCTCCTGTGGGGGCTGGATTTCGGAGGAACCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGC  
CTCTGGGACCAAAACCAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAG  
CAGAAGACACAGCGCTTCTACCTATCTTGCTTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCAGCCACTGAGA  
GACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAGGACAACCTTTATGGAGGTGTTGAAG  
GCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTTACCCTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGC  
AATGTTATCCAGGTGGACCAGTCTGGGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAG  
AAAGTGCTCACTGCCTATCTGGATTACATGGAGGAACTGGGGATGCTGCTGGGTGGGCGGGCCACCTCCACGAGG  
GAGCAGATGCAGCAGGTGCTGGAGTTGGAGATACAGCTGGCCAACATCACAGTGCCCCAGGACCAGCGCGCGAC  
GAGGAGAAGATCTACCACAAGATGAGCATTTCGGAGCTGCAGGCTCTGGCGCCCTCCATGGACTGGCTTGAGTTC  
CTGTCTTTCTTGCTGTCACCATTGGAGTTGAGTGACTCTGAGCCTGTGGTGGTGTATGGGATGGATTATTTGCAG  
CAGGTGTCAGAGCTCATCAACCGCACGGAACCAAGCATCCTGAACAATTACCTGATCTGGAACCTGGTGCAAAG  
ACAACCTCAAGCCTGGACCGACGCTTTGAGTCTGCACAAGAGAAGCTGCTGGAGACCCTCTATGGCACTAAGAAG  
TCCTGTGTGCCGAGGTGGCAGACCTGCATCTCCAACACGGATGACGCCCTTGGCTTTGCTTTGGGGTCACTCTTC  
GTGAAGGCCACGTTTGACCGGCAAAGCAAAGAAATTGCAGAGGGGATGATCAGCGAAATCCGGACCGCATTTGAG  
GAGGCCCTGGGACAGCTGGTTTGGATGGATGAGAAGACCCGCCAGGCAGCCAAGGAGAAAGCAGATGCCATCTAT  
GATATGATTGGTTTCCCAGACTTTATCCTGGAGCCCCAAAGAGCTGGATGATGTTTATGACGGGTACGAAATTTCT  
GAAGATTCTTTCTTCCAAAACATGTTGAATTTGTACAACCTTCTTGCCAAGGTTATGGCTGACCAGCTCCGCAAG  
CCTCCCAGCCGAGACCAGTGGAGCATGACCCCCCAGACAGTGAATGCCTACTACCTTCCAACCTAAGAATGAGATC  
GTCTTCCCCGCTGGCATCCTGCAGGCCCCCTTCTATGCCCGCAACCACCCCAAGGCCCTGAACTTCGGTGGCATC  
GGTGTGGTCATGGGCCATGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTG  
CGGCCCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCACACGGCCTGCATGGAGGAACAGTACAATCAA  
TACCAGGTCAATGGGGAGAGGCTCAACGGCCGCCAGACGCTGGGGGAGAACATTACTGACAACGGGGGGCTGAAG  
GCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATGGGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACC  
AACCACAGCTCTTCTTCGTGGGATTTGCCAGGTGTGGTGTCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGG  
CTGGTGACCGACCCCCACAGCCCTGCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTTCCTGCGG  
CACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACCTGGATCAGGGGA  
GAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGTTTGCTCTTGGGTGGGAGGAAGCAA  
ATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACAGGTGACATGAGTACAGACCCTCCTCAATCACCACATTG  
TGCTCTGCTTTGGGGGTGCCCTGCCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTCCGTGTCACCT  
GCCTGGAAGAGGTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCC

**FIGURE 225**

MNVALQELGAGSNVGFQKGTRQLLGSRTQLELVLAGASLLLAALLLGCLVALGVQYHRDPSH  
STCLTEACIRVAGKILES LDRGVSPCEDFYQFSCGGWIRRNPLPDGRSRWNTFNSLWDQNQA  
ILKHLLENTTFNSSSEAEQKTQRFYLSCLQVERIEELGAQPLRDLIEKIGGWNITGPWDQDN  
FMEVLKAVAGTYRATPFFT VYISADSKSSNSNVIQVDQSGFLPSRDYYLNRTANEKVL TAY  
LDYMEELGMLLGGRPTSTREQMQQVLELEIQ LANITVPQDQRRDEEKIYHKMSISELQALAP  
SMDWLEFLSFLLSPLELSDSEPVVVYGM DYLQQVSELINRTEPSILNNYLIWNLVQKTTSSL  
DRRFESAQEKLLETLYGTKKSCVPRWQTCISNTDDALGFALGSLFVKATFDRQSKEIAEGMI  
SEIRTA FEEALGQLVWMDEKTRQAAKEKADAIYDMIGFPDFILEPKELDDVYDGYEISEDSF  
FQNMLNLYNFS AKVMADQLRKPPSRDQWSMTPQTVNAYYLPTKNEIVFPAGILQAPFYARNH  
PKALNFGGIGVVMGHELTHAFDDQGREYDKEGNLRPWWQNESLAAFRNHTACMEEQYNQYQV  
NGERLNGRQTLGENITDNGGLKAAYNAYKAWLRKHGEEQQLPVGLTNHQLFFVGFAQVWCS  
VRTPESSHEGLVTDPHSPARFRVLGTLSNSRDFLRHFGCPVGSPMNP GQLCEVW

**Type II Transmembrane domain:**

amino acids 32-57



**FIGURE 226**

GCCCCGGCCCTCCGCCCCCTCCGCACTCCCGCCTCCCTCCCTCCGCCCCGCTCCCGCGCCCTCCTCCCTCCCTCCTCCC  
CAGCTGTCCCGTTTCGCGTCATGCCGAGCCTCCCGGCCCGGCCGCCCGCTGCTGCTCCTCGGGCTGCTGCTGCT  
CGGCTCCCGGCCGGCCCCGCGGCGCCGGCCAGAGCCCCCGTGCTGCCATCCGTTCTGAGAAGGAGCCGCTGCC  
CGTTCCGGGAGCGGCAGGTAGGTGGGCGCCCGGGGAGGCGCGGGCGGGGAGTCCGGCTCGGGGCGAGTCAGCGC  
CAGCCCCGAGGGGGCGCGGGGCGCAGGTGGCTCGGCGCGGCGGGCGGCCCGGAGGGTGGGCGGGGGCAGAAGGGC  
GCGGTGCCTGGGACCCGGGACCCGCGGGCAGCCCCCGGGGCGGCACACGGCGCGAGCTGGGCAGCGGCTCCAGC  
CAAGCCCCGTCCCCGAGGCTGCACCTTCGGCGGGAAGGTCTATGCCTTGGACGAGACGTGGCACCCGGACCTAGG  
GGAGCCATTCCGGGTGATGCGCTGCGTGTGTGCGCCTGCGAGGCGCAGTGGGGTCCCGTACCAGGGGCCCTGG  
CAGGGTCAGCTGCAAGAACATCAAACCAGAGTGGCCAACCCCGGCTGTGGGCAGCCGCGCCAGCTGCCGGGACA  
CTGCTGCCAGACCTGCCCCAGGACTTCGTGGCGCTGCTGACAGGGCCGAGGTGCGAGGCGGTGGCACGAGCCCG  
AGTCTCGCTGCTGCGCTCTAGCCTCCGCTTCTCTATCTCTACAGGCGGCTGGACCGCCCTACCAGGATCCGCTT  
CTCAGACTCCAATGGCAGTGTCTGTGAGCACCCTGCAGCCCCCACCAGATGGCCTGGTCTGTGGGGTGTG  
GCGGGCAGTGCCTCGGTTGTCTCTGCGGCTCCTTAGGGCAGAACAGCTGCATGTGGCACTTGTGACACTCACTCA  
CCCTTCAGGGGAGGTCTGGGGGCTCTCATCCGGCACCGGGCCCTGTCCCCAGAGACCTTCAGTGCCATCCTGAC  
TCTAGAAGGCCCCACCAGCAGGGCGTAGGGGGCATCACCTGCTCACTCTCAGTGACACAGAGGACTCCTTGCA  
TTTTTTGCTGCTCTTCCGAGGCCTTGCAAGGACTAACCCAGGTTCCCTTGAGGCTCCAGATTCTACACCAGGGGCA  
GCTACTGCGAGAACTTCAGGCCAATGTCTCAGCCCAGGAACCAGGCTTTGCTGAGGTGCTGCCCAACCTGACAGT  
CCAGGAGATGGACTGGCTGGTGTGGGGGAGCTGCAGATGGCCCTGGAGTGGGCAGGCAGGCCAGGGCTGCGCAT  
CAGTGGACACATTGCTGCCAGGAAGAGCTGCGACGTCTGCAAAGTGTCTTTGTGGGGCTAATGCCCTGATCCC  
AGTCCAAACGGGTGCTGCCGGCTCAGCCAGCCTCACTCTGCTAGGAAATGGCNCCCTGATCCTCCAGGTGCAATT  
GGTAGGGACAACCAGTGAGGTGGTGGCCATGACACTGGAAACCAAGCCTCAGCGGAGGGATCAGCCCCACTGTCT  
GTGCCACATGGCTGGCCTATCCTCCCCCTGCCCCAGGCCGTGGGTATCTGCCCTGGGCTGGGGTGCCCCAGGGGC  
TCATATGCTGCTGCAGAAATGAGCTCTTCTGAACGTGGGCACCAAGGACTTCCAGACGGAGAGCTTCGGGGGCA  
ACGTGGCTGCCCTGCCCTACTGTGGGGCATAGCGCCCGCCCTGCCCGTGCCCTAGCAGGAGCCCTGGTGCTACC  
CCCTGTGAAGAGCCAAGCAGCAGGGCACGCTGGCTTTCCTTGGAATACCACTGTACCTGCACATGAAGTGCT  
GCTGGCTGGGCTTGGTGGCTCAGAACAAAGGCACTGTCACTGCCACCTCCTTGGGGCTCCTGGAACGCCAGGGCC  
TCGGCGGCTGCTGAAGGGATTCTATGGCTCAGAGGCCAGGGTGTGGTGAAGGACCTGGAGCCGGAACCTGCTGCG  
GCACCTGGCAAAAGGCATGGCTTCCCTGATGATCACCAACCAAGGTAGCCCCAGAGGGGAGCTCCGAGGGCAGCCT  
CTCCTCCCAGGTGCACATAGCCAACCAATGTGAGGTTGGCGGACTGCGCCTGGAGGCGGCCGGGGCCGAGGGGGT  
GCGGGCGCTGGGGGCTCCGGATACAGCCTCTGCTGCGCCGCTGTGGTGCCTGGTCTCCCGGCCCTAGCGCCCGC  
CAAACCTGGTGGTCTTGGGCGGCCCGAGACCCCAACACATGCTTCTTCGAGGGGCAGCAGCGCCCCCACGGGGC  
TCGCTGGGCGCCCAACTACGACCCGCTCTGCTCACTCTGCACCTGCCAGAGACGAACGGTGATCTGTGACCCGGT  
GGTGTGCCACCGGCCAGCTGCCACACCCGGTGCAGGCTCCCGACCACTGCTGCCCTGTTTGGCCTGGCTGCTA  
TTTTGATGGTGACCGGAGCTGGCGGGCAGCGGGTACGCGGTGGCACCCCGTTGTGCCCCCTTTGGCTTAATTAA  
GTGTGCTGTCTGCACCTGCAAGCAGGGGGGCACTGGAGAGGTGCACTGTGAGAAGGTGCACTGTCCCCGGCTGGC  
CTGTGCCAGCCTGTGCGTGTCAACCCACCGACTGCTGCAAACAGTGTCCAGGTGAGGCCACCCCCAGCTGGG  
GGACCCCATGCAGGCTGATGGGCCCCGGGGCTGCCGTTTTGCTGGGCAGTGGTTCCAGAGAGTCAGAGCTGGCA  
CCCCCTCAGTGCCCCCGTTTTGGAGAGATGAGCTGTATCACCTGCAGATGTGGGGTAAGTGGGGAGCAGAGGCTTGT  
GTGAGGTGGGTACTGGGAGCCTGGTCTGGAGTAGGGAGACCTTCCAGGGAGGTCCCTGAAGAAGCTGAAGGTCA  
CTGTGTCCAGTGCCCTCTGGGGGACACTCAGTGTCTGCTCTGTCTTGTACCAGGCAGGGGTGCCTCACTGTGAGC  
GGGATGACTGTTCACTGCCACTGTCTGTGGCTCGGGGAAGGAGAGTCGATGCTGTTCCCGCTGCACGGCCCCACC  
GGCGGCGTAAGTGAGGGAGTCCAGGGTCAGCAGCTGTGAGTGGAGGGCTCACCTGCCTGTGGGACTCCTGATCAG  
GGAAGGGAGCACTCACTGTGTGCAGGAACAGTGCAGCCTGCCTCACAAGTGCCATTCCAATCCACCTCACAGCA  
ACCTGGTGGAATTGTTATTTATGACCTTTTCTTTACAAATGAGATTTCTGAAGCTCAGAGAAATTAAGCAACGAG  
ATGAAGGTACCCAGCTGTGTGCACTGACCTGTTAGAAAATACTGGCCTTTCTGGGACCAAGGCAGGGATGCTT  
TGCCCTGCCCTCTATGCCTCTCTGTGCCTCTCCACTCCCTCTCCCTCCTCCAACATTCCTCCCTTCTGTCTCC  
AGCAGCCCCAGAGACCAGAACTGATCCAGAGCTGGAGAAAGAAGCCGAAGGCTCTTAGGGAGCAGCCAGAGGGCC  
AAGTGACCAAGAGGATGGGGCCTGAGCTGGGGAAGGGGTGGCATCGAGGACCTTCTTGCAATTCTCCTGTGGGAAG  
CCCAGTGCCCTTTGCTCCTCTGTCTGCTCTACTCCCACCCCACTACCTCTGGGAACCAACAGCTCCACAAGGGG  
GAGAGGCAGCTGGGCCAGACCGAGGTACAGCCACTCCAAGTCTGCCCTGCCACCTCGGCCTCTGTCTCTGGAA  
GCCCCACCCCTTTCTTCTGTACATAATGTCACTGGCTTGTGGGATTTTTAATTTATCTTCACTCAGCACCAG  
GGCCCCGGACACTCCACTCCTGCTGCCCTGAGCTGAGCAGAGTCATTATTGGAGAGTTTTGTATTTATTAAC  
ATTTCTTTTTTCAGTCTTTGGGCATGAGGTTGGCTCTTTGTGGCCAGGAACCTGAGTGGGGCCTGGTGGACAAGGG  
GCNGAGAGTAGGAGGTGAGAGAGAGGAGCTCTGACACTTGGGGAGCTGAAAGAGACCTGGAGAGGCAGAGGATAG  
CGTGGCNNTTGGCTGGCATNCCTGGGTTCGCGCAGAGGGGCTGGGGATGGTTCTTGAGATGGTCTAGAGACTCAAG  
AATTTAGGGGAAGTAGAAGCAGGATTTGACTCAAGTTTAGTTTCCACATCGCTGGCCTGTTTGCTGACTTCATG  
TTTGAAGTTGCTCCAGAGAGAGAATCAAAGGTGTACCAAGCCCTCTCTCCCTCCTTCCCTTCCCTTCCCTTTCT  
TTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCCCTCC



**FIGURE 227**

GGCCGAGCGGGGGTGCTGCGCGGCGGCCGTGATGGCTGGTGACGGCGGGGCCGGGCAGGGGA  
CCGGGGCCGCGGGCCCGGGAGCGGGCCAGCTGCCGGGAGCCCTGAATCACCGCCTGGCCCCGAC  
TCCACCATGAACGTGCGGCTGCAGGAGCTGGGAGCTGGCAGCAACGTGGGATTCCAGAAGGG  
GACAAGACAGCTGTTAGGCTCACGCACGCAGCTGGAGCTGGTCTTAGCAGGTGCCTCTCTAC  
TGCTGGCTGCACTGCTTCTGGGCTGCCTTGTGGCCCTAGGGGTCCAGTACCACAGAGACCCA  
TCCCACAGCACCTGCCTTACAGAGGCCTGCATTTCGAGTGGCTGGAAAAATCCTGGAGTCCCT  
GGACCGAGGGGTGAGCCCCCTGTGAGGACTTTTACCAGTTCTCCTGTGGGGGCTGGATTGGA  
GGAACCCCCTGCCCGATGGGCGTTCTCGCTGGAACACCTTCAACAGCCTCTGGGACCAAAAC  
CAGGCCATACTGAAGCACCTGCTTGAAAACACCACCTTCAACTCCAGCAGTGAAGCTGAGCA  
GAAGACACAGCGCTTCTACCTATCTTGCCTACAGGTGGAGCGCATTGAGGAGCTGGGAGCCC  
AGCCACTGAGAGACCTCATTGAGAAGATTGGTGGTTGGAACATTACGGGGCCCTGGGACCAG  
GACAACTTTATGGAGGTGTTGAAGGCAGTAGCAGGGACCTACAGGGCCACCCCATTTCTCAC  
CGTCTACATCAGTGCCGACTCTAAGAGTTCCAACAGCAATGTTATCCAGGTGGACCAGTCTG  
GGCTCTTTCTGCCCTCTCGGGATTACTACTTAAACAGAACTGCCAATGAGAAAGTAAGGAAC  
ATCTTCCGAACCCCCATCCCTACCCCTGGCTGAGCTGGGCTGATCCCTGTTGACTTTTCCCT  
TTGCCAAGGGTCAGAGCAGGGAAGGTGAGCCTATCCTGTCACCTAGTGAACAACTGCCCCCT  
CCTTTCTTTCTTCTTTCTTCTCCTCCCTCCCTCCCTTTCTTCCCCTTTTCTTCTCCTTCCTTCCTTCC  
TCTTATTCTTCTAGTAGGTTTCATAGACACCTACTGTGTGCCAGGTCCAGTGGGGGAATTG  
GAGATATAAGTTTCCGAGCCATTGCCACAGGAAGCGTTCAGTGTGATGGGTTCATGGACCT  
AGATAGGCTGATAACAAAGCTCACAAGAGGGTCCTGAGGATTCAGGAGAGACTTATGGAGCC  
AGCAAAGTCTTCTGAAGAGATTGCATTTGAGCCAGGTCCTGTAG

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**FIGURE 228**

ATGCCTACTACCTTCCAATAAGAATGAGATCGTCTTCCCCGCTGGCATCCTGCAGGCCCCC  
TTCTATGCCCCGAACCAACCCCAAGGCCCTGAACTTCGGTGGCATCGGTGTGGTCATGGGCCA  
TGAGTTGACGCATGCCTTTGATGACCAAGGGCGCGAGTATGACAAAGAAGGGAACCTGCGGC  
CCTGGTGGCAGAATGAGTCCCTGGCAGCCTTCCGGAACCAACACGGCCTGCATGGAGGAACAG  
TACAATCAATACCAGGTCAATGGGGAGAGGGCTCAACGGCCGCCAGACGCTGGGGGAGAACAT  
TGCTGACAACGGGGGGCTGAAGGCTGCCTACAATGCTTACAAAGCATGGCTGAGAAAGCATG  
GGGAGGAGCAGCAACTGCCAGCCGTGGGGCTCACCAACCACCAGCTCTTCTTCGTGGGATTT  
GCCCAGGTGTGGTGCTCGGTCCGCACACCAGAGAGCTCTCACGAGGGGGCTGGTGACCGACCC  
CCACAGCCCTGCCCCGCTTCCGCGTGCTGGGCACTCTCTCCAACCTCCCGTGACTIONCCTGCGGC  
ACTTCGGCTGCCCTGTGCGCTCCCCCATGAACCCAGGGCAGCTGTGTGAGGTGTGGTAGACC  
TGGATCAGGGGAGAAATGGCCAGCTGTCACCAGACCTGGGGCAGCTCTCCTGACAAAGCTGT  
TTGCTCTTGGGTGGGAGGAAGCAAATGCAAGCTGGGCTGGGTCTAGTCCCTCCCCCCCACA  
GGTGACATGAGTACAGACCCTCCTCAATCACCACATTGTGCCTCTGCTTTGGGGGTGCCCT  
GCCTCCAGCAGAGCCCCCACCATTCACTGTGACATCTTTCCGTGTCACCCTGCCTGGAAGAG  
GTCTGGGTGGGGAGGCCAGTTCCCATAGGAAGGAGTCTGCCTCTTCTGTCCCCAGGCTCACT  
CAGCCTGGCGGCCATGGGGCCTGCCGTGCCCTGCCCCACTGTGACCCACAGGCCTGGGTGGTG  
TACCTCCTGGACTTCTCCCCAGGCTCACTCAGTGCGCACTTAGGGGTGGACTCAGCTCTGTC  
TGGCTCACCCCTCACGGGCTACCCCCACCTCACCTGTGCTCCTTGTGCCACTGCTCCCAGTG  
CTGCTGCTGACCTTCACTGACAGCTCCTAGTGGAAGCCCAAGGGCCTCTGAAAGCCTCCTGC  
TGCCCCACTGTTTCCCTGGGCTGAGAGGGGAAGTGCAATATGTGTAGCGGGTACTGGTTCCTGT  
GTCTTAGGGCACAAGCCTTAGCAAATGATTGATTCTCCCTGGACAAAGCAGGAAAGCAGATA  
GAGCAGGGAAAAGGAAGAACAGAGTTTATTTTTTACAGAAAAGAGGGTGGGAGGGTGTGGTCT  
TGGCCCTTATAGGACC

**FIGURE 229**

CCCACGCGTCCGAGCCGCCCGAGAATTAGACACACTCCGGACGCGGCCAAAAGCAACCGAGA  
 GGAGGGGAGGCCAAAAACACCGAAAAACAAAAGAGAGAAACAACACCCAACAACCTGGGGTGG  
 GGGGAAGAAAGAAAGAAAAGAAACCCACCCACCCACCAAAAAAAAAAAAAAAAAAAAAA  
 AAAAAAAAAAAATCCTGTGGCGCGCCGCCCTGGTTCCCGGGAAGACTCGCCAGCACCAGGGGG  
 TGGGGGAGTGCGAGCTGAAAGCTGCTGGAGAGTGAGCAGCCCTAGCAGGGGATGGACATGATG  
 CTGTTGGTGCAGGGTGCTTGTTGCTCGAACCAGTGGCTGGCGGCGGTGCTCCTCAGCCTGTG  
 CTGCCTGCTACCCTCCTGCCTCCCGGCTGGACAGAGTGTGGACTTCCCCTGGGCGGCCGTGG  
 ACAACATGATGGTCAGAAAAGGGGACACGGCGGTGCTTAGGTGTTATTTGGAAGATGGAGCT  
 TCAAAGGGTGCCTGGCTGAACCGGTCAAGTATTATTTTTGCGGGAGGTGATAAGTGGTCAGT  
 GGATCCTCGAGTTTCAATTTCAACATTGAATAAAAGGGACTACAGCCTCCAGATACAGAATG  
 TAGATGTGACAGATGATGGCCCATACACGTGTTCTGTTCAAGTCAACATACACCCAGAACA  
 ATGCAGGTGCATCTAAGTGTGCAAGTTCCTCCTAAGATATATGACATCTCAAATGATATGAC  
 CGTCAATGAAGGAACCAACGTCACTCTTACTTGTTTGGCCACTGGGAAACCAGAGCCTTCCA  
 TTTCTTGGCGACACATCTCCCCATCAGCAAAACCATTTGAAAATGGACAATATTTGGACATT  
 TATGGAATTACAAGGGACCAGGCTGGGGAATATGAATGCAGTGCGGAAAATGCTGTGTCAATT  
 CCCAGATGTGAGGAAAGTAAAAGTTGTTGTCAACTTTGCTCCTACTATTCAGGAAATTAAAT  
 CTGGCACCGTGACCCCCGGACGCAGTGGCCTGATAAGATGTGAAGGTGCAGGTGTGCCGCCCT  
 CCAGCCTTTGAATGGTACAAAGGAGAGAAGAAGCTCTTCAATGGCCAACAAGGAATTATTAT  
 TCAAATTTTAGCACAAAGATCCATTCTCACTGTTACCAACGTGACACAGGAGCACTTCGGCA  
 ATTATACCTGTGTGGCTGCCAACAAGCTAGGCACAACCAATGCGAGCCTGCCTCTTAACCCT  
 CCAAGTACAGCCCAGTATGGAATTACCGGGAGCGCTGATGTTCTTTTCTCCTGCTGGTACCT  
 TGTGTTGACACTGTCCTCTTTCACCAGCATATTCTACCTGAAGAATGCCATTCTACAATAA  
 TTCAAAGACCCATAAAAGGCTTTTAAGGATTCTCTGAAAGTGCTGATGGCTGGATCCAATCT  
 GGTACAGTTTGTTAAAAGCAGCGTGGGATATAATCAGCAGTGCTTACATGGGGATGATCGCC  
 TTCTGTAGAATTGCTCATTATGTAAATACTTTAATTCTACTCTTTTTTTGATTAGCTACATTA  
 CCTTGTGAAGCAGTACACATTGTCCTTTTTTTTAAGACGTGAAAGCTCTGAAATTACTTTTAG  
 AGGATATTAATTGTGATTTTCATGTTTGTAATCTACAACCTTTTCAAAGCATTTCAGTCATGGT  
 CTGCTAGGTTGCAGGCTGTAGTTTACAAAACGAATATTGCAGTGAATATGTGATTCTTTAA  
 GGCTGCAATACAAGCATTTCAGTTCCTGTTCATAAAGAGTCAATCCACATTTTACAAAGATG  
 CATTTTTTTCTTTTTTTGATAAAAAAGCAAATAATATTGCCTTCAGATTATTTCTTCAAATA  
 TAACACATATCTAGATTTTTCTGCTTGCATGATATTCAGGTTTCAGGAATGAGCCTTGTAAT  
 ATAAGTGGCTGTGCAGCTCTGCTTCTCTTTCTGTAAAGTTCAGCATGGGTGTGCCTTCATAC  
 AATAATATTTTTCTCTTTGTCTCCAATAATAAAATGTTTTGCTAAATCTTACAATTTGA  
 AAGTAAAAATAAACCAGAGTGATCAAGTTAAACCATACACTATCTCTAAGTAACGAAGGAGC  
 TATTGGACTGTAAAAATCTCTTCCTGCACTGACAATGGGGTTTGAGAATTTTGCCCCACACT  
 AACTCAGTTCTTGTGATGAGAGACAATTTAATAACAGTATAGTAAATATACCATATGATTTCT  
 TTTAGTTGTAGCTAAATGTTAGATCCACCGTGGGAAATCATTCCTTTTAAATGACAGCACA  
 GTCCACTCAAAGGATTGCCTAGCAATACAGCATCTTTTCCTTTCACTAGTCCAAGCCAAAAA  
 TTTTAAGATGATTTGTGAGAAAGGGCACAAAGTCCTATCACCTAATATTACAAGAGTTGGTA  
 AGCGCTCATCATTAATTTTATTTTGTGGCAGGTATTATGACAGTCGACCTGGAGGGTATGGA  
 TATGGATATGGACGTTCCAGAGACTATAATGGCAGAAACCAGGGTGGTTATGACCGCTACTC  
 AGGAGGAAATTACAGAGACAATTATGACAACCTGAAATGAGACATGCACATAATATAGATACA  
 CAAGGAATAATTTCTGATCCAGGATCGTCCTTCCAAATGGCTGTATTTATAAAGGTTTTTGG  
 AGCTGCACTGAAGCATCTTATTTTATAGTATATCAACCTTTTGTTTTTAAATTGACCTGCCA  
 AGGTAGCTGAAGACCTTTTAGACAGTTCATCTTTTTTTTTTAAATTTTTTCTGCCTATTTAA  
 AGACAAATTATGGGACGTTTGTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 230**

MMLLVQGACCSNQWLAAVLLSLCCLLPSCLPAGQSVDFPWAAVDNMMVRKGD TAVLR CYLED  
GASKGAWLNRSSIIIFAGGDKWSVDPRVSISTLNKR DYSLQIQNV DVTDDGPYTCSVQTQHTP  
RTMQVHLTVQVPPKIYDISNDMTVNEG TNVTLTCLATGKPEPSISWRHISPSAKPFENGQYL  
DIYGITRDQAGEYECSAENAVSFDPVRKVKVVVNFAPT IQEIKSGTVTPGRSGLIRCEGAGV  
PPPAFEWYKGEKKLFNGQQGII IQNFSTRSILTVTNVTQEHFGNYTCVAANKLGTTNASLPL  
NPPSTAQYGITGSADVLFSCWYLVLTLS SFTSIFYLKNAILQ

**Important features of the protein:****Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 326-345

**N-glycosylation sites.**

amino acids 71-75, 153-157, 273-277, 284-288, 292-296, 305-309

**Casein kinase II phosphorylation site.**

amino acids 147-151, 208-212, 224-228

**Tyrosine kinase phosphorylation site.**

amino acids 178-186

**N-myristoylation sites.**amino acids 7-13, 63-70, 67-73, 151-157, 239-245, 291-297,  
302-308, 319-325**Myelin P0 protein:**

amino acids 92-121

**FIGURE 231**

AGTGGTTCGATGGGAAGGATCTTTCTCCAAGTGGTTCCTCTTGAGGGGAGCATTCTGCTGG  
CTCCAGGACTTTGGCCATCTATAAAGCTTGGCAATGAGAAATAAGAAAATTCTCAAGGAGGA  
CGAGCTCTTGAGTGAGACCCAACAAGCTGCTTTTCACCAAATTGCAATGGAGCCTTTCGAAA  
TCAATGTTCCAAAGCCCAAGAGGAGAAATGGGGTGAACCTTCTCCCTAGCTGTGGTGGTCATC  
TACCTGATCCTGCTCACCGCTGGCGCTGGGCTGCTGGTGGTCCAAGTTCTGAATCTGCAGGC  
GCGGCTCCGGGTCCTGGAGATGTATTTCTCAATGACACTCTGGCGGCTGAGGACAGCCCGT  
CCTTCTCCTTGCTGCAGTCAGCACACCCTGGAGAACACCTGGCTCAGGGTGCATCGAGGCTG  
CAAGTCCTGCAGGCCCAACTCACCTGGGTCCGCGTCAGCCATGAGCACTTGCTGCAGCGGGT  
AGACAACTTCACTCAGAACCCAGGGATGTTTCAGAATCAAAGGTGAACAAGGCGCCCCAGGTC  
TTCAAGGTCACAAGGGGGGCCATGGGCATGCCTGGTGCCCCCTGGCCCCGCCGGGACCACCTGCT  
GAGAAGGGAGCCAAGGGGGCTATGGGACGAGATGGAGCAACAGGCCCCCTCGGGACCCCAAGG  
CCCACCGGGAGTCAAGGGAGAGGCGGGCCTCCAAGGACCCCAAGGGTGCTCCAGGGAAGCAAG  
GAGCCACTGGCACCCCAGGACCCCAAGGAGAGAAGGGCAGCAAAGGCGATGGGGGTCTCATT  
GGCCCCAAAAGGGGAAACTGGAATAAGGGAGAGAAAGGAGACCTGGGTCTCCCAGGAAGCAA  
AGGGGACAGGGGCATGAAAGGAGATGCAGGGGTGATGGGGCCTCCTGGAGCCCAGGGGAGTA  
AAGGTGACTTCGGGAGGCCAGGCCCACCAGGTTTGGCTGGTTTTCTTGAGCTAAAGGAGAT  
CAAGGACAACCTGGACTGCAGGGTGTTCCGGGGCCCTCCTGGTGCAGTGGGACACCCAGGTGC  
CAAGGGTGAGCCTGGCAGTGCTGGCTCCCCTGGGCGAGCAGGACTTCCAGGGAGCCCCGGGA  
GTCCAGGAGCCACAGGCCTGAAAGGAAGCAAAGGGGACACAGGACTTCAAGGACAGCAAGGA  
AGAAAAGGAGAATCAGGAGTTCCAGGCCCTGCAGGTGTGAAGGGAGAACAGGGGAGCCCAGG  
GCTGGCAGGTCCCAAGGGAGCCCCTGGACAAGCTGGCCAGAAGGGAGACCAGGGAGTGAAAG  
GATCTTCTGGGGAGCAAGGAGTAAAGGGAGAAAAAGGTGAAAGAGGTGAAAACCTCAGTGTCC  
GTCAGGATTGTCGGCAGTAGTAACCGAGGCCGGGCTGAAGTTTACTACAGTGGTACCTGGGG  
GACAATTTGCGATGACGAGTGGCAAAATTCTGATGCCATTGTCTTCTGCCGCATGCTGGGTT  
ACTCCAAAGGAAGGGCCCTGTACAAAGTGGGAGCTGGCACTGGGCAGATCTGGCTGGATAAT  
GTTCAAGTGTGGGGCACGGAGAGTACCCTGTGGAGCTGCACCAAGAATAGCTGGGGCCATCA  
TGAAGTGCAGCCACGAGGAGGACGCAGGCGTGGAGTGCAGCGTCTGAACCCGGAAACCCTTTCA  
CTTCTCTGCTCCCGAGGTGTCCTCGGGCTCATATGTGGGAAGGCAGAGGATCTCTGAGGAGT  
TCCCTGGGGACAACCTGAGCAGCCTCTGGAGAGGGGCCATTAATAAAGCTCAACATCATTGA



**FIGURE 232**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA68886

><subunit 1 of 1, 520 aa, 1 stop

><MW: 52658, pI: 9.16, NX(S/T): 3

MRNKKILKEDELLSETQQAAFHQIAMEPFEINVPKPKRRNGVNFSLAVVVIYLILLTAGAGL  
LVVQVLNLQARLRVLEMYFLNDTLAAEDSPSFSLLQSAHPGEHLAQGASRLQVLQAQLTWVR  
VSHEHLLQRVDNFTQNPGMFRIKGEQGAPGLQGHKGAMGMPGAPGPPGPPAEKGAKGAMGRD  
GATGPSGPQGPPGVKGEAGLQGPQAPGKQGATGTPGPQGEKGSKGDGGLIGPKGETGTKGE  
KGDGLPGSKGDRGMKGDAGVMGPPGAQGSKGDFGRPGPPGLAGFPGAKGDQGPGLQGVPG  
PPGAVGHPPGAKGEPGSAGSPGRAGLPGSPGSPGATGLKGSKGDGLQGGQGRKGESGVPGPA  
GVKGEQGSPLAGPKGAPGQAGQKGDQGVKGSSGEQGVKGEKGERGENSVSVRIVGSSNRGR  
AEVYYSGTWGTICDDEWQNSDAIVFCRMLGYSKGRALYKVGAGTGQIWLDNVQCRGTESTLW  
SCTKNSWGHHDCSHEEDAGVECSV

**Transmembrane domain:**

amino acids 47-66 (type II)

**N-glycosylation sites.**

amino acids 43-47, 83-87, 136-140

**Tyrosine kinase phosphorylation site.**

amino acids 432-440

**N-myristoylation sites.**

amino acids 41-47, 178-184, 253-259, 274-280, 340-346, 346-352,  
400-406, 441-447, 475-481, 490-496, 515-521

**Amidation site.**

amino acids 360-364

**Leucine zipper pattern.**

amino acids 56-78

**Speract receptor repeat**

amino acids 422-471, 488-519

**C1q domain proteins.**

amino acids 151-184, 301-334, 316-349



**FIGURE 233**

CCCACGCGTCCGAAGGCAGACAAAGGTTCAATTTGTAAAGAAGCTCCTTCCAGCACCTCCTCT  
CTTCTCCTTTTGCCCAAACCTCACCCAGTGAGTGTGAGCATTTAAGAAGCATCCTCTGCCAAG  
ACCAAAAGGAAAGAAGAAAAAGGGCCAAAAGCCAAAATGAAACTGATGGTACTTGTTTTTCAC  
CATTGGGCTAACTTTGCTGCTAGGAGTTCAAGCCATGCCTGCAAATCGCCTCTCTTGCTACA  
GAAAGATACTAAAAGATCACAACTGTCACAACCTTCCGGAAGGAGTAGCTGACCTGACACAG  
ATTGATGTCAATGTCCAGGATCATTTCTGGGATGGGAAGGGATGTGAGATGATCTGTTACTG  
CAACTTCAGCGAATTGCTCTGCTGCCCAAAGACGTTTTCTTTGGACCAAAGATCTCTTTTCG  
TGATTCCTTGCAACAATCAATGAGAATCTTCATGTATTCTGGAGAACACCATTCCTGATTTTC  
CCACAACTGCACTACATCAGTATAACTGCATTTCTAGTTTCTATATAGTGCAATAGAGCAT  
AGATTCTATAAATTCTTACTTGTCTAAGACAAGTAAATCTGTGTAAACAAGTAGTAATAAA  
AGTTAATTCAATCTAAAAAAAAAAAAAA

**FIGURE 234**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA52758

<subunit 1 of 1, 98 aa, 1 stop

<MW: 11081, pI: 6.68, NX(S/T): 1

MKLMVLVFTIGLTLLLG VQAMPANRLSCYRKILKDHNCHNLPEGVADLTQIDVNVQDHFWDG

KGCEMICYCNFSELLCCPKDVFFGPKISFVIPCNNQ

**Important features:****Signal peptide:**

amino acids 1-20

**N-glycosylation site.**

amino acids 72-76

**Tyrosine kinase phosphorylation site.**

amino acids 63-71

**FIGURE 235**

CCCACGCGTCCGCGGACGCGTGGGCTGGACCCCAGGTCTGGAGCGAATTCCAGCCTGCAGGG  
CTGATAAGCGAGGCATTAGTGAGATTGAGAGAGACTTTACCCCGCCGTGGTGGTTGGAGGGC  
GCGCAGTAGAGCAGCAGCACAGGCGCGGGTCCCGGGAGGCCGGCTCTGCTCGCGCCGAGATG  
TGGAATCTCCTTCACGAAACCGACTCGGCTGTGGCCACCGCGCGCCGCCCGCGCTGGCTGTG  
CGCTGGGGCGCTGGTGTGGCGGGTGGCTTCTTTCTCCTCGGCTTCCTCTTCGGGTGGTTTA  
TAAAATCCTCCAATGAAGCTACTAACATTACTCCAAAGCATAATATGAAAGCATTTTTGGAT  
GAATTGAAAGCTGAGAACATCAAGAAGTTCTTACATAATTTTACACAGATACCACATTTAGC  
AGGAACAGAACAAAACCTTTCAGCTTGCAAAGCAAATTCAATCCCAGTGGAAGAATTTGGCC  
TGGATTCTGTTGAGCTAGCTCATTATGATGTCCTGTTGTCCTACCCAAATAAGACTCATCCC  
AACTACATCTCAATAATTAATGAAGATGGAAATGAGATTTTCAACACATCATTATTTGAACC  
ACCTCCTCCAGGATATGAAAATGTTTCGGATATTGTACCACCTTTCAGTGCTTTCTCTCCTC  
AAGGAATGCCAGAGGGCGATCTAGTGTATGTTAACTATGCACGAACTGAAGACTTCTTTAAA  
TTGGAACGGGACATGAAAATCAATTGCTCTGGGAAAATTGTAATTGCCAGATATGGGAAAGT  
TTTCAGAGGAAATAAGGTTAAAAATGCCAGCTGGCAGGGGGCCAAAGGAGTCATTCTCTACT  
CCGACCCTGCTGACTACTTTGCTCCTGGGGTGAAGTCCTATCCAGACGGTTGGAATCTTCCT  
GGAGGTGGTGTCCAGCGTGGAAATATCCTAAATCTGAATGGTGCAGGAGACCCTCTCACACC  
AGGTTACCCAGCAAATGAATATGCTTATAGGCGTGGAATTGCAGAGGCTGTTGGTCTTCCAA  
GTATTCTGTTCATCCAATTGGATACTATGATGCACAGAAGCTCCTAGAAAAAATGGGTGGC  
TCAGCACCAACAGATAGCAGCTGGAGAGGAAGTCTCAAAGTGCCCTACAATGTTGGACCTGG  
CTTTACTGGAACTTTTCTACACAAAAAGTCAAGATGCACATCCACTCTACCAATGAAGTGA  
CGAGAATTTACAATGTGATAGGTAATCTCAGAGGAGCAGTGGAACCAGACAGATATGTCATT  
CTGGGAGGTCACCGGGACTCATGGGTGTTTGGTGGTATTGACCCTCAGAGTGGAGCAGCTGT  
TGTTTCATGAAATTGTGAGGAGCTTTGGAACACTGAAAAAGGAAGGGTGGAGACCTAGAAGAA  
CAATTTTGTGTTGCAAGCTGGGATGCAGAAGAATTTGGTCTTCTTGGTTCTACTGAGTGGGCA  
GAGGAGAATTCAAGACTCCTTCAAGAGCGTGGCGTGGCTTATATTAATGCTGACTCATCTAT  
AGAAGGAACTACACTCTGAGAGTTGATTGTACACCGCTGATGTACAGCTTGGTACACAACC  
TAACAAAAGAGCTGAAAAGCCCTGATGAAGGCTTTGAAGGCAAATCTCTTTATGAAAGTTGG  
ACTAAAAAAGTCCTTCCCCAGAGTTCAGTGGCATGCCAGGATAAGCAAATTGGGATCTGG  
AAATGATTTTGAAGTGTTCTTCCAACGACTTGGAATTGCTTCAGGCAGAGCACGGTATACTA  
AAAATTGGGAAACAAACAAATTCAGCGGCTATCCACTGTATCACAGTGTCTATGAAACATAT  
GAGTTGGTGGAAAAGTTTTATGATCCAATGTTTAAATATCACCTCACTGTGGCCAGGTTTCG  
AGGAGGGATGGTGTGTTGAGCTAGCCAATTCCATAGTGCTCCCTTTTGATTGTCGAGATTATG  
CTGTAGTTTTAAGAAAGTATGCTGACAAAATCTACAGTATTTCTATGAAACATCCACAGGAA  
ATGAAGACATACAGTGTATCATTTGATTCACTTTTTTCTGCAGTAAAGAATTTTACAGAAAT  
TGCTTCCAAGTTCAGTGAGAGACTCCAGGACTTTGACAAAAGCAACCCAATAGTATTAAGAA  
TGATGAATGATCAACTCATGTTTCTGGAAAGAGCATTATTTGATCCATTAGGGTTACCAGAC  
AGGCCTTTTTTATAGGCATGTCATCTATGCTCCAAGCAGCCACAACAAGTATGCAGGGGAGTC  
ATTCCCAGGAATTTATGATGCTCTGTTTGATATTGAAAGCAAAGTGGACCCTTCCAAGGCCT  
GGGGAGAAGTGAAGAGACAGATTTATGTTGCAGCCTTCACAGTGCAGGCAGCTGCAGAGACT  
TTGAGTGAAGTAGCCTAAGAGGATTTTTTTAGAGAATCCGTATTGAATTTGTGTGGTATGTCA  
CTCAGAAAGAATCGTAATGGGTATATTGATAAATTTTAAATTGGTATATTTGAAATAAAGT  
TGAATATTATATATAA

**FIGURE 236**

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA52756  
><subunit 1 of 1, 750 aa, 1 stop  
><MW: 84305, pI: 6.93, NX(S/T): 10  
MWNLLHETDSAVATARRPRWLCAGALVLAGGFFLLGFLFGWFIKSSNEATNITPKHNMKAFL  
DELKAENIKKFLHNFTQIPHLAGTEQNFQLAKQIQSQWKEFGLDSVELAHYDVLLSYPNKTH  
PNYISIINEDGNEIFNTSLFEP PPPGYENVSDIVPPFSAFSPQGMPEGDLVYVNYARTEDFF  
KLERDMKINCSGKIVARIYGVFRGNKVKNALAGAKGVILYSDPADYFAPGVKSYPDGWNL  
PGGGVQVRGNILNLNGAGDPLTPGYPANAYARRGIAEAVGLPSIPVHPIGYYDAQKLEKMG  
GSAPPDSSWRGSLKVPYNVGPFTGNFSTQKV KMHISTNEVTRIYNVIGTLRGAVEPDRYV  
ILGGHRDSWVFGGIDPQSGAAVVHEIVRSFGTLKKEGWRPRRTILFASWDAEEFGLLGSTEW  
AEENSRLQERGVAYINADSSIEGNYTLRVDCTPLMYSLVHNLTKELKSPDEGFEGKSLYES  
WTKKSPSPEFSGMPRISKLGSGNDFEVFFQRLGIASGRARYTKNWETNKFSGYPLYHSVYET  
YELVEKFYDPMFKYHLTVAQVRGGMVFELANSIVLPFDCRDYAVVLRKYADKIYSISMKHPQ  
EMKTYSVSFDLSLFAVKNFTEIASKFSERLQDFDKSNPIVLRMMNDQLMFLERAFIDPLGLP  
DRPFYRHVIYAPSSH NKYAGESFPGIYDALFDIESKVDPSKAWGEVKRQIYVAAFTVQAAAE  
TLSEVA

**Signal sequence:**

amino acids 1-40

**N-glycosylation sites.**amino acids 76-80, 121-125, 140-144, 153-157, 195-199, 336-340,  
459-463, 476-480, 638-642**Tyrosine kinase phosphorylation sites.**

amino acids 363-372, 605-613, 606-613, 617-626

**N-myristoylation sites.**amino acids 85-91, 168-174, 252-258, 256-262, 282-288, 335-341,  
360-366, 427-433, 529-535, 707-713

(19) World Intellectual Property Organization  
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PCT

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15/63, 5/10, 1/21, 1/19, C07K 14/47, 14/705, 19/00, 16/18,  
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PCT/US99/31274	30 December 1999 (30.12.1999)	US
PCT/US00/00219	5 January 2000 (05.01.2000)	US
PCT/US00/00277	6 January 2000 (06.01.2000)	US
PCT/US00/00376	6 January 2000 (06.01.2000)	US

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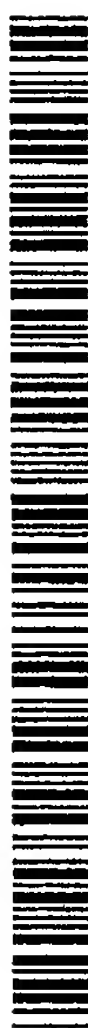
(74) Agents: KRESNAK, Mark, T. et al.; Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080-4990 (US).

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[Continued on next page]

(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.



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(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

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**Published:**

— *With international search report.*



## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/04341

## A. CLASSIFICATION OF SUBJECT MATTER

IPC 7	C12N15/12	C12N15/63	C12N5/10	C12N1/21	C12N1/19
	C07K14/47	C07K14/705	C07K19/00	C07K16/18	C07K16/28
	G01N33/68	G01N33/543	A61K47/48	A61K51/08	A61K38/17

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K G01N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 57983 A (ZYMOGENETICS INC) 23 December 1998 (1998-12-23)  the whole document	1-3, 5-13, 15-21
A	--- KLEIN R D ET AL: "Selection for genes encoding secreted proteins and receptors" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, US, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, no. 93, 1 July 1996 (1996-07-01), pages 7108-7113, XP002077277 ISSN: 0027-8424 the whole document --- -/-	



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

## \* Special categories of cited documents:

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

20 July 2000

Date of mailing of the international search report

18.10.00

Name and mailing address of the ISA

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Authorized officer

Smalt, R

## INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/04341

## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	YOKOYAMA-KOBAYASHI M ET AL: "A signal sequence detection system using secreted protease activity as an indicator" GENE,NL,ELSEVIER BIOMEDICAL PRESS. AMSTERDAM, vol. 163, no. 2, 3 October 1995 (1995-10-03), pages 193-196, XP004041983 ISSN: 0378-1119 the whole document ---	
A	EP 0 834 563 A (SMITHKLINE BEECHAM CORP) 8 April 1998 (1998-04-08) the whole document ---	
A	WO 97 07198 A (GENETICS INST) 27 February 1997 (1997-02-27) the whole document ---	
P,X, L	WO 99 46281 A (BAKER KEVIN P ;CHEN JIAN (US); GENENTECH INC (US); GURNEY AUSTIN () 16 September 1999 (1999-09-16) whole document, particularly the passages referring to PR0213 (e.g. pages 2,50,123,183), and the claims ---	1-3, 5-13, 15-21
P,X	WO 99 54437 A (MILLENNIUM BIOTHERAPEUTICS INC) 28 October 1999 (1999-10-28) the whole document -----	1-3, 5-13, 15-21

# INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US 00/04341

## Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

## Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Invention 1 : claims 1-3, 5-13, 15-21, all partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 1: claims 1-3,5-13,15-21, all partially

Nucleic acid with seq.ID.1, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.2 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.2 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide.

Invention 2: claims 1-29,38-43, and 50-53,  
all partially

Nucleic acid with seq.ID.611, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.612 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.612 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO337 (seq.ID.523) using its interaction with PRO4993 (seq.ID.612), method for linking a bioactive molecule to a cell expressing PRO337 through the use of PRO4993, and method of modulating at least one activity of said cell thereby.

... Invention 3: claims 1-29,38-43, and 50-53,  
all partially

Nucleic acid with seq.ID.522, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.523 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.523 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PRO4993 (seq.ID.612) using its interaction with PRO337 (seq.ID.523), method for linking a bioactive molecule to a cell expressing PRO4993 through the use of PRO337, and method of modulating at least one activity of said cell thereby.

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Invention 4: claims 1-21,30-37,44-49, and 54-57,  
all partially

Nucleic acid with seq.ID.613, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.614 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.614 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR0700 (seq.ID.523), PR0725 (seq.ID.616) and/or PR0739 (seq.ID.618) using their interaction with PR01559 (seq.ID.614), method for linking a bioactive molecule to a cell expressing PR0700, PR0725 or PR0739 through the use of PR01559, and method of modulating at least one activity of said cell thereby.

Invention 5: claims 1-21,30-37,44-49, and 54-57,  
all partially

Nucleic acid with seq.ID.89, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.90 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.90 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of said peptide fused to a heterologous sequence, isolated extracellular domain of said protein or said protein lacking its signal peptide, and an antibody against said polypeptide. Also a method of detecting PR01559 (seq.ID.614) using its interaction with PR0700 (seq.ID.90), method for linking a bioactive molecule to a cell expressing PR01559 through the use of PR0700, and method of modulating at least one activity of said cell thereby.

Invention 6: claims 1-21,30-37,44-49, and 54-57,  
all partially

Nucleic acid with seq.ID.615, encoding a polypeptide comprising the amino acid sequence as represented in seq.ID.616 or a nucleic acid having at least 80% homology thereto, vector comprising said nucleic acid, host cell comprising said vector, process for producing the protein of seq.ID.616 using said host, the isolated protein or one having at least 80% homology thereto, a chimeric protein of

## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

PR0381, as represented by seq.ID's 144 and 145,  
PR0386, as represented by seq.ID's 149 and 150,  
PR0540, as represented by seq.ID's 156 and 157,  
PR0615, as represented by seq.ID's 161 and 162,  
PR0618, as represented by seq.ID's 168 and 169,  
PR0719, as represented by seq.ID's 177 and 178,  
PR0724, as represented by seq.ID's 182 and 183,  
PR0772, as represented by seq.ID's 189 and 190,  
PR0852, as represented by seq.ID's 195 and 196,  
PR0853, as represented by seq.ID's 205 and 206,  
PR0860, as represented by seq.ID's 210 and 211,  
PR0846, as represented by seq.ID's 215 and 216,  
PR0862, as represented by seq.ID's 220 and 221,  
PR0864, as represented by seq.ID's 225 and 226,  
PR0792, as represented by seq.ID's 230 and 231,  
PR0866, as represented by seq.ID's 235 and 236,  
PR0871, as represented by seq.ID's 244 and 245,  
PR0873, as represented by seq.ID's 253 and 254,  
PR0940, as represented by seq.ID's 258 and 259,  
PR0941, as represented by seq.ID's 263 and 264,  
PR0944, as represented by seq.ID's 269 and 270,  
PR0983, as represented by seq.ID's 283 and 284,

## Claim : 9

PR01057, as represented by seq.ID's 295 and 296,  
PR01071, as represented by seq.ID's 300 and 301,  
PR01072, as represented by seq.ID's 302 and 303,  
PR01075, as represented by seq.ID's 308 and 309,  
PR0181, as represented by seq.ID's 321 and 322,  
PR0195, as represented by seq.ID's 329 and 330,  
PR0865, as represented by seq.ID's 336 and 337,  
PR0827, as represented by seq.ID's 345 and 346,  
PR01114, as represented by seq.ID's 351 and 352,  
PR0237, as represented by seq.ID's 357 and 358,  
PR0541, as represented by seq.ID's 362 and 363,  
PR0273, as represented by seq.ID's 369 and 370,  
PR0701, as represented by seq.ID's 374 and 375,  
PR0704, as represented by seq.ID's 379 and 380,  
PR0706, as represented by seq.ID's 384 and 385,  
PR0707, as represented by seq.ID's 389 and 390,  
PR0322, as represented by seq.ID's 394 and 395,  
PR0526, as represented by seq.ID's 399 and 400,  
PR0531, as represented by seq.ID's 404 and 405,  
PR0534, as represented by seq.ID's 409 and 410,  
PR0697, as represented by seq.ID's 414 and 415,  
PR0717, as represented by seq.ID's 419 and 420,  
PR0731, as represented by seq.ID's 424 and 425,  
PR0218, as represented by seq.ID's 429 and 430,  
PR0768, as represented by seq.ID's 436 and 437,  
PR0771, as represented by seq.ID's 441 and 442,  
PR0733, as represented by seq.ID's 446 and 447,  
PR0162, as represented by seq.ID's 451 and 452,  
PR0788, as represented by seq.ID's 453 and 454,



## FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

PR01008, as represented by seq.ID's 455 and 456,  
PR01012, as represented by seq.ID's 458 and 459,  
PR01014, as represented by seq.ID's 463 and 464,  
PR01017, as represented by seq.ID's 465 and 466,  
PR0474, as represented by seq.ID's 467 and 468,  
PR01031, as represented by seq.ID's 469 and 470,  
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PR0285, as represented by seq.ID's 495 and 496,  
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For the sake of conciseness, the first subject matter is explicitly defined, the other subject matters are defined by analogy thereto.

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